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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 08:53:09 : Search time 71.703 Seconds
(without alignments)
8725.170 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atgtgtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 15

Total number of hits satisfying chosen parameters: 11554

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued_Patents.NA.*

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
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4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/6C.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	US-09-605-785-375	Sequence 375, App
2	2040	100.0	2040	US-09-439-313-375	Sequence 375, App
3	2040	100.0	2040	US-09-352-616A-375	Sequence 375, App
4	1551	76.0	2000	US-09-605-785-374	Sequence 374, App
5	1551	76.0	2000	US-09-439-313-374	Sequence 374, App
6	1551	76.0	2000	US-09-352-616A-374	Sequence 374, App
7	1128	55.3	1155	US-09-605-785-373	Sequence 373, App
8	1128	55.3	1155	US-09-439-313-373	Sequence 373, App
9	1128	55.3	1155	US-09-352-616A-373	Sequence 373, App
10	491	24.1	1512	US-09-605-785-368	Sequence 368, App
11	491	24.1	1512	US-09-439-313-368	Sequence 368, App
12	491	24.1	1512	US-09-352-616A-368	Sequence 368, App
13	491	24.1	1512	US-09-605-785-369	Sequence 369, App
14	252	12.4	1853	US-09-605-785-369	Sequence 369, App
15	252	12.4	1853	US-09-439-313-369	Sequence 369, App
16	252	12.4	1853	US-09-352-616A-369	Sequence 369, App
17	252	12.4	1853	US-09-605-785-368	Sequence 368, App
18	120	5.9	1059	US-09-605-785-368	Sequence 368, App
19	120	5.9	1059	US-09-439-313-368	Sequence 368, App
20	120	5.9	1059	US-09-352-616A-368	Sequence 368, App
21	120	5.9	1059	US-09-605-785-369	Sequence 369, App
22	120	5.9	1059	US-09-439-313-369	Sequence 369, App
23	120	5.9	1059	US-09-352-616A-369	Sequence 369, App
24	120	5.9	1059	US-09-605-785-368	Sequence 368, App
25	120	5.9	1059	US-09-439-313-368	Sequence 368, App
26	120	5.9	1059	US-09-352-616A-368	Sequence 368, App
27	120	5.9	1059	US-09-605-785-369	Sequence 369, App

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c	29	120	5.9	1852	4	US-09-605-785-530	Sequence 530, App
c	30	120	5.9	1852	4	US-09-439-313-530	Sequence 530, App
c	31	120	5.9	1853	4	US-09-605-785-371	Sequence 371, App
c	32	120	5.9	1853	4	US-09-439-313-371	Sequence 371, App
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c	34	120	5.9	1855	4	US-09-439-313-371	Sequence 371, App
c	35	120	5.9	2184	4	US-09-352-616A-371	Sequence 371, App
c	36	120	5.9	2184	4	US-09-605-785-370	Sequence 370, App
c	37	120	5.9	2184	4	US-09-439-313-370	Sequence 370, App
c	38	120	5.9	2184	4	US-09-352-616A-370	Sequence 367, App
c	39	118	5.8	668	4	US-09-605-785-367	Sequence 367, App
c	40	118	5.8	668	4	US-09-439-313-367	Sequence 367, App
c	41	118	5.8	668	4	US-09-352-616A-367	Sequence 367, App
c	42	118	5.8	668	4	US-09-605-785-367	Sequence 367, App
c	43	109	5.3	454	4	US-08-991-789A-211	Sequence 211, App
c	44	109	5.3	454	4	US-09-062-451-211	Sequence 211, App
c	45	109	5.3	454	4	US-09-598-326-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-605-785-375
Sequence 375, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Hitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yeasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-375
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGTTGATTCATGCGGCTGCTTCTTCTGTGAAGACCATTTGGTCTC 60
DB 1 ATGTGTTGAGTTGATTCATGCGGCTGCTTCTTCTGTGAAGACCATTTGGTCTC 60
QY 61 AGGAGCAAGTGGGCAAGTGGTGGTCCGCTCCCGGCAAGGAGGAGGCAAG 120
DB 61 AGGAGCAAGTGGGCAAGTGGTGGTCCGCTCCCGGCAAGGAGGAGGCAAG 120
QY 121 AGCAAGTGGGCAAGTGGTGGGCAAGTGGTGGTCCGCTCCCGGCAAGGAGGCAAG 180
DB 121 AGCAAGTGGGCAAGTGGTGGGCAAGTGGTGGTCCGCTCCCGGCAAGGAGGCAAG 180

OY	181	ATGGGCAAGTGTGGCGGCGCACCTCTCCCTGCTGAGGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGTGGCGGCGCACCTCTCCCTGCTGAGGGGGAGTGGCAAGCAAGCTG	240
OY	241	GGCGCTTCTGAGAGCCAGCAGCAGCTGCGTATCAACACACTGAGAACAGATGTGGCAAG	300
Db	241	GGCGCTTCTGAGAGCCAGCAGCAGCTGCGTATCAACACACTGAGAACAGATGTGGCAAG	300
OY	301	TGTGTGTCCACTGTCTTCCCTGCTGAGGGGGAGCGGCAAGCAAGTGGGCGCTTGG	360
Db	301	TGTGTGTCCACTGTCTTCCCTGCTGAGGGGGAGCGGCAAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTTCAGTGTACAGTGGCTTCATGAGAGCCAGGCTACCACTGCGTGGAGAAATCTG	420
Db	361	GGAGACTTCAGTGTACAGTGGCTTCATGAGAGCCAGGCTACCACTGCGTGGAGAAATCTG	420
OY	421	GACAACTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCTATCGTCATG	480
Db	421	GACAACTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCTATCGTCATG	480
OY	481	CTCAGGGGACATGTACGCGTAACAAAGAGAGCAACCAAGACAGTGTCTACATCTGGCC	540
Db	481	CTCAGGGGACATGTACGCGTAACAAAGAGAGCAACCAAGACAGTGTCTACATCTGGCC	540
OY	541	TCTGCGCAATGGGAATTCAGAAAGTAACTCTGCTGAGACAGATGTCTCACTTAAAT	600
Db	541	TCTGCGCAATGGGAATTCAGAAAGTAACTCTGCTGAGACAGATGTCTCACTTAAAT	600
OY	601	GTCCTTGACAAACAAAAGAGACAGCTCTGTATTAAGCCGTCACAAATGCGCAGAGATGA	660
Db	601	GTCCTTGACAAACAAAAGAGACAGCTCTGTATTAAGCCGTCACAAATGCGCAGAGATGA	660
OY	661	TGTGGTTAATGTTGCTGAGAAACATGGCAGCTGATCCAAATATTTCCAGATGAGTGAAT	720
Db	661	TGTGGTTAATGTTGCTGAGAAACATGGCAGCTGATCCAAATATTTCCAGATGAGTGAAT	720
OY	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTGA	780
Db	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTGA	780
OY	781	TATGGTGTGATTCGAATCAAAAAACAAGCATGGCGCTCACACCACTGTACTTGGTGA	840
Db	781	TATGGTGTGATTCGAATCAAAAAACAAGCATGGCGCTCACACCACTGTACTTGGTGA	840
OY	841	CATGAGCAAAAAACGCAAGTGTGAAATTTTTATTCAGAAAAAAGCGAATTTAAATGCA	900
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OY	901	CTGGATGATATTGGAAGAGCTGCGTCATCTGCGTATGTTGATGAGATCACACAGTATA	960
Db	901	CTGGATGATATTGGAAGAGCTGCGTCATCTGCGTATGTTGATGAGATCACACAGTATA	960
OY	961	GTCAGCCTTACTTGTGACAAAAATATTGATGTATCTTCCAAGATCTATCTGGACAGAGC	1020
Db	961	GTCAGCCTTACTTGTGACAAAAATATTGATGTATCTTCCAAGATCTATCTGGACAGAGC	1020
OY	1021	GCCAGAGATGTGCTGTTTCTAGTCATCATATGTATTTGGCCAGTACTTTCAGTAC	1080
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Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTTGGAAGACAGAAATCCAGAACAGACTTAAAG	1140
OY	1141	CTGACATCAGAGGAAGTCAACAAGGTTCAAGGAGTGAATAATAGCCAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAGTCAACAAGGTTCAAGGAGTGAATAATAGCCAGCCAGAGAAA	1200
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Db	1261	AAGCATGAAGTATATATGTTGGATTTACTAGAAAACCTGACATAAAGGTGCTACGTCTGGC	1320
QY	1321	AATGGTGTATATGATTAATTTCTTCAAAGGAGAGCAGAAACCTCGAATAATCAGCAATTT	1380
Db	1321	AATGGTGTATATGATTAATTTCTTCAAAGGAGAGCAGAAACCTCGAATAATCAGCAATTT	1380
QY	1381	CTTGACAAACGAAAGTGAAGGTATCACAGAAATTTGCGAATTTGTTTCTGACTACAAAGAA	1440
Db	1381	CTTGACAAACGAAAGTGAAGGTATCACAGAAATTTGCGAATTTGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTCTTGAAAACACGACACCCGAAACCAAGACTTAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTCTTGAAAACACGACACCCGAAACCAAGACTTAAGCTGACA	1500
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Db	1621	GAAATGAAGAAAGCAGCGAAGTACTCATGTCTGGATTTCCCGAGAAAACCTGACTAATATGCTGCC	1680
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QY	1741	CAGCAATTTCTCTGACACTGTGAATGGAAGATCACAGTGCAGAACCAAAATGATATCTCAG	1800
Db	1741	CAGCAATTTCTCTGACACTGTGAATGGAAGATCACAGTGCAGAACCAAAATGATATCTCAG	1800
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Db	1801	AAGCAATTTTGTGAAGAACAGAACACTCTGGAAATTTACAGATGAGATTTCTGATTCATGAA	1860
QY	1861	GAAAGACGATAGAGAGGTGTTGAAAAAATGCAATTCGACCTTCTCTAGTTGTGAAGAA	1920
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QY	1921	GAAGAAAGCATCTTGATGTAAGAAATAGTACGTTGCCGGAAGAAATTTGCCATGCTAAGACTG	1980
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Db	1981	GAGCTAGACACATGAAACATCTCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT	2040

; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-375

Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGAGCAAGATGGGCAAGTGTGTGCGCGTTGCTCCCTGCTGCAAGGAGCGGCAAG 120
OY 121 AGCAACGTGGGACATCTTGGAGACCAACGACCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGACATCTTGGAGACCAACGACCTGCTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGTGGCGGCACTGCTCCCTGCTGAGGGGAGGAGGCAAGACGTCG 240
DB 181 ATGGGCAAGTGTGGCGGCACTGCTCCCTGCTGAGGGGAGGAGGCAAGACGTCG 240
OY 241 GCGCGTTCTGAGACACGACGACTCTGCTATGAAGACACTCAGAAACAAGATGGGCAAG 300
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OY 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGATCACGTCGCGGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGATCACGTCGCGGGAGAGATCTG 420
OY 421 GACAAGCTCCACAGACGTCCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTGCATG 480
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DB 661 TGTGCGTTAATGTGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
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DB 721 ACCACTGCACTACGCTATCTATATGAAGATTAATTAATGCGCAACACACTGCTTA 780
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DB 781 TATGGTGTGATATGAAATCAAAAAACAAGATGGCTCACACCACTGTACTTGGTGA 840
OY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900

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DB 901 CTGATATGATATGAAGACAGCTGCTCATACTTGGCTATGTTGGATCAGCAAGTATA 960
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DB 961 GTACGCTTCTACTTGGACCAAAATATGATGTATCTTCAAGATCTATCTGACAGACG 1020
OY 1021 GCCAAGATATGCTGTTCTGTCATCATCTGATTAATTTGCCATTAATCTTCTGACATC 1080
DB 1021 GCCAAGATATGCTGTTCTGTCATCATCTGATTAATTTGCCATTAATCTTCTGACATC 1080
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DB 1081 AAGAAAAACAGATCTAAAAATCTTCTGAAAAACAGCAATCCAGAACACTTAAAG 1140
OY 1141 CTGACATCAGAGAAAGTCCAAAGGTTCAAAAGCAGTGAATAATGACCAGCAAGAA 1200
DB 1141 CTGACATCAGAGAAAGTCCAAAGGTTCAAAAGCAGTGAATAATGACCAGCAAGAA 1200
OY 1201 ATGCTCAAGAACCAAAATTAATTAAGATGGTGAATGAGAGAGGTTGAAGAAGATGAG 1260
DB 1201 ATGCTCAAGAACCAAAATTAATTAAGATGGTGAATGAGAGAGGTTGAAGAAGATGAG 1260
OY 1261 AAGCATGAAAGTAAATATGATGATTAATCTTCAAAAGAGCAGAACCTGAAAAATGCAATTT 1320
DB 1261 AAGCATGAAAGTAAATATGATGATTAATCTTCAAAAGAGCAGAACCTGAAAAATGCAATTT 1320
OY 1321 AATGGTATTAATGATTAATCTTCAAAAGAGCAGAACCTGAAAAATGCAATTT 1380
DB 1321 AATGGTATTAATGATTAATCTTCAAAAGAGCAGAACCTGAAAAATGCAATTT 1380
OY 1381 CCTGACACGAAAGTGAAGATGATCAACAATTTTGGATTTAGTTCTCTACATCAAGAA 1440
DB 1381 CCTGACACGAAAGTGAAGATGATCAACAATTTTGGATTTAGTTCTCTACATCAAGAA 1440
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DB 1501 TCAGAGGAAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAAGAAAGATCT 1560
OY 1561 CAAGAACCAGAAATTAATTAAGATGGTGAATGAAGACTTGAATAATTTATGGCTATCGAA 1620
DB 1561 CAAGAACCAGAAATTAATTAAGATGGTGAATGAAGACTTGAATAATTTATGGCTATCGAA 1620
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OY 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAGAACACCTGAAAC 1740
DB 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAGAACACCTGAAAC 1740
OY 1741 CAGCAATTTCTGACACTGAGATGAAGATGATCAGAGTGAAGCAAGCAAAATGATCTCAG 1800
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OY 1801 AAGCAATTTTGAAGAAACAGAACTGGAATATTAACAGATGAGATGATGATTCATGAA 1860
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OY 1861 GAAAGCAGATAGAAAGTGTGAAAAAATGAATTCCTGACCTTCTTATGTTGAAGAA 1920
DB 1861 GAAAGCAGATAGAAAGTGTGAAAAAATGAATTCCTGACCTTCTTATGTTGAAGAA 1920
OY 1921 GAAAAAGACATCTTGATCAAAAAATGATACGTTGGGGAAGAAATTCCTGCTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGATCAAAAAATGATACGTTGGGGAAGAAATTCCTGCTAAGACTG 1980
OY 1981 GAGCTAGACAAATGAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAAT 2040

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Db 1981 GAGCTAGACAAATGAAACATCAGAGCCAGCTAAAAA 2040
RESULT 3
US-09-352-616A-375
Sequence 375, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
Applicant: Dillion, Davlin C.
Applicant: Harlocker, Susan Louise
Applicant: Jiang, Yugu
Applicant: Xu, Jiangchun
Applicant: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352, 616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-375

Query Match      100.0% Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTTGAGGTTGATTCATGCGGCTCTCTTCTGTGAAGAGCCATTTGTCTC 60
Db 1 ATGTGGTTGAGGTTGATTCATGCGGCTCTCTTCTGTGAAGAGCCATTTGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTCTGCTCCCTTCTCTGCGAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTCTGCTCCCTTCTCTGCGAGGAGCGGCAAG 120
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Db 661 TGTGCGTAAATGTTGCTGGAACATGGCATGATCAATAATTTCCAGATGATGTAAT 720
QY 721 ACCACTGTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGACATGCTCTTA 780
Db 721 ACCACTGTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGACATGCTCTTA 780
QY 781 TATGTCCTATATCCGAATTAATAAACAAGCATGGCTCCACACACTGATCTGTTGTA 840
Db 781 TATGTCCTATATCCGAATTAATAAACAAGCATGGCTCCACACACTGATCTGTTGTA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
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Db 901 CTGGATGATATGGAAGAGCTGCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGAGACAGC 1020
Db 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGAGACAGC 1020
QY 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAAAGAAAACAGATGCTAAATAATCTCTTGTGAAGACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAAAAGAAAACAGATGCTAAATAATCTCTTGTGAAGACAGCAATCCAGAACAGCTTAAG 1140
QY 1141 CTGACATCAAGAGAAAGTACAAAAGTTCAAGGCGTGAATAATGGCCAGCAAGAAA 1200
Db 1141 CTGACATCAAGAGAAAGTACAAAAGTTCAAGGCGTGAATAATGGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATGTTGGGATTAATGAAAACCTGATAATGCTGCTGCGC 1320
Db 1261 AAGCATGAAAGTAAATGTTGGGATTAATGAAAACCTGATAATGCTGCTGCGC 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGGAGCAAGCACTGTAATTCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGGAGCAAGCACTGTAATTCAGCAATTT 1380
QY 1381 CTTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCAAAATTAATCTTCTGAAAACAGCAAGCAAGCAAGCACTTAAGCTGACA 1500
Db 1441 AAAAGATGCAAAATTAATCTTCTGAAAACAGCAAGCAAGCAAGCACTTAAGCTGACA 1500
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QY 1561 CAAGAAGCAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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QY 1621 GAATGAAAGAGACGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 GAATGAAAGAGACGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740

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QY 1741 CAGCAATTTCTGACACTGAGATGAGATATCACAGTACAGCAAAATGATCTCAG 1800
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Db 1741 CAGCAATTTCTGACACTGAGATGAGATATCACAGTACAGCAAAATGATCTCAG 1800
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Db 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
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Db 1861 GAAAAGCAGATGAGATGAGTGTGTAATAAATGAAATTTCTGAGCTTTCTTGTAGTGAAGAA 1920
QY 1921 GAAAAGCAGATGAGTGTGTAATAAATGAAATTTCTGAGCTTTCTTGTAGTGAAGAA 1980
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Db 1921 GAAAAGCAGATGAGTGTGTAATAAATGAAATTTCTGAGCTTTCTTGTAGTGAAGAA 1980
QY 1981 GAGCTAGACACAAATGAAATCATCAGAGCAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040
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Db 1981 GAGCTAGACACAAATGAAATCATCAGAGCAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 4

US-09-605-785-374
Sequence 374, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vegdick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-374

Query Match 76.0%; Score 1551; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTGGATTCATGCGGCGCTCTCTGCTGTAAGCAAGCATTTGGTCTC 60
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Db 1 ATGGTGGTTGAGTGGATTCATGCGGCGCTCTCTCTGCTGTAAGCAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGTCTGCGTTGCTTCCCTGCTGAGAGGAGCGGCAAG 120
|||
Db 61 AGGAGCAAGATGGGCAAGTGTGTCTGCGTTGCTTCCCTGCTGAGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCAAGCACTGCTATGAGAGCACTAGAGCAAG 180
|||
Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCAAGCACTGCTATGAGAGCACTAGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGCGCCACTGTTCCCTCTGCTGAGGGGAGTGGCAAGAGCAACGTG 240
|||
Db 181 ATGGGCAAGTGGTGGCGCCACTGTTCCCTCTGCTGAGGGGAGTGGCAAGAGCAACGTG 240
QY 241 GCGGCTTCTGGAGACCAAGAGCACTCTGCTATGAAAGCACTGAGAACAAAGTGGGCAAG 300
|||
Db 241 GCGGCTTCTGGAGACCAAGAGCACTCTGCTATGAAAGCACTGAGAACAAAGTGGGCAAG 300
QY 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
|||
Db 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GAGAGTACAGATGAGACAGTCTTCAATGAGCCAGGATACAGTCTGCTGAGAAATCTG 420
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Db 361 GAGAGTACAGATGAGACAGTCTTCAATGAGCCAGGATACAGTCTGCTGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTATCTCATG 480
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QY 481 CTCAGGAGACCTGAGCTGTAACAAGAGCAAGCAAGAGAGCACTGCTTACATCTGGCC 540
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QY 541 TCTGCCAATGGGAATTCAGAAATGATGAAATCTCTGCTGAGAGAGATGCACTTAAT 600
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QY 661 TGTGCGTTAATGTGTGCTGGAACATGCGCACTGATCCAAATTTCCAGATGATGGAAT 720
|||
Db 661 TGTGCGTTAATGTGTGCTGGAACATGCGCACTGATCCAAATTTCCAGATGATGGAAT 720
QY 721 ACCACTCTGCTACGCTCTATATGAAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
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QY 781 TATGTTGCTGATATGAAATCAAAAAAAGCAATGCGCTCACACACTGTTACTTGGTGA 840
|||
Db 781 TATGTTGCTGATATGAAATCAAAAAAAGCAATGCGCTCACACACTGTTACTTGGTGA 840
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Db 841 CATGAGCAAAAAAGCAAGTGTGAAATTTTATATCAGAAAAAAGCGAATTTAATGCA 900
QY 901 CTGATATGATGAGAGAGAGCTGCTCATACTGCTGATGTTGTTGATCAGCAAGTATA 960
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Db 901 CTGATATGATGAGAGAGAGCTGCTCATACTGCTGATGTTGTTGATCAGCAAGTATA 960
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Db 961 GTACGCTTCTACTTGGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
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Db 1021 GCCAGAGATATGCTGTTTCTACTCATCATCATATTTTGGCAGTTACTTTCTGACTAC 1080
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Db 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAAGCGATGAAATAGCCAGCAGAGAAA 1200
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Db 1201 ATGTCTCAAGAACCAAGAAATTAATGATGATGATGAGAGCTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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Db 1381 CCTGACAGCAAGAGTGAAGATATCACAGATTTGGCAATTTCTGACTACAAAGAA 1440
QY 1441 AAACACATGCCAAATACTCTTGTAAAACAGCAACCCAGACAGACTTAAAGCTGACA 1500
Db 1441 AAACACATGCCAAATACTCTTGTAAAACAGCAACCCAGACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATCACAAAGGCTTGAGGGGCGTGAAGAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGATCACAAAGGCTTGAGGGGCGTGAAGAAATGGCCAGCCAGAG 1551

RESULT 5
US-09-439-313-374

; Sequence 374 Application US/09439313
; Patent No. 6329305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-374

Query Match 76.0%; Score 1551; DB 4; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCTTGAGGTGATTCATCGCGGCTGCTCTTGTGTAAGAAGCCATTTGGTCTC 60
Db 1 ATGTGCTTGAGGTGATTCATCGCGGCTGCTCTTGTGTAAGAAGCCATTTGGTCTC 60
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Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTTGGAGACCAAGCACTGCTATGAAGCACTCAGGAACAAGATGGGCAAG 300
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QY 301 TGGTGTGCCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
Db 301 TGGTGTGCCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
QY 361 GGAGACTAGCATATGAGTGTGCTTCAATGAGCCCAAGGTACCACTCCGTGGAAGAATCTG 420
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QY 421 GACAACTCCACAGAGCTGCTGGGGGTAAAGTCCCGAAGAAGATCTCATGCTCATG 480
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Db 601 GTCTTGACAAACAAAAGAGACAGCTGTATTAAGGCGCTACAAATGCGCAAGATGAA 660
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACATGATCCAAATATTCAGATGATGAAAT 720
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Db 721 ACCACTGTGCATACGTATCTATTAATGAAGATTAATTAATGGCCAAAGACATGCTTAA 780
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Db 1141 CTGACATCAGAGGAAGTGTACAAAGGTTCAAGGCGCTGAATAATAGCCAGCAAGAAA 1200
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Db 1201 ATGTCTCAAGAACAGAAATTAAGATGATATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGATTAATGAAGAAACCTGACTATGTGCTGCTG 1320
Db 1261 AAGCATGAAGATTAATATGTTGGATTAATGAAGAAACCTGACTATGTGCTGCTG 1320
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QY 1381 CCTGACAAAGAAAGTGAAGATATCACAGATTTGGCAATTTCTGACTACAAAGAA 1440

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Db 1381 CCTGACACGAAGTGAAGATATCAGCAATTTGGGAATTAAGTTCTGACATCAAGAA 1440
Oy 1441 AAGAGATGCCAAATFACTCTTCTGAAACAGACACCCGAAGACAGATTAAAGCTGACA 1500
Db 1441 AAGAGATGCCAAATFACTCTTCTGAAACAGACACCCGAAGACAGATTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 6
US-09-352-616A-374
Sequence 374, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jlang, Yuguil
APPLICANT: Xu, Jlangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 76.0%; Score 1551; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGTGGTGGAGTGGATTCATGCCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 AAGGTGGTGGAGTGGATTCATGCCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Oy 61 AAGAGCAAGATGGCAAGTGGTGGTCCGTTGCTCCCTGCGAGGGAGAGCGGCAAG 120
Db 61 AAGAGCAAGATGGCAAGTGGTGGTCCGTTGCTCCCTGCGAGGGAGAGCGGCAAG 120
Oy 121 AAGCAAGTGGGCACTTCTGGAGACCAAGACGACTGTGTATGAAGACACTCAGAGCAAG 180
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Oy 181 AAGGGCAATGGTGGCGCCACAGTCCCTGCTGTCAGAGGGAGTGGCAAGCAACGTG 240
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Oy 241 AAGGGCAATGGTGGCGCCACAGTCCCTGCTGTCAGAGGGAGTGGCAAGCAACGTG 240
Db 241 AAGGGCAATGGTGGCGCCACAGTCCCTGCTGTCAGAGGGAGTGGCAAGCAACGTG 240
Oy 301 TGGTGGTGGCACTGCTCCCTGCTGTCAGAGGGAGTGGCAAGCAACGTG 360
Db 301 TGGTGGTGGCACTGCTCCCTGCTGTCAGAGGGAGTGGCAAGCAACGTG 360
Oy 361 GGAAGTACAGATGACAGTCCCTTCTGATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 361 GGAAGTACAGATGACAGTCCCTTCTGATGAAGACACTCAGAGCAAGATGGGCAAG 300
Oy 421 GACAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCATCGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCATCGTCATG 480
Oy 481 CTCAGGGACACTGACGTGAACAAGAAAGCAAGCAAGAGACTCTCTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAGAAAGCAAGCAAGAGACTCTCTACATCTGGCC 540

Db 481 CTCAGGGACACTGACGTGAACAAGAAAGCAAGCAAGAGACTCTCTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGAGACAGAGATGTAACCTAAT 600
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Oy 601 GTCCCTTGACAAACAAAAGAGAGACAGTCTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGACAGTCTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
Oy 661 TGTGGCTTAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGCTTAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTCTGACCTACGCTATCTAATGAAGATTAATGGCCAAACAGCTGCTTAA 780
Db 721 ACCACTCTGACCTACGCTATCTAATGAAGATTAATGGCCAAACAGCTGCTTAA 780
Oy 781 TATGGTGTGATATCAATCAAAAAACAAGCATGGCTCAGACACCTGTTACTTGGTGA 840
Db 781 TATGGTGTGATATCAATCAAAAAACAAGCATGGCTCAGACACCTGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
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Db 901 CTGGATATGATATGGAAGAGTGTCTCATCTGCTGATGTTGTGGATCAGCAATATA 960
Oy 961 GTGAGCCTTCTACTTGAAGAAAAATTTGATGATCTTCAAGATCATCTGAGACAGAG 1020
Db 961 GTGAGCCTTCTACTTGAAGAAAAATTTGATGATCTTCAAGATCATCTGAGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGATGATTAATTTCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGATGATTAATTTCCAGTTACTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAACAGCTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAACAGCTTAAAG 1140
Oy 1141 CTGACATCAGAGAAAGTACAAAGGTTCAAAAGAGTGAAGAAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAAAGTACAAAGGTTCAAAAGAGTGAAGAAATAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
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Oy 1261 AAGCATGAAAGTAAATATGGGATTAATGAAGAAACCTGACTAATGGTCACTGGTGC 1320
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Oy 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGAATTAATTTCTGACTCAAAAGAA 1440
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Oy 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 7
US-09-605-785-373

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; Sequence 373, Application US/09605785
; Patent No. 632176
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-785-373
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Query Match          55.3%; Score 1128; DB 4; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGCTGTTGAGTGTGATTCATCCCGGCTGCTCTTCTGTGAAGAGCCATTGCTCTC 60
DB 1 ATGCTGTTGAGTGTGATTCATCCCGGCTGCTCTTCTGTGAAGAGCCATTGCTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTCTGAGGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTCTGAGGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGGAGACACGACCTCTGTATGAAGACCTAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTGTGGAGACACGACCTCTGTATGAAGACCTAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTCCGCTGCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG 240
DB 181 ATGGGCAAGTGTGCTGCTCCGCTGCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG 240
QY 241 GGGCTCTTGTGAGACACGACGACTCTGTATGAAGACACTACAGAAACAGATGGCAAG 300
DB 241 GGGCTCTTGTGAGACACGACGACTCTGTATGAAGACACTACAGAAACAGATGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCTGAGGGGAGCGGCAAGGAGTGGGCGTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCTGAGGGGAGCGGCAAGGAGTGGGCGTTGG 360
QY 361 GGAGACTACGATGACAGTGTGCTTGTGAGAGCCAGGTACACGTCGCTGAGAAAGATCTG 420
DB 361 GGAGACTACGATGACAGTGTGCTTGTGAGAGCCAGGTACACGTCGCTGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGACACTGACGTAACAAAGAGCAAGCAAGAAAGAGATGCTCTTACATCTGACC 540
DB 481 CTCAGGGACACTGACGTAACAAAGAGCAAGCAAGAAAGAGATGCTCTTACATCTGACC 540
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QY 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGAGACAGATGTCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGACAGCTGTGTAAAGGCCCTACATAGCCAGGAAGATGAA 660
DB 601 GTCTTGACAAACAAAAGAGACAGCTGTGTAAAGGCCCTACATAGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACATGATCCAAATATATCCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACATGATCCAAATATATCCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTAATGAGATGAATTAATGATGATGATGATGATGATG 780
DB 721 ACCACTGTGACACTACGCTATCTAATGAGATGAATTAATGATGATGATGATGATGATG 780
QY 781 TATGCTGTGATATGCAATCAAAAACAGATGGCCCTACACACACATGTTACTTGCTGA 840
DB 781 TATGCTGTGATATGCAATCAAAAACAGATGGCCCTACACACACATGTTACTTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAATCAAGAAAAGCAATTTAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAATCAAGAAAAGCAATTTAATGCA 900
QY 901 CTGGATAGATATGGAAGGACTGCTCTCATACCTGCTGATGTTGATGATGATGATGATG 960
DB 901 CTGGATAGATATGGAAGGACTGCTCTCATACCTGCTGATGTTGATGATGATGATGATG 960
QY 961 GTGAGCTTCTACTTGTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
DB 961 GTGAGCTTCTACTTGTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
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RESULT 8
US-09-439-313-373
; Sequence 373, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Stolk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-439-313-373

Query Match          55.3%; Score 1128; DB 4; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ATGTGTGTGAGTGTATTCATGCGGGCTCTTGTGTAAGAGCCATTTGGTTC 60
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    1 ATGTGTGTGAGTGTATTCATGCGGGCTCTTGTGTAAGAGCCATTTGGTTC 60
OY 61 AGGACCAAGANTGGCAAGTGTGTGCGGTTCCTCCCTGCTGCAGGAGAGCGGCAAG 120
    |||
    61 AGGACCAAGANTGGCAAGTGTGTGCGGTTCCTCCCTGCTGCAGGAGAGCGGCAAG 120
OY 121 AGCAACGTGGGACCTTTCTGGAGACCAAGCACTGTGCTATGAAACACTCAGAGCAAG 180
    |||
    121 AGCAACGTGGGACCTTTCTGGAGACCAAGCACTGTGCTATGAAACACTCAGAGCAAG 180
OY 181 ATGGCAAGTGTGGCGGCACCTGTCCCTGCTGCAGGAGGAGTGGCAAGCAAGCTG 240
    |||
    181 ATGGCAAGTGTGGCGGCACCTGTCCCTGCTGCAGGAGGAGTGGCAAGCAAGCTG 240
OY 241 GCGGCTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGAACAAAGATGGGCAAG 300
    |||
    241 GCGGCTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGAACAAAGATGGGCAAG 300
OY 301 TGTGCTGCTGCTGCTTCCCTGCTGCAGGAGGAGCGGCAAGCAAGTGGCGCTTGG 360
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    301 TGTGCTGCTGCTGCTTCCCTGCTGCAGGAGGAGCGGCAAGCAAGTGGCGCTTGG 360
OY 361 GGAGACTAGATGACAGTGTCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
    |||
    361 GGAGACTAGATGACAGTGTCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
OY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
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    421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
OY 481 CTCAGGAGACCTGAGGTGAACAAGAGCAAGCAAGAGACCTCTTACATCTGGCC 540
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    481 CTCAGGAGACCTGAGGTGAACAAGAGCAAGCAAGAGACCTCTTACATCTGGCC 540
OY 541 TGTGCCAATGGGAATTCAGAACTCTGCTGCAGAGAGATGTCAACTTAAT 600
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    541 TGTGCCAATGGGAATTCAGAACTCTGCTGCAGAGAGATGTCAACTTAAT 600
OY 601 GTCCCTTGACACAAAAAGAGACAGCTCTGATAAAGCCGCTACAAATGCCAGGAATGAA 660
    |||
    601 GTCCCTTGACACAAAAAGAGACAGCTCTGATAAAGCCGCTACAAATGCCAGGAATGAA 660
OY 661 TGTGGCTTAATGTGTGTGTAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
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    661 TGTGGCTTAATGTGTGTGTAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
OY 721 ACCACTCTGCTAGCGCTATCTATTAATGAAGTAAATTAATGAGCCAAAGCACTGCTTA 780
    |||
    721 ACCACTCTGCTAGCGCTATCTATTAATGAAGTAAATTAATGAGCCAAAGCACTGCTTA 780
OY 781 TATGTGCTGATATGCAATCAAAAAAGCAATGAGCTCACAACACTGTTACTGTGTA 840
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    781 TATGTGCTGATATGCAATCAAAAAAGCAATGAGCTCACAACACTGTTACTGTGTA 840
OY 841 CATGAGCAAAAAAGCAAGTGTGAATTTTAATCAAAAAAGCGAATTTAAATGCA 900
    |||
    841 CATGAGCAAAAAAGCAAGTGTGAATTTTAATCAAAAAAGCGAATTTAAATGCA 900
OY 901 CTGAGATAGTATGGAAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAATGTA 960
    |||
    901 CTGAGATAGTATGGAAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAATGTA 960
OY 961 GTGAGCTTCTACTTGAGCAAAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
    |||
    961 GTGAGCTTCTACTTGAGCAAAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
OY 1021 GCGAGAGATATGCTGTTCTAGTCAATCATGATGATGATGATGATGATGATGATGATG 1080
    |||
    1021 GCGAGAGATATGCTGTTCTAGTCAATCATGATGATGATGATGATGATGATGATGATG 1080
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OY 1081 AAAGAAAAACAGATGCTAAATAATCTCTGTAAGAACAGCAATCCAGAA 1128
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    1081 AAAGAAAAACAGATGCTAAATAATCTCTGTAAGAACAGCAATCCAGAA 1128
RESULT 9
US-09-352-616A-373
; Sequence 373, Application US/09352616A
; Patent No. 6195278
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuguai
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-373
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Query Match 55.3%; Score 1128; DB 4; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ATGTGTGTGAGTGTATTCATGCGGGCTCTTGTGTAAGAGCCATTTGGTTC 60
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    1 ATGTGTGTGAGTGTATTCATGCGGGCTCTTGTGTAAGAGCCATTTGGTTC 60
OY 61 AGGACCAAGANTGGCAAGTGTGTGCGGTTCCTCCCTGCTGCAGGAGAGCGGCAAG 120
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    61 AGGACCAAGANTGGCAAGTGTGTGCGGTTCCTCCCTGCTGCAGGAGAGCGGCAAG 120
OY 121 AGCAACGTGGGACCTTTCTGGAGACCAAGCACTGTGCTATGAAACACTCAGAGCAAG 180
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    121 AGCAACGTGGGACCTTTCTGGAGACCAAGCACTGTGCTATGAAACACTCAGAGCAAG 180
OY 181 ATGGCAAGTGTGGCGGCACCTGTCCCTGCTGCAGGAGGAGTGGCAAGCAAGCTG 240
    |||
    181 ATGGCAAGTGTGGCGGCACCTGTCCCTGCTGCAGGAGGAGTGGCAAGCAAGCTG 240
OY 241 GCGGCTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGAACAAAGATGGGCAAG 300
    |||
    241 GCGGCTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGAACAAAGATGGGCAAG 300
OY 301 TGTGCTGCTGCTGCTTCCCTGCTGCAGGAGGAGCGGCAAGCAAGTGGCGCTTGG 360
    |||
    301 TGTGCTGCTGCTGCTTCCCTGCTGCAGGAGGAGCGGCAAGCAAGTGGCGCTTGG 360
OY 361 GGAGACTAGATGACAGTGTCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
    |||
    361 GGAGACTAGATGACAGTGTCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
OY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
    |||
    421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
OY 481 CTCAGGAGACCTGAGGTGAACAAGAGCAAGCAAGAGACCTCTTACATCTGGCC 540
    |||
    481 CTCAGGAGACCTGAGGTGAACAAGAGCAAGCAAGAGACCTCTTACATCTGGCC 540
OY 541 TGTGCCAATGGGAATTCAGAACTCTGCTGCAGAGAGATGTCAACTTAAT 600
    |||
    541 TGTGCCAATGGGAATTCAGAACTCTGCTGCAGAGAGATGTCAACTTAAT 600
OY 601 GTCCCTTGACACAAAAAGAGACAGCTCTGATAAAGCCGCTACAAATGCCAGGAATGAA 660
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Db 601 GTCTTACACAAAAAGAGACAGCTGTGTAAGCCCGACAAATCCAGGAGATGAA 660
OY 661 TGTGCGTAAATGTTGCGAAGACGACATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTAAATGTTGCGAAGACGACATGATCCAAATATTCAGATGATGAAAT 720
OY 721 ACCACTGTGACATGACATCTATATATGAATAAATTAATGCGCAAGCCTGCTTA 780
Db 721 ACCACTGTGACATGACATCTATATATGAATAAATTAATGCGCAAGCCTGCTTA 780
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Db 781 TATGTCCTGATATGATCAATCAAAAACAGCAGGCGCTCACACCTGTTACTGTGTA 840
OY 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
OY 901 CTGATGATATGGAAGAGCTGCTCTCATCTTCTGTATGTTGGATCAGCAATATA 960
Db 901 CTGATGATATGGAAGAGCTGCTCTCATCTTCTGTATGTTGGATCAGCAATATA 960
OY 961 GTGACGCTTCTACTTGACAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGACGCTTCTACTTGACAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
OY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGTAATTTGGCAGTACTTCTGACATC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGTAATTTGGCAGTACTTCTGACATC 1080
OY 1081 AAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
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RESULT 10
US-09-605-785-368
; Sequence 368, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-368

Query Match 24.18; Score 491; DB 4; Length 1512;
Best Local Similarity 99.44; Pred. No. 8.9e-198;
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Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 34 TCTCTGTGAAGAACCATTTGCTCTCAGAGCAAGATGGGCAAGTGGTGGCTGGC 93
Db 256 TCTTCTGTGAAGAACCATTTGCTCTCAGAGCAAGATGGGCAAGTGGTGGCTGGC 315
OY 94 TTCCCTGTCTGACAGAGAGCGGCAAGAGCAAGCTGGGCACTTGTGAGACACAGCAGAC 153
Db 316 TTCCCTGTCTGACAGAGAGCGGCAAGAGCAAGCTGGGCACTTGTGAGACACAGCAGAC 375
OY 154 TCTGTATGAAGACATCAGAGACAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGG 213
Db 376 TCTGTATGAAGACATCAGAGACAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGG 435
OY 214 TGCAGGGGAGTGGCAAGAGCAAGCTGGGCACTTGTGAGACACAGCAAGCTGTATG 273
Db 436 TGCAGGGGAGTGGCAAGAGCAAGCTGGGCACTTGTGAGACACAGCAAGCTGTATG 495
OY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 333
Db 496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 555
OY 334 AGCGCAAGAGCAAGTGGGCGCTTGGGGAACATACATGACATGACATGACATGACATGAC 393
Db 556 AGCGCAAGAGCAAGTGGGCGCTTGGGGAACATACATGACATGACATGACATGACATGAC 615
OY 394 AGTACACAGCTGCTGAGAGATCTGGACAACTCCACAGAGCTGCTGGTGGTGGTGGTGG 453
Db 616 AGTACACAGCTGCTGAGAGATCTGGACAACTCCACAGAGCTGCTGGTGGTGGTGGTGG 675
OY 454 GTCCCAAGAAAGATCTCATCTGATGCTCAGGACACTGACGTAACAGAGAGCAAG 513
Db 676 GTCCCAAGAAAGATCTCATCTGATGCTCAGGACACTGACGTAACAGAGAGCAAG 735
OY 514 CAAAAGGAGTGTCTACATCTGGCCCTGCAATGGGAATTCAGAAATGTAATTAATCTC 573
Db 736 CAAAAGGAGTGTCTACATCTGGCCCTGCAATGGGAATTCAGAAATGTAATTAATCTC 795
OY 574 CTGCTGACAGACATGTCATTAATGCTCTTGACAAACAAAAGAGACAGCTGTGATA 633
Db 796 STGCTGACAGACATGTCATTAATGCTCTTGACAAACAAAAGAGACAGCTGTGATA 855
OY 634 AAGCCCTGACAAATCCAGAGAAATGATGCGTTAATGTTGCTGGAACATGACATGAT 693
Db 856 AAGCCCTGACAAATCCAGAGAAATGATGCGTTAATGTTGCTGGAACATGACATGAT 915
OY 694 CCAATATTCAGATGATGATAATACCACTCT 728
Db 916 CCAATATTCAGATGATGATAATACCACTCT 950
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RESULT 11
US-09-439-313-368
; Sequence 368, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
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SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 368
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-368

Query Match 24.1%; Score 491; DB 4; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8.9e-198;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGAGAGAGCCATTTGGTCTCAGAGACAGATGGGCAATGGTGTGCGGTTGC 93
DB 256 TCTTCTGAGAGAGCCATTTGGTCTCAGAGACAGATGGGCAATGGTGTGCGGTTGC 315
QY 94 TTCCCTCTCTCAGAGAGAGGCGGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGAC 153
DB 316 TTCCCTCTCTCAGAGAGAGGCGGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGAC 375
QY 154 TCTGCTATGAGACACCTCAGAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTGC 213
DB 376 TCTGCTATGAGACACCTCAGAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAGAGAGCAAGCTGGGCGCTTCTGAGACCAAGCACTCTCTATG 273
DB 436 TGCAGGGGAGTGGCAGAGAGCAAGCTGGGCGCTTCTGAGACCAAGCACTCTCTATG 495
QY 274 AAGACACTCAGAGACACATATGGGCAAGTGGTGGTCCACTGCTTCCCTGCTGCAGGGGG 333
DB 496 AAGACACTCAGAGACACATATGGGCAAGTGGTGGTCCACTGCTTCCCTGCTGCAGGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGAGCC 615
QY 394 AGGTACACAGCTCCGTGGAAGATCTGCACAACTCCAGAGAGTGCCTGAGGGGTAA 453
DB 616 AGGTACACAGCTCCGTGGAAGATCTGCACAACTCCAGAGAGTGCCTGAGGGGTAA 675
QY 454 GTCCCAAGAAAGATCTATGCTCATGCTCAGGAGCACTGACGTGACAGAGAGCAAG 513
DB 676 GTCCCAAGAAAGATCTATGCTCATGCTCAGGAGCACTGACGTGACAGAGAGCAAG 735
QY 514 CAAAAGAGAGCTGCTCATGCTGCGCTGCGCAATGGGAATTGCAAGTACTAAACTC 573
DB 736 CAAAAGAGAGCTGCTCATGCTGCGCTGCGCAATGGGAATTGCAAGTACTAAACTC 795
QY 574 CTGCTGACAGACGATGTCACCTTATGCTTGCACAAACAAAGAGACAGCTCTGATA 633
DB 796 STGCTGACAGACGATGTCACCTTATGCTTGCACAAACAAAGAGACAGCTCTGATA 855
QY 634 AAGCCCGTACAAATGCGCAGAGAGATGCGCTTAATGTTGCTGGAACATGGCACTGAT 693
DB 856 AAGCCCGTACAAATGCGCAGAGAGATGCGCTTAATGTTGCTGGAACATGGCACTGAT 915
QY 694 CCAATATTCCAGATGATGGAATACCACTCT 728
DB 916 CCAATATTCCAGATGATGGAATACCACTCT 950

RESULT 12

US-09-062-451-294

Sequence 294, Application US/09062451

Patent No. 6344550

GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

NUMBER OF SEQUENCES: 297

CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 294:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-294

Query Match 24.1%; Score 491; DB 4; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8.9e-198;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGAGAGAGCCATTTGGTCTCAGAGACAGATGGGCAATGGTGTGCGGTTGC 93
DB 256 TCTTCTGAGAGAGCCATTTGGTCTCAGAGACAGATGGGCAATGGTGTGCGGTTGC 315
QY 94 TTCCCTCTCTCAGAGAGAGGCGGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGAC 153
DB 316 TTCCCTCTCTCAGAGAGAGGCGGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGAC 375
QY 154 TCTGCTATGAGACACCTCAGAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTGC 213
DB 376 TCTGCTATGAGACACCTCAGAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAGAGAGCAAGCTGGGCGCTTCTGAGACCAAGCACTCTCTATG 273
DB 436 TGCAGGGGAGTGGCAGAGAGCAAGCTGGGCGCTTCTGAGACCAAGCACTCTCTATG 495
QY 274 AAGACACTCAGAGACACATATGGGCAAGTGGTGGTCCACTGCTTCCCTGCTGCAGGGGG 333
DB 496 AAGACACTCAGAGACACATATGGGCAAGTGGTGGTCCACTGCTTCCCTGCTGCAGGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGAGCC 615
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DB 616 AGGTACACAGCTCCGTGGAAGATCTGCACAACTCCAGAGAGTGCCTGAGGGGTAA 675
QY 454 GTCCCAAGAAAGATCTATGCTCATGCTCAGGAGCACTGACGTGACAGAGAGCAAG 513
DB 676 GTCCCAAGAAAGATCTATGCTCATGCTCAGGAGCACTGACGTGACAGAGAGCAAG 735
QY 514 CAAAAGAGAGCTGCTCATGCTGCGCTGCGCAATGGGAATTGCAAGTACTAAACTC 573
DB 736 CAAAAGAGAGCTGCTCATGCTGCGCTGCGCAATGGGAATTGCAAGTACTAAACTC 795
QY 574 CTGCTGACAGACGATGTCACCTTATGCTTGCACAAACAAAGAGACAGCTCTGATA 633
DB 796 STGCTGACAGACGATGTCACCTTATGCTTGCACAAACAAAGAGACAGCTCTGATA 855

Db 556 AGC 558

RESULT 15
US-09-439-313-369
; Sequence 369, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqul
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien.
US-09-439-313-369

Query Match 12.4%; Score 252; DB 4; Length 1853;
Best Local Similarity 99.7%; Pred. No. 3.6e-97;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGTCCTGC 93
DB 256 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGTCCTGC 315
QY 94 TTCCCTGCTGCAGGAGGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGCAGCAG 153
DB 316 TTCCCTGCTGCAGGAGGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGCAGCAG 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCGCCACTGCTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCGCCACTGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGCAGCAGTCTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGCAGCAGTCTGCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCTGCTTCCCTGTCAGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCTGCTTCCCTGTCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 16
US-09-062-451-295
; Sequence 295, Application US/09062451
; Patent No. 6344350
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 295:
SEQUENCE CHARACTERISTICS:
LENGTH: 1853 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-295

Query Match 12.4%; Score 252; DB 4; Length 1853;
Best Local Similarity 99.7%; Pred. No. 3.6e-97;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGTCCTGC 93
DB 256 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGTCCTGC 315
QY 94 TTCCCTGCTGCAGGAGGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGCAGCAG 153
DB 316 TTCCCTGCTGCAGGAGGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGCAGCAG 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCGCCACTGCTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCGCCACTGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGCAGCAGTCTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGCAGCAGTCTGCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCTGCTTCCCTGTCAGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCTGCTTCCCTGTCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 17
US-09-352-616A-369
; Sequence 369, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqul
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A

;; CURRENT FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 472
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 369
;; LENGTH: 1853
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-952-616a-369

Query Match 12.4%; Score 252; DB 4; Length 1853;
Best Local Similarity 99.7%; Pred. No. 3.6e-97;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGCTGCGCTGC 93
DB 256 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGCTGCGCTGC 315
QY 94 TTCCCTGTCGAGGAGAGACCGGCAAGACAACTGGGCACTTTGGAGACAGAGAGAC 153
DB 316 TTCCCTGTCGAGGAGAGACCGGCAAGACAACTGGGCACTTTGGAGACAGAGAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTCCCTGC 435
QY 214 TGCAGGGGGAGTGCGCAAGCAACGTGGGCTTCTGAGACACAGAGACTGCTATG 273
DB 436 TGCAGGGGGAGTGCGCAAGCAACGTGGGCTTCTGAGACACAGAGACTGCTATG 495
QY 274 AAGGACTCTCAGAACAGATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGAGGGGG 333
DB 496 AAGGACTCTCAGAACAGATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGAGGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 18

US-09-605-785-531
; Sequence 531, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-531

Query Match 5.9%; Score 120; DB 4; Length 879;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 566
DB 333 GGACAGCAAAAGAGAGACTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 392
QY 567 AAAACTCTGCTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
DB 393 AAAACTCTGCTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 452
QY 627 TCTGATTAAGGCGGTACAAATGCCAGGAAGATGAATGTGCTTAATGTCTGGAACATGG 686
DB 453 TCTGATTAAGGCGGTACAAATGCCAGGAAGATGAATGTGCTTAATGTCTGGAACATGG 512
QY 687 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 728
DB 513 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 554

RESULT 19

US-09-439-313-531
; Sequence 531, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqul
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-531

Query Match 5.9%; Score 120; DB 4; Length 879;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 566
DB 333 GGACAGCAAAAGAGAGACTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 392
QY 567 AAAACTCTGCTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
DB 393 AAAACTCTGCTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 452
QY 627 TCTGATTAAGGCGGTACAAATGCCAGGAAGATGAATGTGCTTAATGTCTGGAACATGG 686
DB 453 TCTGATTAAGGCGGTACAAATGCCAGGAAGATGAATGTGCTTAATGTCTGGAACATGG 512
QY 687 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 728
DB 513 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 554

RESULT 20

US-09-605-785-372

```
; Sequence 372, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-372
```

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Query Match          5.9%; Score 120; DB 4; Length 1059;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGT 566
    |||||||
DB 276 GGACAAGCAAAAAGAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGT 335

QY 567 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACCAACAAAAAGAGACAGC 626
    |||||||
DB 336 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACCAACAAAAAGAGACAGC 395

QY 627 TCTGATTAAGGCCGTACATGCGCAGAGATGATGTCGTTAATGTTGCTGGAACATGG 686
    |||||||
DB 396 TCTGATTAAGGCCGTACATGCGCAGAGATGATGTCGTTAATGTTGCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 728
    |||||||
DB 456 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 497
```

```
RESULT 21
US-09-439-313-372
; Sequence 372, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reiter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
```

```
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-372
```

```
Query Match          5.9%; Score 120; DB 4; Length 1059;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGT 566
    |||||||
DB 276 GGACAAGCAAAAAGAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGT 335

QY 567 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACCAACAAAAAGAGACAGC 626
    |||||||
DB 336 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACCAACAAAAAGAGACAGC 395

QY 627 TCTGATTAAGGCCGTACATGCGCAGAGATGATGTCGTTAATGTTGCTGGAACATGG 686
    |||||||
DB 396 TCTGATTAAGGCCGTACATGCGCAGAGATGATGTCGTTAATGTTGCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 728
    |||||||
DB 456 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 497
```

```
RESULT 22
US-09-352-616A-372
; Sequence 372, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-372
```

```
Query Match          5.9%; Score 120; DB 4; Length 1059;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGT 566
    |||||||
DB 276 GGACAAGCAAAAAGAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGT 335

QY 567 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACCAACAAAAAGAGACAGC 626
    |||||||
DB 336 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACCAACAAAAAGAGACAGC 395

QY 627 TCTGATTAAGGCCGTACATGCGCAGAGATGATGTCGTTAATGTTGCTGGAACATGG 686
    |||||||
DB 396 TCTGATTAAGGCCGTACATGCGCAGAGATGATGTCGTTAATGTTGCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 728
    |||||||
DB 456 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 497
```


RESULT 23
US-08-991-789A-291/C
Sequence 291, Application US/08991789A
Patent No. 6225054
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
Reed, Steven G.
Smith, John M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potler, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
FAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-08-991-789A-291
Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 507 GGACAAGCAAAAGAGAGCTGCTTACATCTGGCCTGCGCAATGGGAATTGAGAAGTACT 566
|||||
DB 791 GGACAAGCAAAAGAGAGCTGCTTACATCTGGCCTGCGCAATGGGAATTGAGAAGTACT 732
QY 567 AAACCTCGCTGCTGAGACAGATGTCACTTAATGTCCTTGACACAAAAAGAGACAGC 636
|||||
DB 731 AAACCTCGCTGCTGAGACAGATGTCACTTAATGTCCTTGACACAAAAAGAGACAGC 672
QY 627 TCTGATTAAGCGCGTCAATGCGAGAAAGTGAATGCGCTTAATGTCGTGAACATG 686
|||||
DB 671 TCTGACAAAGCGCGTCAATGCGAGAAAGTGAATGCGCTTAATGTCGTGAACATG 612
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
|||||
DB 611 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 570
RESULT 24
US-09-605-785-366/C
Sequence 366, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 366
LENGTH: 1851
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-366
Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 507 GGACAAGCAAAAGAGAGCTGCTTACATCTGGCCTGCGCAATGGGAATTGAGAAGTACT 566
|||||
DB 791 GGACAAGCAAAAGAGAGCTGCTTACATCTGGCCTGCGCAATGGGAATTGAGAAGTACT 732
QY 567 AAACCTCGCTGCTGAGACAGATGTCACTTAATGTCCTTGACACAAAAAGAGACAGC 636
|||||
DB 731 AAACCTCGCTGCTGAGACAGATGTCACTTAATGTCCTTGACACAAAAAGAGACAGC 672
QY 627 TCTGATTAAGCGCGTCAATGCGAGAAAGTGAATGCGCTTAATGTCGTGAACATG 686
|||||
DB 671 TCTGACAAAGCGCGTCAATGCGAGAAAGTGAATGCGCTTAATGTCGTGAACATG 612
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
|||||
DB 611 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 570

RESULT 25
US-09-439-313-366/C
Sequence 366, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 366

LENGTH: 1851
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-366

Query Match 5.9%; Score 120; DB 4; Length 1851;

Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTCGCAATGGGAATTCAGAACTAGT 566
DB 791 GGACAGCAAAAGAGAGAGACTGCTCTACATCTGGCCCTCGCAATGGGAATTCAGAACTAGT 732
QY 567 AAAACTCGTCTGGAGACAGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCGTCTGGAGACAGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATTAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGACAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTATCCCAATATTCAGATGAGATGGAATACCACTCT 728
DB 611 CACTATCCCAATATTCAGATGAGATGGAATACCACTCT 570

RESULT 26

US-09-062-451-291/c
Sequence 291, Application US/09062451
Patent No. 6344550

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 291:

SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-291

Query Match 5.9%; Score 120; DB 4; Length 1851;

Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTCGCAATGGGAATTCAGAACTAGT 566

DB 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTCGCAATGGGAATTCAGAACTAGT 732
QY 567 AAAACTCGTCTGGAGACAGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCGTCTGGAGACAGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATTAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGACAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTATCCCAATATTCAGATGAGATGGAATACCACTCT 728
DB 611 CACTATCCCAATATTCAGATGAGATGGAATACCACTCT 570

RESULT 27

US-09-062-451-292/c
Sequence 292, Application US/09062451
Patent No. 6344550

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 292:

SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-292

Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTCGCAATGGGAATTCAGAACTAGT 566
DB 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTCGCAATGGGAATTCAGAACTAGT 732
QY 567 AAAACTCGTCTGGAGACAGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCGTCTGGAGACAGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATTAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGACAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612

```
QY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
|||||
Db 611 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 570

RESULT 28
US-09-352-616A-366/c
; Sequence 366, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-366

Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 566
|||||
Db 791 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 732

QY 567 AAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
|||||
Db 731 AAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 672

QY 627 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTAATGTCTGGAACATGG 686
|||||
Db 671 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTAATGTCTGGAACATGG 612

QY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
|||||
Db 611 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 570

RESULT 29
US-09-605-785-530
; Sequence 530, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-530

Query Match 5.9%; Score 120; DB 4; Length 1852;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 566
|||||
Db 1062 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 1121

QY 567 AAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
|||||
Db 1122 AAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 1181

QY 627 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTAATGTCTGGAACATGG 686
|||||
Db 1182 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTAATGTCTGGAACATGG 1241

QY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
|||||
Db 1242 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 1283

RESULT 30
US-09-439-313-530
; Sequence 530, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-530

Query Match 5.9%; Score 120; DB 4; Length 1852;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 566
|||||
Db 1062 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 1121

QY 567 AAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
|||||
Db 1122 AAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 1181
```

QY 627 TCTGATTAAGCGCGTACATGCCAGAAATGATGTCGCTTAACTGCTGGAACATGG 686
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1182 TCTGACAAAGCGCGTACATGCCAGAAATGATGTCGCTTAACTGCTGGAACATGG 1241
QY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1242 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 1283

RESULT 31
US-09-605-785-371

; Sequence 371, Application US/09605785
; Patent No. 6321716

; GENERAL INFORMATION:

; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1855)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-371

Query Match 5.9%; Score 120; DB 4; Length 1855;

Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1072 GGACAGCAAAAGAGAGAGACTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 1131
QY 567 AAACTCTGCTGCGACAGACGATGTCACCTTAATGCTCTTGACACAAAAAGAGAGACAGC 626
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1132 AAACTCTGCTGCGACAGACGATGTCACCTTAATGCTCTTGACACAAAAAGAGAGACAGC 1191
QY 627 TCTGATTAAGCGCGTACATGCCAGAAATGATGTCGCTTAACTGCTGGAACATGG 686
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1192 TCTGACAAAGCGCGTACATGCCAGAAATGATGTCGCTTAACTGCTGGAACATGG 1251
QY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1252 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 1293

RESULT 32
US-09-439-313-371
; Sequence 371, Application US/09439313

; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1855)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-371

Query Match 5.9%; Score 120; DB 4; Length 1855;

Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1072 GGACAGCAAAAGAGAGAGACTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 1131
QY 567 AAACTCTGCTGCGACAGACGATGTCACCTTAATGCTCTTGACACAAAAAGAGAGACAGC 626
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1132 AAACTCTGCTGCGACAGACGATGTCACCTTAATGCTCTTGACACAAAAAGAGAGACAGC 1191
QY 627 TCTGATTAAGCGCGTACATGCCAGAAATGATGTCGCTTAACTGCTGGAACATGG 686
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1192 TCTGACAAAGCGCGTACATGCCAGAAATGATGTCGCTTAACTGCTGGAACATGG 1251
QY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1252 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 1293

RESULT 33
US-09-062-451-297

; Sequence 297, Application US/09062451
; Patent No. 6344550

; GENERAL INFORMATION:

; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/062,451
: FILING DATE: 04-APR-1997
:
: CLASSIFICATION:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: MAKI, David J.
: REGISTRATION NUMBER: 31,392
: REFERENCE/DOCKET NUMBER: 210121.419C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
:
: INFORMATION FOR SEQ ID NO: 297:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1855 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-062-451-297

```

Query Match	5.9%	Score 120;	DB 4;	Length 1855;
Best Local Similarity	99.1%	Pred. No. 1.3e-41;		
Matches 220;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;
QY 507	GGACAGCAAAAAGAGAGCTGCTCTACATCTGCGCTCTGGCAATGGGAATTCAGAAAGTAGT			566
Db 1072	GGACAGCAAAAAGAGAGCTGCTCTACATCTGCGCTCTGGCAATGGGAATTCAGAAAGTAGT			1131
QY 567	AAAACTCCTGCTGGAGCAGACGATGTCAACTTATATGTCCCTTGACAAACAAAAGAGCAGC			626
Db 1132	AAAACTCGTGGCGAGCAGACGATGTCAACTTATATGTCCCTTGACAAACAAAAGAGCAGC			1191
QY 627	TCTGTAAAGGCCGTCACATGCGCAGGAAGATGAATGTGGCTTAATGTTGCTGGAACATGG			686
Db 1192	TCTGCAAAAGGCCGTCACATGCGCAGGAAGATGAATGTGGCTTAATGTTGCTGGAACATGG			1251
QY 687	CACGTATCCAAATATTCAGATGAATATGGAATACCACTCT			728
Db 1252	CACGTATCCAAATATTCAGATGAATATGGAATACCACTCT			1293

```

RESULT 34
US-09-352-616A-371
Sequence 371, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42768
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 371
LENGTH: 1855
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1855)
OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-371

```

Query Match	5.98;	Score 120;	DB 4;	Length 1855;
Best Local Similarity	99.18;	Pred. NO. 1.3e-41;		
Matches 220;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Q7 507 GGACAAGCAAAAGAGGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTCGAAGTACT 566

Db	1072	GGACAGCAAAAGGAGCTGCTTACCTCTGGCCCTTGCCCAATGGAAATTCAGAACTGT	1133
0y	567	AAAATCCCTGGTGACAGACGATGTCACTTAATGTCTTGCACACAAAAAGAGCAGC	626
Db	1132	AAAACCTGCTGGACAGACAGATGTCACTTAATGTCTTGCACACAAAAAGAGCAGC	1191
0y	627	TCTGATAAGGCCCTACAAATGCCAGAAATGAAATGGTAAATGTTGCTGGAACATGG	686
Db	1132	TCTGACAAAGGCCCTACAAATGCCAGAAATGAAATGGTAAATGTTGCTGGAACATGG	1251
0y	687	CACATGATCAAAATATTCACAGATGATGTGAATATACACTCT	728
Db	1232	CACATGATCAAAATATTCACAGATGATGTGAATATACACTCT	1293

```

RESULT 35
US-09-605-785-370
; Sequence 370, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT FILING DATE: 2000-06-27
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-370

```

Query Match	Score	ID	Length
Best Local Similarity	99.1%	Pred. No. 1,3e-41	
Matches	220	Conservative	0
		Mismatches	2
		Indels	0
		Gaps	0
QY	507	GGACAGCAAGAAAAGAGACTGCTCTACATCTGCGCTCTGTGCCAATGGGAATTCAAGAGTAGT	566
DB	1061	GGACAGCAAGCAAAAAGAGAGACTCTCTACATCTGCGCTCTGTGCCAATGGGAATTCAAGAGTAGT	1120
QY	567	AAACTCCGCTGGAGCAAGCATGTCACTTAATGCTTGAACAAAAGAGAGCAGC	626
DB	1121	AAAACTCGTGGAGCAAGCATGTCACTTAATGCTTGAACAAAAGAGAGCAGC	1180
QY	627	TCTGTAAAGGCCGTACATGCGCAGGAAGATGAATGTGGTTAATGTGCTGGAACATGG	686
DB	1181	TCTGCAAAAAGCCGTACATGCGCAGGAAGATGAATGTGGTTAATGTGCTGGAACATGG	1240
QY	687	CACGTATCCAAATATTCAGATGAGTATGGAAATACCACTCT	728
DB	1241	CACGTATCCAAATATTCAGATGAGTATGGAAATACCACTCT	1282

RESULT 36

US-09-439-313-370
Sequence 370, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiongchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Relfer, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439, 313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 370
LENGTH: 2184
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-370

Query Match 5.9%; Score 120; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAAGAGACTGCTCTACATCTGCGCTGCCAATGGGAATTCAGAGTAGT 566
DB 1061 GGACAGCAAAAAGAGACTGCTCTACATCTGCGCTGCCAATGGGAATTCAGAGTAGT 1120
QY 567 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAAGAGACAGC 626
DB 1121 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAAGAGACAGC 1180
QY 627 TCTGATAAGGCCGTCACATGTCAGAGATGATGATGTCGTTAATGTTGCTGGAACATGG 686
DB 1181 TCTGATAAGGCCGTCACATGTCAGAGATGATGATGTCGTTAATGTTGCTGGAACATGG 1240
QY 687 CACTGATCCAAATATTCAGATGATGATGAAATACCACTCT 728
DB 1241 CACTGATCCAAATATTCAGATGATGATGAAATACCACTCT 1282

RESULT 37
US-09-062-451-296
Sequence 296, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 296:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-296

Query Match 5.9%; Score 120; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAAGAGACTGCTCTACATCTGCGCTGCCAATGGGAATTCAGAGTAGT 566
DB 1061 GGACAGCAAAAAGAGACTGCTCTACATCTGCGCTGCCAATGGGAATTCAGAGTAGT 1120
QY 567 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAAGAGACAGC 626
DB 1121 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAAGAGACAGC 1180
QY 627 TCTGATAAGGCCGTCACATGTCAGAGATGATGATGTCGTTAATGTTGCTGGAACATGG 686
DB 1181 TCTGATAAGGCCGTCACATGTCAGAGATGATGATGTCGTTAATGTTGCTGGAACATGG 1240
QY 687 CACTGATCCAAATATTCAGATGATGATGAAATACCACTCT 728
DB 1241 CACTGATCCAAATATTCAGATGATGATGAAATACCACTCT 1282

RESULT 38
US-09-352-616A-370
Sequence 370, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, David C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiongchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352, 616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 370
LENGTH: 2184
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-370

Query Match 5.9%; Score 120; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAAGAGACTGCTCTACATCTGCGCTGCCAATGGGAATTCAGAGTAGT 566
DB 1061 GGACAGCAAAAAGAGACTGCTCTACATCTGCGCTGCCAATGGGAATTCAGAGTAGT 1120
QY 567 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAAGAGACAGC 626
DB 1121 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTCTTGACACAAAAGAGACAGC 1180

OY 627 TCGATTAAGGCGGTACATGCGCAGAGATGATGCGTTATGCTGGAACATGG 686
DB 1181 TCTGACAAAGCGGTACATGCGCAGAGATGATGCGTTATGCTGGAACATGG 1240
OY 687 CACTGATCCAAATATTCGAGATGATGGAATACCACCTCT 728
DB 1241 CACTGATCCAAATATTCGAGATGATGGAATACCACCTCT 1282

RESULT 39

US-09-605-785-367/C
Sequence 367, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqul
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 367
LENGTH: 668
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-367

Query Match 5.8%; Score 118; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 520 AGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGTAAACTCTGCTG 579
DB 548 AGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGTAAACTCTGCTG 489
OY 580 GACAGACGATGCACTTAATGCTCTTGACACAAAAAGAGCAGCTCTGATTAAGG 637
DB 488 GACAGACGATGCACTTAATGCTCTTGACACAAAAAGAGCAGCTCTGATTAAGG 431

RESULT 40

US-09-439-313-367/C
Sequence 367, Application US/09439313
Patent No. 6329505

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqul
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John

APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 367
LENGTH: 668
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-367

Query Match 5.8%; Score 118; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 520 AGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGTAAACTCTGCTG 579
DB 548 AGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGTAAACTCTGCTG 489
OY 580 GACAGACGATGCACTTAATGCTCTTGACACAAAAAGAGCAGCTCTGATTAAGG 637
DB 488 GACAGACGATGCACTTAATGCTCTTGACACAAAAAGAGCAGCTCTGATTAAGG 431

RESULT 41

US-09-062-451-293/C
Sequence 293, Application US/09062451
Patent No. 6344550

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 293:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-293

Query Match 5.8%; Score 118; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 AGAGCTGCTTACATCTGGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 579
 |||||||
 DB 548 AGACAGCTCTACATCTGGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 489
 |||||||
 QY 580 GACAGCAGTGTCACTTAATGTCTTGACACAAAGAGGACAGCTGTGATAAGG 637
 |||||||
 DB 488 GACAGCAGTGTCACTTAATGTCTTGACACAAAGAGGACAGCTGTGATAAGG 431
 |||||||

RESULT 42

US-09-352-616A-367/c
 ; Sequence 367, Application US/09352616A
 ; Patent No. 6395278
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.427C8
 ; CURRENT APPLICATION NUMBER: US/09/352,616A
 ; NUMBER OF SEQ ID NOS: 472
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 367
 ; LENGTH: 668
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-352-616A-367

Query Match 5.8%; Score 118; DB 4; Length 668;
 Best Local Similarity 100.0%; Fred. No. 9.7e-41;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 AGAGCTGCTTACATCTGGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 579
 |||||||
 DB 548 AGACAGCTCTACATCTGGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 489
 |||||||
 QY 580 GACAGCAGTGTCACTTAATGTCTTGACACAAAGAGGACAGCTGTGATAAGG 637
 |||||||
 DB 488 GACAGCAGTGTCACTTAATGTCTTGACACAAAGAGGACAGCTGTGATAAGG 431
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RESULT 43

US-08-991-789A-211/c
 ; Sequence 211, Application US/08991789A
 ; Patent No. 6225054
 ; GENERAL INFORMATION:
 ; APPLICANT: Frudakis, Tony N.
 ; Smith, John M.
 ; Reed, Steven G.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT AND DIAGNOSIS OF BREAST CANCER
 ; NUMBER OF SEQUENCES: 292
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed IP Law Group
 ; STREET: 701 Fifth Avenue, Suite 6300
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/991,789A
 ; FILING DATE: 11-Dec-1997
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 210121.419C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 211:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 454 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 211:

US-08-991-789A-211

Query Match 5.3%; Score 109; DB 4; Length 454;
 Best Local Similarity 99.1%; Fred. No. 6.1e-37;
 Matches 209; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGCTGCTTACATCTGGCTCTGCGCAATGGGAATTCAGAACTAGT 566
 |||||||
 DB 418 GGACAGCAAAAGAGAGCTGCTTACATCTGGCTCTGCGCAATGGGAATTCAGAACTAGT 359
 |||||||
 QY 567 AAACCTCTGCTGAGAGAGATGTCACTTAATGTCTTGACACAAAGAGAGAGC 626
 |||||||
 DB 358 AAACCTGCTGCTGAGAGAGATGTCACTTAATGTCTTGACACAAAGAGAGAGC 299
 |||||||
 QY 627 TCTGATTAAGGCGGTACATCCAGGAAGATGTCCTTAATGTCTGGAACATGG 686
 |||||||
 DB 298 TCTGACAAAGGCGGTACATCCAGGAAGATGTCCTTAATGTCTGGAACATGG 239
 |||||||
 QY 687 CACTGATCCAAATATTCAGATGATGGA 717
 |||||||
 DB 238 CACTGATCCAAATATTCAGATGATGGA 208
 |||||||

RESULT 44

US-09-062-451-211/c
 ; Sequence 211, Application US/09062451
 ; Patent No. 6344350
 ; GENERAL INFORMATION:
 ; APPLICANT: Frudakis, Tony N.
 ; Smith, John M.
 ; Reed, Steven G.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT AND DIAGNOSIS OF BREAST CANCER
 ; NUMBER OF SEQUENCES: 297
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/062,451
 ; FILING DATE: 04-Apr-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Makl, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.419C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 211:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 454 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-211

Query Match 5.38; Score 109; DB 4; Length 454;
Best Local Similarity 99.18; Pred. No. 6.1e-37;
Matches 209; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 566
DB 418 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 359
QY 567 AAACTCTGCTGGACAGACGATGTCAACTTAATGCTTGCCTTGACAACAAGAGAGACAGC 626
DB 358 AAACTCTGCTGGACAGACGATGTCAACTTAATGCTTGCCTTGACAACAAGAGAGACAGC 299
QY 627 TCTGATAAAGCGCTGACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 686
DB 298 TCTGACAAGCGCTGACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 239
QY 687 CACTGATCCAATAATATTCAGATGAGTATGA 717
DB 238 CACTGATCCAATAATATTCAGATGAGTATGA 208

RESULT 45

US-09-598-326-211/C
Sequence 211, Application US/09598326
Patent No. 6423496

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
Reed, Steven G.
Smith, John M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 247

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,326

FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.41901

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4800

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 211:

SEQUENCE CHARACTERISTICS:

LENGTH: 454 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 211:

US-09-598-326-211

QY 507 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 566
DB 418 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 359
QY 567 AAACTCTGCTGGACAGACGATGTCAACTTAATGCTTGCCTTGACAACAAGAGAGACAGC 626
DB 358 AAACTCTGCTGGACAGACGATGTCAACTTAATGCTTGCCTTGACAACAAGAGAGACAGC 299
QY 627 TCTGATAAAGCGCTGACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 686
DB 298 TCTGACAAGCGCTGACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 239
QY 687 CACTGATCCAATAATATTCAGATGAGTATGA 717
DB 238 CACTGATCCAATAATATTCAGATGAGTATGA 208

Search completed: November 8, 2002, 13:36:08
Job time: 110.703 secs

Query Match 5.38; Score 109; DB 4; Length 454;
Best Local Similarity 99.18; Pred. No. 6.1e-37;

Matches 209; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 06:30:33 ; Search time 379.723 Seconds
(without alignments)
12098.502 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atggtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaa 2040

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 15

Total number of hits satisfying chosen parameters: 113580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	21 AAC81013	Human B1Agl antiig
2	2040	100.0	2040	22 AA167213	B305D Isoform C sp
3	2040	100.0	2040	22 AAS63809	Human prostate cdn
4	2040	100.0	2040	22 AAH93716	Human prostate-cpn
5	2040	100.0	2040	22 AAH85030	Human prostate-spe
6	2040	100.0	2040	22 AAH02781	Prostate tumour an
7	2040	100.0	2040	24 ABL95180	Human B305D splice
8	2040	100.0	2040	24 AAS99859	Breast tumour-spec
9	1989	97.5	2040	21 AAA06600	Human immunogenic

10	1551	76.0	2000	21 AAC81012	Human B1Agl antiig
11	1551	76.0	2000	22 AA167212	B305D Isoform C sp
12	1551	76.0	2000	22 AAS63808	Human prostate cdn
13	1551	76.0	2000	22 AAH93715	Human prostate-spe
14	1551	76.0	2000	22 AAH85029	Human prostate-spe
15	1551	76.0	2000	22 AAH02780	Prostate tumour an
16	1551	76.0	2000	24 ABL95179	Human B305D splice
17	1551	76.0	2000	24 AAS99857	Breast tumour-spec
18	1500	73.5	2000	21 AAA06599	Human immunogenic
19	1128	55.3	1155	21 AAC81011	Human B1Agl antiig
20	1128	55.3	1155	21 AAA06598	Human immunogenic
21	1128	55.3	1155	22 AA167211	B305D Isoform C sp
22	1128	55.3	1155	22 AAS63807	Human prostate cdn
23	1128	55.3	1155	22 AAH93714	Human prostate-cpn
24	1128	55.3	1155	22 AAH85028	Human prostate-spe
25	1128	55.3	1155	22 AAH02779	Prostate tumour an
26	1128	55.3	1155	24 ABL95178	Human B305D splice
27	1128	55.3	1155	24 AAS99857	Breast tumour-spec
28	1044	51.2	1590	24 AAS99869	Breast tumour-spec
29	975	47.8	1155	24 AAS99872	Breast tumour-spec
30	491	24.1	1512	19 AAV68995	DNA molecule encod
31	491	24.1	1512	21 AAC81006	Human B1Agl antiig
32	491	24.1	1512	21 AAA06593	Human immunogenic
33	491	24.1	1512	22 AAS63802	Human prostate cdn
34	491	24.1	1512	22 AAH93709	Human prostate-spe
35	491	24.1	1512	22 AAH85023	Human prostate-spe
36	491	24.1	1512	22 AAH02774	Prostate tumour an
37	491	24.1	1512	24 ABL95173	Human B305D splice
38	491	24.1	1512	24 AAB46896	Human breast tumou
39	491	24.1	1512	24 AAS99852	Breast tumour-spec
40	252	12.4	1853	19 AAV68996	DNA molecule encod
41	252	12.4	1853	21 AAC81007	Human B1Agl antiig
42	252	12.4	1853	21 AAA06594	Human immunogenic
43	252	12.4	1853	22 AAS63803	Human prostate cdn
44	252	12.4	1853	22 AAH93710	Human prostate-spe
45	252	12.4	1853	22 AAH85024	Human prostate-spe

ALIGNMENTS

RESULT 1
AAC81013
ID AAC81013 strand: cDNA; 2040 BP.
AAC81013:
13-FEB-2001 (first entry)
Human B1Agl antigen splice isoform B1C-9-16 cDNA.
Human; breast tumour-specific antigen; cytosolic; vaccine;
breast cancer; B1Agl; B1Agl; B1Agl; ss.
Homo sapiens.
WO200061753-A2.
19-OCT-2000.
07-APR-2000; 2000WO-US09312.
09-APR-1999; 99US-0288198.
28-OCT-1999; 99US-0428735.
23-MAR-2000; 2000US-0534825.
(CORI-) CORIXA CORP.
Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
WPI; 2000-628403/60.
P-PSDB; AAB28630.

PT An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX
PS Claim 4; Page 178; 187pp; English.
XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumor tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;.
Query Match 100.0%; Score 2040; DB 21; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTTGAGTGAATCCATCCGCGTCCCTCTTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGTGAATCCATCCGCGTCCCTCTTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAACCTGGGCACTTCTGGAGACAGAGACTCTGCTATGAAGACACTAGAGCAAG 180
DB 121 AGCAACCTGGGCACTTCTGGAGACAGAGACTCTGCTATGAAGACACTAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCTTCTGGAGACAGAGACTCTGCTATGAAGACACTAGAGCAAGTGGGCAAG 300
DB 241 GGGCTTCTGGAGACAGAGACTCTGCTATGAAGACACTAGAGCAAGTGGGCAAG 300
QY 301 TGGTGGTGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB 301 TGGTGGTGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
QY 361 GGAAGCTACAGTACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
DB 361 GGAAGCTACAGTACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
QY 421 GACAAAGCTCCACAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
DB 421 GACAAAGCTCCACAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
QY 481 CTCAGGGAACCTGACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGGGAACCTGACGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGACAGACAGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGACAGACAGTCACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGGCCGATCAATGACAGAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGGCCGATCAATGACAGAGATGAA 660
QY 661 TGTGCGTTAATGTGTGGAACATGGCACTGATCAATATTTCCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTGTGGAACATGGCACTGATCAATATTTCCAGATGATGAAAT 720

QY 721 ACCACTGGACACTACGCTATCTATATGAAGATTAATTAAGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTGGACACTACGCTATCTATATGAAGATTAATTAATTAAGCCAAAGCACTGCTCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAACAGCAGTGGCTCACACCAGTCTTGGTGTGA 840
DB 781 TATGTCCTGATATGCAATCAAAAACAGCAGTGGCTCACACCAGTCTTGGTGTGA 840
QY 841 CATAGCAAAAACAGCAAGTCTGCAATTTTATTCAGAAAAAGCAATTTAAAGCA 900
DB 841 CATAGCAAAAACAGCAAGTCTGCAATTTTATTCAGAAAAAGCAATTTAAAGCA 900
QY 901 CTGATGATATGGAAGAGAGCTCTCATATCTTATGTTGGATGATGAGCAAGTATA 960
DB 901 CTGATGATATGGAAGAGAGCTCTCATATCTTATGTTGGATGATGAGCAAGTATA 960
QY 961 GTCAGCTTCTACTTGAACCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTCAGCTTCTACTTGAACCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGTCTCAAGGCGAGTCAAAATAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAAAAAGTCTCAAGGCGAGTCAAAATAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGCTAATTAATGATTAATCTCTCAAAAGAGAGCAAGACCTGAAATACAGCAATTT 1380
DB 1321 AATGCTAATTAATGATTAATCTCTCAAAAGAGAGCAAGACCTGAAATACAGCAATTT 1380
QY 1381 CCTGCAACGAAATGAAAGATATCACAGATTTGCGAATTAATGATTTGATGACTACAAAGAA 1440
DB 1381 CCTGCAACGAAATGAAAGATATCACAGATTTGCGAATTAATGATTTGATGACTACAAAGAA 1440
QY 1441 AAACGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
DB 1441 AAACGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACAAAAGCTTGAAGGCGAGTCAAAAATGGCCAGCCAGAGAAAAATCT 1560
DB 1501 TCAGAGAGAGAGTACAAAAGCTTGAAGGCGAGTCAAAAATGGCCAGCCAGAGAAAAATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 CAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 GAAATGAAGAGAGAGAGTACTCATGCGATTTCCAGAAAACTGACTTAATGATGACC 1680
DB 1621 GAAATGAAGAGAGAGAGTACTCATGCGATTTCCAGAAAACTGACTTAATGATGACC 1680
QY 1681 ACTGCTGGCAATGGTGAATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ACTGCTGGCAATGGTGAATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGCAAAAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGCAAAAATGATACTCAG 1800

OY 1801 AAGCAATTTTGTGAAGAACAGACACTGGAATATTAACAGATGAGATTCTGATTATGAA 1860
 |||||||
 Db 1801 AAGCAATTTTGTGAAGAACAGACACTGGAATATTAACAGATGAGATTCTGATTATGAA 1860
 OY 1861 GAAAGCAGATGAGATGTTGTTGAAAAATGAATTCGACCTTTCTTGTGTTAAGAA 1920
 |||||||
 Db 1861 GAAAGCAGATGAGATGTTGTTGAAAAATGAATTCGACCTTTCTTGTGTTAAGAA 1920
 OY 1921 GAAAAAGACATCTTCGATGAAAAATAGTAGTTCGGGGAAGAAATGCGCATGAGACTG 1980
 |||||||
 Db 1921 GAAAAAGACATCTTCGATGAAAAATAGTAGTTCGGGGAAGAAATGCGCATGAGACTG 1980
 OY 1981 GAGCTAGACACATGAATGAAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
 |||||||
 Db 1981 GAGCTAGACACATGAATGAAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040

RESULT 2

AA167213 standard; cDNA: 2040 BP.

AA167213;

11-FEB-2002 (first entry)

B305D isoform C splice variant 3 encoding cDNA.

Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
 cancer: B305D; ss.

Homo sapiens.

Location/Qualifiers

Key 1.2016

/tag= a /Product= "B305D isoform C splice variant"

W0200175171-A2.

11-OCT-2001.

02-APR-2001; 2001WO-US10631.

03-APR-2000; 2000US-194241P.

20-JUL-2000; 2000US-219862P.

27-JUL-2000; 2000US-221300P.

18-DEC-2000; 2000US-256592P.

(CORI-) CORIXA CORP.

Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;

WPI: 2001-626449/72.

P-PSDB; AAG65978.

Identifying tissue (tumour)-specific polynucleotides overexpressed in

tissue of interest as compared to control tissue, for detecting cancer

cells in patient. comprises DNA microarray analysis or quantitative

polymerase chain reaction -

Claim 4; Page 94-95; 127pp; English.

The invention relates to identifying tissue-specific polynucleotides (P)
 that involves performing a genetic subtraction to identify pool of (P)
 from tissue of interest (TI), performing DNA microarray analysis to
 identify first subset of polynucleotides (SP1) at least 2-fold over
 expressed in TI, and performing quantitative polymerase chain reaction
 (PCR) analysis on SP1 to identify second subset of (P). The method is
 useful for determining the presence or absence of a cancer cell in a
 patient, monitoring the progression of cancer in a patient using a
 biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
 urine or a tumour biopsy sample. The methods are useful for determining
 the presence or absence of or monitoring progression of prostate, breast,

CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
 CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
 CC sequence represents a cDNA encoding a B305D isoform C splice variant.
 XX

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 100.0%; Score 2040; DB 22; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGTTGAGGTGATTCATGCGCGCTGCTCTTGTGAAGAACCATTTGGTCTC 60
 |||||||
 Db 1 ATGGTGTTGAGGTGATTCATGCGCGCTGCTCTTGTGAAGAACCATTTGGTCTC 60
 OY 61 AAGACCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
 |||||||
 Db 61 AAGACCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
 OY 121 ACGAAGTGGGACCTTCTGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAG 180
 |||||||
 Db 121 ACGAAGTGGGACCTTCTGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAG 180
 OY 181 ATGGGCAAGTGTGCGCCGACCTGCTCCCTGCTCAGGGGAGTGGCAAGACAGTG 240
 |||||||
 Db 181 ATGGGCAAGTGTGCGCCGACCTGCTCCCTGCTCAGGGGAGTGGCAAGACAGTG 240
 OY 241 GGGCGTTCTGGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
 |||||||
 Db 241 GGGCGTTCTGGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
 OY 301 TGGTCTGCGACCTGCTCCCTGCTGAGGGGAGCGGCAAGAGAGTGGGCGCTGG 360
 |||||||
 Db 301 TGGTCTGCGACCTGCTCCCTGCTGAGGGGAGCGGCAAGAGAGTGGGCGCTGG 360
 OY 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGACAGCTCCGTGAGAAATGTG 420
 |||||||
 Db 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGACAGCTCCGTGAGAAATGTG 420
 OY 421 GACAAAGCTCCACAGAGTGCCTTTCATGAGCCAGGACAGCTCCGTGAGAAATGTG 480
 |||||||
 Db 421 GACAAAGCTCCACAGAGTGCCTTTCATGAGCCAGGACAGCTCCGTGAGAAATGTG 480
 OY 481 CTCGAGGACACTGAGCTGATGACAAAGGACAAAGAGAGTCTCATATCTGGCC 540
 |||||||
 Db 481 CTCGAGGACACTGAGCTGATGACAAAGGACAAAGAGAGTCTCATATCTGGCC 540
 OY 541 TCTGCCAATGGGAATTCAGAAATGATAAACTCTGCTGACAGACGATGCACTTAAT 600
 |||||||
 Db 541 TCTGCCAATGGGAATTCAGAAATGATAAACTCTGCTGACAGACGATGCACTTAAT 600
 OY 601 GTCTTTGACAAACAAAGAGACAGCTCTGATTAAGGCCGTCACATGCGAGAAATGAA 660
 |||||||
 Db 601 GTCTTTGACAAACAAAGAGACAGCTCTGATTAAGGCCGTCACATGCGAGAAATGAA 660
 OY 661 TGTGGTTAATGTTGCTGTAACATGGAAGTCCCAATTTCCAGATGAGATGGAAT 720
 |||||||
 Db 661 TGTGGTTAATGTTGCTGTAACATGGAAGTCCCAATTTCCAGATGAGATGGAAT 720
 OY 721 ACCACTGTCACCTAGCTATCTATATGAAGTAATTAATGAGCAAGCACTGCTTTA 780
 |||||||
 Db 721 ACCACTGTCACCTAGCTATCTATATGAAGTAATTAATGAGCAAGCACTGCTTTA 780
 OY 781 TATGTTGCTGATATGATTCAAAAAACAAGCATGAGCTTCACACCTTTACTTGGTGA 840
 |||||||
 Db 781 TATGTTGCTGATATGATTCAAAAAACAAGCATGAGCTTCACACCTTTACTTGGTGA 840
 OY 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAGCAATTTAAATCA 900
 |||||||
 Db 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAGCAATTTAAATCA 900
 OY 901 CTGATAGATATGGAAGAGCTCTCTCATACTTCTGATGTTGATGATCAGCAAGTATA 960
 |||||||
 Db 901 CTGATAGATATGGAAGAGCTCTCTCATACTTCTGATGTTGATGATCAGCAAGTATA 960

121 AGCAAGTGGGCACTTGTGGAGACCAGAGACTGTATGAAGACACTCAGAGCAAG 180
121 AGCAAGTGGGCACTTGTGGAGACCAGAGACTGTATGAAGACACTCAGAGCAAG 180
181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGCgtg 240
181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGCgtg 240
241 GGGCGTCTGGAGACCAGACGACTGCTATGAAGACTCAGGAACAAGATGGCAAG 300
241 GGGCGTCTGGAGACCAGACGACTGCTATGAAGACTCAGGAACAAGATGGCAAG 300
301 TGGTGTGGCACTGCTTCCCTGCTGAGGGGGAGGGAAGCAAGGAGGGGCGTGG 360
301 TGGTGTGGCACTGCTTCCCTGCTGAGGGGGAGGGAAGCAAGGAGGGGCGTGG 360
361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACAGGTCCGTGGAGAAATCTg 420
361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACAGGTCCGTGGAGAAATCTg 420
421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCATGCTATg 480
421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCATGCTATg 480
481 CTCAGGACACTGACGCTGAACAAGAGCAAGCAAAAGAGGCTGCTACACTGGGC 540
481 CTCAGGACACTGACGCTGAACAAGAGCAAGCAAAAGAGGCTGCTACACTGGGC 540
541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACGAGATGTCAACTTAAT 600
541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACGAGATGTCAACTTAAT 600
601 GTCCCTTGAACAACAAAAGAGGACAGCTGTGATTAAGCCGTACATGCCAGAAATGAA 660
601 GTCCCTTGAACAACAAAAGAGGACAGCTGTGATTAAGCCGTACATGCCAGAAATGAA 660
661 TGTGCGTAAATGTGCTGGAAACATGGCAGTCCAAATATTCCAGATGATGTAAGAAAT 720
661 TGTGCGTAAATGTGCTGGAAACATGGCAGTCCAAATATTCCAGATGATGTAAGAAAT 720
721 ACCACTGTGACACTGACGCTATCTATAATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
721 ACCACTGTGACACTGACGCTATCTATAATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
781 TATGGCTGTGATATGCAATCAAAAACAGCATGGCCTCACACCTGTACTTGGTGA 840
781 TATGGCTGTGATATGCAATCAAAAACAGCATGGCCTCACACCTGTACTTGGTGA 840
841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAAAACAGCAATTTAAATGCA 900
841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAAAACAGCAATTTAAATGCA 900
901 CTGGATAGATATGAAGAAGTCTCTCATATCTGTATGTTGTGATCAGCAAGTATA 960
901 CTGGATAGATATGAAGAAGTCTCTCATATCTGTATGTTGTGATCAGCAAGTATA 960
961 GTGAGCGCTCTACTGTGAGCAAAATATGATGTATCTTCAAGATATATCTGACAGAG 1020
961 GTGAGCGCTCTACTGTGAGCAAAATATGATGTATCTTCAAGATATATCTGACAGAG 1020
1021 GCCAGAGATATGCTTCTATGATCATCATGTAATTTGGCAGTACTTCTGCTAC 1080
1021 GCCAGAGATATGCTTCTATGATCATCATGTAATTTGGCAGTACTTCTGCTAC 1080
1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAAAGGCAAGTGAAGATGAGCCAGAGAAA 1200
1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAAAGGCAAGTGAAGATGAGCCAGAGAAA 1200

1201 ATGCTCAAGAACCAAAATTAATTAAGATGTGATAGAGAGGTGAAGAAATGAAG 1260
1201 ATGCTCAAGAACCAAAATTAATTAAGATGTGATAGAGAGGTGAAGAAATGAAG 1260
1261 AAGCATGAAGATTAATGTGGATTACTAGAAAACCTGACTAATGTGCTACTGTGGC 1320
1261 AAGCATGAAGATTAATGTGGATTACTAGAAAACCTGACTAATGTGCTACTGTGGC 1320
1321 AATGTGATTAATGGATTAATTCCTCAAGAGAGAGCAAAACCTGAAAAATGCAATTT 1380
1321 AATGTGATTAATGGATTAATTCCTCAAGAGAGAGCAAAACCTGAAAAATGCAATTT 1380
1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGGCAATTTAGTTCTGCTCAAGAA 1440
1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGGCAATTTAGTTCTGCTCAAGAA 1440
1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACCTTAAAGCTGACA 1500
1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACCTTAAAGCTGACA 1500
1501 TCAGAGGAAGAGTCACAAAAGCTTGAAGGCGAGTGAAGATGGCCAGAGAAAGATCT 1560
1501 TCAGAGGAAGAGTCACAAAAGCTTGAAGGCGAGTGAAGATGGCCAGAGAAAGATCT 1560
1561 CAAGAACCAAGAAATTAATTAAGATGGTGAATGAGAGCTGAAAAATTTTATGGCTATCGAA 1620
1561 CAAGAACCAAGAAATTAATTAAGATGGTGAATGAGAGCTGAAAAATTTTATGGCTATCGAA 1620
1621 GAAATGAAGAGCAGGAAAGTACTCATGTGCGATTCAGAAAACTGACTAATGGTGGC 1680
1621 GAAATGAAGAGCAGGAAAGTACTCATGTGCGATTCAGAAAACTGACTAATGGTGGC 1680
1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGCAAAACCTGAAAGC 1740
1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGCAAAACCTGAAAGC 1740
1741 CAGCAATTTCTGACACTGGAATGAAGATCAACAGTACAGCAACAAAATGATACTCAG 1800
1741 CAGCAATTTCTGACACTGGAATGAAGATCAACAGTACAGCAACAAAATGATACTCAG 1800
1801 AAGCAATTTTGTGAAGAAACAGAACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
1801 AAGCAATTTTGTGAAGAAACAGAACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
1861 GAAAACAGATAGAAATGCTGTGAAAAAATGAATTTGAGCTTCTCTGTAGTGAAGAAA 1920
1861 GAAAACAGATAGAAATGCTGTGAAAAAATGAATTTGAGCTTCTCTGTAGTGAAGAAA 1920
1921 GAAAAAGACATCTTGCATGAAAAATAGATTGCGGGAAGAAATTCCTGCTAAGACTG 1980
1921 GAAAAAGACATCTTGCATGAAAAATAGATTGCGGGAAGAAATTCCTGCTAAGACTG 1980
1981 GAGCTAGACAAATGAAGATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040
1981 GAGCTAGACAAATGAAGATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040

RESULT 4
AAH93716
ID AAH93716 standard; cDNA; 2040 BP.
XX
XX AAH93716;
AC
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #10.
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX Homo sapiens.
XX
PN WO200151633-A2.

XX 19-JUL-2001.
PD
XX 16-JAN-2001: 2001MO-US01574.
PF
XX 14-JAN-2000: 2000US-0483672.
PR
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kales MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skeiky YAW,
PI Wang A, Mesgher MJ;
XX WPI: 2001-425873/45.
DR
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
PS
XX Claim 1: Page 348; 543pp: English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 2040 BP: 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCGGCTGCTCTCTCTGTGAAGAAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATGCGGCTGCTCTCTCTGTGAAGAAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGAGGAGAGGCGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGAGGAGAGGCGCAAG 120
QY 121 AGCAACGTGGGCACTTGTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTGTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAACGTG 240
QY 241 GGGCTCTTGTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAG 300
DB 241 GGGCTCTTGTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGAGGAGGAGGCGCAAGAGGTTGGGCTTGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGAGGAGGAGGCGCAAGAGGTTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCACTCCGTTGGAAGATCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCACTCCGTTGGAAGATCTG 420
QY 421 GACAACTCCACAGAGTGGTGGTGAAGTCCCAAGAAAGATCTCATGTGATG 480
DB 421 GACAACTCCACAGAGTGGTGGTGAAGTCCCAAGAAAGATCTCATGTGATG 480

QY 481 CTCAGGACACTGACGTGAACAAGAAAGACAAAGAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAAAGACAAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTGAGAGTAAGTAAACCTCTGCTGGACAGACATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTGAGAGTAAGTAAACCTCTGCTGGACAGACATGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGACAGCTGTGTAAGGCCGTACAAATCCAGGAAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGACAGCTGTGTAAGGCCGTACAAATCCAGGAAGATGAA 660
QY 661 TGTGCGTTAAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGTAAT 720
DB 661 TGTGCGTTAAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGTAAT 720
QY 721 ACCACTCTGCACCTACCTATCTATTAAGATTAATGATGATGATGATGATGATGATGAT 780
DB 721 ACCACTCTGCACCTACCTATCTATTAAGATTAATGATGATGATGATGATGATGATGAT 780
QY 781 TATGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TATGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGAGAGAGACTCTCTCATACTGCTGTATGTTGATGATGATGATGATGAT 960
DB 901 CTGATGATATGAGAGAGACTCTCTCATACTGCTGTATGTTGATGATGATGATGATGAT 960
QY 961 GTGAGCTTCTACTGTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 GTGAGCTTCTACTGTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCGATAC 1080
DB 1021 GCCAGAGATGATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCGATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACGCAATCCAGAAACAGATTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACGCAATCCAGAAACAGATTAAAG 1140
QY 1141 CTGACATCAGAGGAAGTACAAAGGTCAAAAGGCAAGTGAATATACCGCCAGAGAA 1200
DB 1141 CTGACATCAGAGGAAGTACAAAGGTCAAAAGGCAAGTGAATATACCGCCAGAGAA 1200
QY 1201 ATGTCTCAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGTCTCAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 AAGCATGAAGTAATTAATGAGGATTAATGAGGATTAATGAGGATTAATGAGGATTAAT 1320
DB 1261 AAGCATGAAGTAATTAATGAGGATTAATGAGGATTAATGAGGATTAATGAGGATTAAT 1320
QY 1321 AATGCTATATGATTAATTAATCTCAAGAGGAAGCAAGCAACCTGAAATTAATGATTAAT 1380
DB 1321 AATGCTATATGATTAATTAATCTCAAGAGGAAGCAAGCAACCTGAAATTAATGATTAAT 1380
QY 1381 CTTGCAACAGAAATGAAAGATATCACAGATTTGCAATTAATGATTAATGATTAATGATTAAT 1440
DB 1381 CTTGCAACAGAAATGAAAGATATCACAGATTTGCAATTAATGATTAATGATTAATGATTAAT 1440
QY 1441 AAACAGATGCCAAATAATCTCTTCTGAAAAACGCAACCCAGAACAGACTTAATGATGAT 1500
DB 1441 AAACAGATGCCAAATAATCTCTTCTGAAAAACGCAACCCAGAACAGACTTAATGATGAT 1500
QY 1501 TCAGAGGAAGAGTACAAAGGCTTGAAGGAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGT 1560
DB 1501 TCAGAGGAAGAGTACAAAGGCTTGAAGGAGTGAAGATGAGGAGGAGGAGGAGGAGGAGT 1560

QY 1561 CAGAACCCAGAAATTAATAGAGTGTATAGAGAGTAAATTTATGCTATCGAA 1620
 |||||||
 Db 1561 CAGAACCCAGAAATTAATAGAGTGTATAGAGAGTAAATTTATGCTATCGAA 1620
 QY 1621 GAAATGAAGAACGACGGAATCTATGTCGATTCGCCAGAAACCTGATAGTGCC 1680
 |||||||
 Db 1621 GAAATGAAGAACGACGGAATCTATGTCGATTCGCCAGAAACCTGATAGTGCC 1680
 QY 1681 ACTGTCGCAATGATGATGATGATTAATCTCTCCAGGAGAGAGAACCTGAAAGC 1740
 |||||||
 Db 1681 ACTGTCGCAATGATGATGATGATTAATCTCTCCAGGAGAGAGAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAGTGCAGAACAAATGATCTGAG 1800
 |||||||
 Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAGTGCAGAACAAATGATCTGAG 1800
 QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGATGATTCATGAA 1860
 |||||||
 Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGATGATTCATGAA 1860
 QY 1861 GAAAAGCAGATGAGAGTGTGTAATAATGAAATTCGAGCTTCTCTAGTTGTAAGAA 1920
 |||||||
 Db 1861 GAAAAGCAGATGAGAGTGTGTAATAATGAAATTCGAGCTTCTCTAGTTGTAAGAA 1920
 QY 1921 GAAAAAGACATCTTGACATGAAATATGACGTTGCGGAGAAATTCGATGTAAGCTG 1980
 |||||||
 Db 1921 GAAAAAGACATCTTGACATGAAATATGACGTTGCGGAGAAATTCGATGTAAGCTG 1980
 QY 1981 GAGCTAGACACAAATGAAATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
 |||||||
 Db 1981 GAGCTAGACACAAATGAAATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 5

AAH85030
 ID AAH85030 standard; cDNA: 2040 BP.

AAH85030;

25-SEP-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #10.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

chromosome 22q11.2; prostate-specific protein; chromosome 1;

prostate specific antigen; PSA; ss.

Homo sapiens.

MO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

Kalos MD, Reltter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;

WPI; 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a

prostate-specific protein, useful in the diagnosis and therapy of prostate cancer -

variant. Also described are polynucleotides (NI) encoding (PI) and (CC (NI) have cytostatic activity and can be used in vaccine production. CC The polypeptides, nucleic acids and antibodies from the present CC Invention are useful in the diagnosis and therapy of prostate cancer. CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome CC region. Prostate specific antigen (PSA) P501S was located on CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99777 represent CC polynucleotide and polypeptide sequences used in the exemplification of the present invention.

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other:

Query Match 100.0%; Score 2040; DB 22; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTGAAAGCCATTTGGTCTC 60

Db 1 ATGTGTGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTGAAAGCCATTTGGTCTC 60

QY 61 AGAGCAAGATGGCGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120

Db 61 AGAGCAAGATGGCGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120

QY 121 AGCAAGTGGGCACTTCTGAGACACGACGACCTGCTGATGAAGACACTCAGAGCAAG 180

Db 121 AGCAAGTGGGCACTTCTGAGACACGACGACCTGCTGATGAAGACACTCAGAGCAAG 180

QY 181 ATGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGCTG 240

Db 181 ATGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGCTG 240

QY 241 GCGCTTCTGAGACACGACGACCTGCTGATGAAGACACTCAGAGCAAGTGGCAAG 300

Db 241 GCGCTTCTGAGACACGACGACCTGCTGATGAAGACACTCAGAGCAAGTGGCAAG 300

QY 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGAGTGGGCGCTGG 360

Db 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGAGTGGGCGCTGG 360

QY 361 GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGAGTACCAAGTCCGTGAGAGATG 420

Db 361 GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGAGTACCAAGTCCGTGAGAGATG 420

QY 421 GACAAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAGATCTCATGCTCATG 480

Db 421 GACAAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAGATCTCATGCTCATG 480

QY 481 CTCAGGACACTGAGCTGAGCAAGAGCAAGAGAGAGAGTCTTACATCTGGCC 540

Db 481 CTCAGGACACTGAGCTGAGCAAGAGCAAGAGAGAGAGTCTTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAGAACTAGTAATAACTCTGCTGAGAGAGATGTCACCTTAAT 600

Db 541 TCTGCCAATGGGAATTCAGAACTAGTAATAACTCTGCTGAGAGAGATGTCACCTTAAT 600

QY 601 GTCTTGGACAAACAAAAGAGACAGCTCTGATTAAGGCGGCTGATGCGCAGAGATGAA 660

Db 601 GTCTTGGACAAACAAAAGAGACAGCTCTGATTAAGGCGGCTGATGCGCAGAGATGAA 660

QY 661 TGTGCTTAATGTTCTGAGACATGCACTGATCCAAATATTCAGATGATGAGAAAT 720

Db 661 TGTGCTTAATGTTCTGAGACATGCACTGATCCAAATATTCAGATGATGAGAAAT 720

QY 721 ACCACTGCACTACGATCTATATATGAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780

Db 721 ACCACTGCACTACGATCTATATATGAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780

QY 781 TATGTGCTGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840

Db 781 TATGTGCTGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840

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QY 841 CATGACCAAAAAACAGCAAGTCGTGAAAATTTTAAATCAGAAAAAGCGAATTTAAATGCA 900
    |||
Db 841 CATGACCAAAAAACAGCAAGTCGTGAAAATTTTAAATCAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGAGATAGATATGGAAGGAGCTGCTCATCTCTGCTGATGATGTTGTGATAGACAAGTATA 960
    |||
Db 901 CTGAGATAGATATGGAAGGAGCTGCTCATCTCTGCTGATGATGTTGTGATAGACAAGTATA 960
QY 961 GTGAGCTTCTACTTGTAGCAAAAATTTGATGTATCTCTCAAGATCTATCTGGACAGAGC 1020
    |||
Db 961 GTGAGCTTCTACTTGTAGCAAAAATTTGATGTATCTCTCAAGATCTATCTGGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTTGACTAC 1080
    |||
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTTGACTAC 1080
QY 1081 AAGAAAAACAGTGTCTAAAAATCTCTTGAAGAACAGCAATCCAGACAAAGCTTAAAG 1140
    |||
Db 1081 AAGAAAAACAGTGTCTAAAAATCTCTTGAAGAACAGCAATCCAGACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGGAGAGTGCACAAAGGTTCAAGGCGAGTAAATAGCCAGCAGAGAAA 1200
    |||
Db 1141 CTGACATCAGAGGAGAGTGCACAAAGGTTCAAGGCGAGTAAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACACAGAAATTAATTAAGATGTATAGAGAGGTTGAAGAAATGAAG 1260
    |||
Db 1201 ATGTCTCAAGAACACAGAAATTAATTAAGATGTATAGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTGGGATTAATGAAAAACCTGACTAATGTGTGCTGCTGCGC 1320
    |||
Db 1261 AAGCATGAAAGTAAATATGTGGGATTAATGAAAAACCTGACTAATGTGTGCTGCTGCGC 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAAGACCTGAAATTCAGCAATTT 1380
    |||
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAAGACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTTCTGACTACAAAGAA 1440
    |||
Db 1381 CCTGACACAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTTCTGACTACAAAGAA 1440
QY 1441 AATGATGCGCAAAATTAATCTTCTGAAAAACAGACCCAGAACGCTTAAAGCTGACAA 1500
    |||
Db 1441 AATGATGCGCAAAATTAATCTTCTGAAAAACAGACCCAGAACGCTTAAAGCTGACAA 1500
QY 1501 TCAGAGGAAGAGTGCACAAAGGCTTGAAGGCGACGTAAGTGGCCAGAGAAAAAGATCT 1560
    |||
Db 1501 TCAGAGGAAGAGTGCACAAAGGCTTGAAGGCGACGTAAGTGGCCAGAGAAAAAGATCT 1560
QY 1561 CAAGAAACAGAAATTAATTAAGATGTTGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
    |||
Db 1561 CAAGAAACAGAAATTAATTAAGATGTTGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
QY 1621 GAATATGAAGAGACGGAAGTACTCATGTGCGATTCGCCAAGAAACCGATATATGTGCC 1680
    |||
Db 1621 GAATATGAAGAGACGGAAGTACTCATGTGCGATTCGCCAAGAAACCGATATATGTGCC 1680
QY 1681 ACTGCTGGCAATGATGATGATTAATCTCTCAAGAGAGAGCAAGACCTGAAAGC 1740
    |||
Db 1681 ACTGCTGGCAATGATGATGATTAATCTCTCTCAAGAGAGAGCAAGACCTGAAAGC 1740
QY 1741 CAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTGAACAAATATGATATCTAG 1800
    |||
Db 1741 CAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTGAACAAATATGATATCTAG 1800
QY 1801 AAGCAATTTTGTGAAGAACGAACTGGAATTTACACATGAGATTCGATTCATGAA 1860
    |||
Db 1801 AAGCAATTTTGTGAAGAACGAACTGGAATTTACACATGAGATTCGATTCATGAA 1860
QY 1861 GAAAAAGAGATAGAGTGTGAAAAAATGAATATCTGAGCTTCTCTTAACTGTAAGAAA 1920
    |||
Db 1861 GAAAAAGAGATAGAGTGTGAAAAAATGAATATCTGAGCTTCTCTTAACTGTAAGAAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTGCCATGCTAAGACTG 1980
    |||

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Db 1921 GAAAAAGACATCTTGATGAAAAATAGTACCTTCGGGAAGAAATTTGCCATGCTAAGACTG 1980
    |||
QY 1981 GAGCTGACACAAATGAACATCAGAGCCAGCTAAAAAATTTAAAAAATTTAAAAA 2040
    |||
Db 1981 GAGCTGACACAAATGAACATCAGAGCCAGCTAAAAAATTTAAAAAATTTAAAAA 2040
    |||

RESULT 6
AAH02781
ID AAH02781 standard; cDNA; 2040 BP.
XX
AC AAH02781;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined cDNA splice variant of B305D #10.
XX
KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200125272-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PA (CORI-) CORIXA CORP.
PI Xu J, Skelky YAW, Reed SG, Cheever MA;
XX
XX WPI; 2001-245062/25.
XX DR P-PSDB; AAB74817.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
XX Claim 50; Page 233; 276pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other:
XX

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGGTGATTCATGCGGCGGCGCTCTGTAAGAAAGCCATTTGGTCTC 60
    |||
Db 1 ATGTGTTGAGGTGATTCATGCGGCGGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
    |||
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
    |||
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
    |||
QY 121 AGCAACGTGGCACTTCTGAGAACACGACGACTCTGCTGTAAGACATCAGAGAGCAAG 180
    |||

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Db 121 AGCAACGTGGGCACTTCTGGAGACCAGACGACTCTGCTATGNAAGCACTCTCAGAGCAAG 180
OY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCGAGGGGGAGTGGCAAGCAAGCAAGTGG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCGAGGGGGAGTGGCAAGCAAGCAAGTGG 240
OY 241 GGGCGTCTTGAGACACGACGACTCTGCTATGAAACACTGAGAAACAAGATGGGCAAG 300
Db 241 GGGCGTCTTGAGACACGACGACTCTGCTATGAAACACTGAGAAACAAGATGGGCAAG 300
OY 301 TGGTGTGCTGCTGCTTCCCTGCTGCTGAGGGGGAGCGCAAGAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCTGCTGCTTCCCTGCTGCTGAGGGGGAGCGCAAGAGCAAGTGGGCGCTTGG 360
OY 361 GGAGACTAGATGACAGTGGCTTCAATGAGCCAGGTACAGCTCCGTTGAGAGAGATCTGG 420
Db 361 GGAGACTAGATGACAGTGGCTTCAATGAGCCAGGTACAGCTCCGTTGAGAGAGATCTGG 420
OY 421 GACAAGCTTCACAGAGCTGCTGCTGGGGTAAAGTCCCGAAGAGAGATCTCATGCTCATG 480
Db 421 GACAAGCTTCACAGAGCTGCTGCTGGGGTAAAGTCCCGAAGAGAGATCTCATGCTCATG 480
OY 481 CTCAGGAGACCTGACGTGAACAAGAGACAAAGAGAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACCTGACGTGAACAAGAGAGACAAAGAGAGAGAGCTGCTTACATCTGGCC 540
OY 541 TGTGGCAATGGGAATTCAGAAATGATGAAATCTCTGCTGAGACAGAGATCTCACTTAAT 600
Db 541 TGTGGCAATGGGAATTCAGAAATGATGAAATCTCTGCTGAGACAGAGATCTCACTTAAT 600
OY 601 GTCTCTTGACAAACAAAAGAGAGAGCTGCTGATTAAGGCGGTACAAATGCCAGAGAAATGAA 660
Db 601 GTCTCTTGACAAACAAAAGAGAGAGCTGCTGATTAAGGCGGTACAAATGCCAGAGAAATGAA 660
OY 661 TGTGCGTATATGTTGCTGAGACATGGGCACTGATCCAAATATTCACAGATGATGGAAT 720
Db 661 TGTGCGTATATGTTGCTGAGACATGGGCACTGATCCAAATATTCACAGATGATGGAAT 720
OY 721 ACCACTCTGACAGCTATCTATATGAAAGATTAATGAGCCAAAGCAAGCTGCTTAA 780
Db 721 ACCACTCTGACAGCTATCTATATGAAAGATTAATGAGCCAAAGCAAGCTGCTTAA 780
OY 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTTGGTGA 840
OY 841 CATGAGCAAAAAACAGCAAGTCTGTAATTTTATTCAGAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGTAATTTTATTCAGAAAAAAGCGAATTTAAATGCA 900
OY 901 CTGGAGTATGATGAAAGCACTGCTCATACTTGTGCTGATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGGAGTATGATGAAAGCACTGCTCATACTTGTGCTGATGTTGTGGATCAGCAAGTATA 960
OY 961 GTGAGGCTTCTACTTGAGCAAAAAATATTGATGTTCTTCAAGATATTATCTGGACAGAG 1020
Db 961 GTGAGGCTTCTACTTGAGCAAAAAATATTGATGTTCTTCAAGATATTATCTGGACAGAG 1020
OY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
OY 1081 AAAAGAAAAACAGATGCTTAAAAATCTTCTGAAACAGCAATCCAGACAGACTTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTTAAAAATCTTCTGAAACAGCAATCCAGACAGACTTTAAAG 1140
OY 1141 CTGACATCTGAGAGAGAGTCAACAAGGTTCAAAAGCGAGTGAAGAAATGCCAGCAGAGAAA 1200
Db 1141 CTGACATCTGAGAGAGAGTCAACAAGGTTCAAAAGCGAGTGAAGAAATGCCAGCAGAGAAA 1200
OY 1201 ATGTCTCAAGAAACAGAAATTAATTAAGATGCTGATAGAGAGGTTGAAGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAAACAGAAATTAATTAAGATGCTGATAGAGAGGTTGAAGAAAGAAATGAAG 1260

OY 1261 AAGCATGAAAGTAAATATGNGGGATTAATAGAAAAACCTGACTAATGTTGCTACTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGNGGGATTAATAGAAAAACCTGACTAATGTTGCTACTGCTGGC 1320
OY 1321 AATGGTATTAATGATTAATTCCTCAAAAGGAGAGAGCAACACCTGAAATACGCAATTT 1380
Db 1321 AATGGTATTAATGATTAATTCCTCAAAAGGAGAGAGCAACACCTGAAATACGCAATTT 1380
OY 1381 CCTGACACGAAAGTAAAGATATCACAGAAATTTGGAAATTTAGTTTCTGACTCAAAAGAA 1440
Db 1381 CCTGACACGAAAGTAAAGATATCACAGAAATTTGGAAATTTAGTTTCTGACTCAAAAGAA 1440
OY 1441 AAACAGATGCAAAATATCTTCTGAAAACAGAACCCAGAAACAAAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCAAAATATCTTCTGAAAACAGAACCCAGAAACAAAGACTTAAAGCTGACA 1500
OY 1501 TCAGAGAGAGTACACAAAGGCTTGAAGGCGAGTGAAGAAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGTACACAAAGGCTTGAAGGCGAGTGAAGAAATGGCCAGCAGAGAAAGATCT 1560
OY 1561 CAAGAACAGAAATTAATTAAGATGCTGATAGAGAGCTAGAAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGCTGATAGAGAGCTAGAAAATTTTATGCTATCGAA 1620
OY 1621 GAAATGAAGACGAGGAGTACTCATGTCGGATTCGCCGAAAACCTGACTAATGTTGGCC 1680
Db 1621 GAAATGAAGACGAGGAGTACTCATGTCGGATTCGCCGAAAACCTGACTAATGTTGGCC 1680
OY 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCAAGGAGAGCAACACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCAAGGAGAGCAACACCTGAAAGC 1740
OY 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGACACAAATGATACTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGACACAAATGATACTCAG 1800
OY 1801 AAGCAATTTTGTGAACACGAACTGGAATTTTCACAGATGATGATGATGATGATGAA 1860
Db 1801 AAGCAATTTTGTGAACACGAACTGGAATTTTCACAGATGATGATGATGATGATGAA 1860
OY 1861 GAAAGCAGATGAAAGTGTGTAAGAAAAATGAAATTCAGAGCTTCTTATGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAAAGTGTGTAAGAAAAATGAAATTCAGAGCTTCTTATGTTGAAGAA 1920
OY 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGGGAGAAATTCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGGGAGAAATTCATGCTAAGACTG 1980
OY 1981 GAGCTAGACCAATGAAACATCTGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAA 2040
Db 1981 GAGCTAGACCAATGAAACATCTGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 2040

RESULT 7
ABL95180
ID ABL95180 standard; cDNA: 2040 BP.
XX
AC ABL95180;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human B305D splice variant cDNA sequence SEQ ID NO 375.
XX
KW Human; cancer; prostate cancer; vaccine; cytosolic; immunostimulant;
XX gene therapy; gene; ss.
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX

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PF 12-JAN-2001; 200105-0759143.
XX 25-FEB-1997; 9705-0806099.
PR 01-AUG-1997; 9705-0904804.
PR 09-FEB-1998; 9805-0020956.
PR 25-FEB-1998; 9805-0030607.
PR 14-JUL-1998; 9805-0115453.
PR 23-SEP-1998; 9805-0159812.
PR 15-JAN-1999; 9905-0232149.
PR 09-APR-1999; 9905-0288946.
PR 13-JUL-1999; 9905-0352616.
PR 12-NOV-1999; 9905-0439313.
PR 18-NOV-1999; 9905-0443686.
PR 14-JAN-2000; 200005-0483672.
PR 27-MAR-2000; 200005-0536857.
PR 09-MAY-2000; 200005-0568100.
PR 12-MAY-2000; 200005-0570737.
PR 13-JUN-2000; 200005-0593793.
PR 27-JUN-2000; 200005-0605783.
PR 10-AUG-2000; 200005-0636215.
PR 29-AUG-2000; 200005-0651236.
PR 06-SEP-2000; 200005-0657279.
PR 02-OCT-2000; 200005-0679426.
PR 10-OCT-2000; 200005-0685166.
XX (XUJ/) XU J.
PA (DIL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETE/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
PS Claim 1; SEQ ID NO 375; 87bp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
Query Match 100.0%; Score 2040; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTTGAGTGTGATTCATGCGGCTCTTCTGTGAAGAACCAATTTGGTCTC 60
DB 1 ATGGTGGTTGAGTGTGATTCATGCGGCTCTTCTGTGAAGAACCAATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGACAGGAGAGCGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGACAGGAGAGCGCAAG 120

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QY 121 AGCAAGTGGGCACTTCTGAGACACGACACTCTGCTATGAAGACATCAGGACAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACGACACTCTGCTATGAAGACATCAGGACAAG 180
QY 181 ATGGGCAAGTGTGCTGCCGCTCTTCCCTGCTGACAGGGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGTGCTGCCGCTCTTCCCTGCTGACAGGGGAGTGGCAAGCACTG 240
QY 241 GGGCCTTCTGAGACACGACACTCTGCTATGAAGACACTCAGGAACCAATGGGCAAG 300
DB 241 GGGCCTTCTGAGACACGACACTCTGCTATGAAGACACTCAGGAACCAATGGGCAAG 300
QY 301 TGGTGTGCTGCCACTCTTCCCTGCTGACAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGCCACTCTTCCCTGCTGACAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGTACACAGTCCGCTGGAGAAATCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGTACACAGTCCGCTGGAGAAATCTG 420
QY 421 GACAAAGTCCACAGAGTGCCTGCTGGGGTAAATCCCAAGAAAGATCTATGCTATG 480
DB 421 GACAAAGTCCACAGAGTGCCTGCTGGGGTAAATCCCAAGAAAGATCTATGCTATG 480
QY 481 CTCAGGCACTGACGTGAAACAAAGAGACAAAGAAAGAGACTGCTACATCTGGCC 540
DB 481 CTCAGGCACTGACGTGAAACAAAGAGACAAAGAAAGAGACTGCTACATCTGGCC 540
QY 541 TGTGCCAATGGGAATTCAGAAATGATTAACCTCTGCTGACAGACGATGCAACTTAAT 600
DB 541 TGTGCCAATGGGAATTCAGAAATGATTAACCTCTGCTGACAGACGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGGACGCTGATTAAGGCCCTGACAAATGCGAGGAATGAA 660
DB 601 GTCTTGAACAACAAAGAGAGGACGCTGATTAAGGCCCTGACAAATGCGAGGAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTATATGAAGATTAATATGATGATGATGATGAT 780
DB 721 ACCACTGTGACACTACGCTATCTATATGAAGATTAATATGATGATGATGATGAT 780
QY 781 TATGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 TATGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGCTGCTCATACCTGCTGATGTTGATGATGATGATGAT 960
DB 901 CTGATATGATATGGAAGAGCTGCTCATACCTGCTGATGTTGATGATGATGATGAT 960
QY 961 GTGAGCCTTCTACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GTGAGCCTTCTACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCATGTAATTTGCCAGTACTTTCAGTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCATGTAATTTGCCAGTACTTTCAGTAC 1080
QY 1081 AAAGAAAAACAGATGCTTAAATATCTCTTGTGAAACAGCAATCCAGAAAGACTTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTTAAATATCTCTTGTGAAACAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGATGACAAAGTTCAGAAAGAGCTGAAATATACGCGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGATGACAAAGTTCAGAAAGAGCTGAAATATACGCGCAGAGAAA 1200

```


QY 481 CTCAGGACACTGACGTGAACAGAGACACAAGCAAAAAGAGACTGCTACATCTGCCC 540
|||||
Db CTCAGGACACTGACGTGAACAGAGACACAAGCAAAAAGAGACTGCTACATCTGCCC 540
QY 541 TCTCCCAATGGGAATTGAGAAGTGTAAACTCTGCTGGACAGACGATGTCAACTTAAT 600
|||||
Db TCTCCCAATGGGAATTGAGAAGTGTAAACTCTGCTGGACAGACGATGTCAACTTAAT 600
QY 601 GTCTTGCACAAACAAAAGAGACAGCTCTGTAAAGGCCGTCACATGCGCAGGAATGAA 660
|||||
Db GTCTTGCACAAACAAAAGAGAGACAGCTCTGTAAAGGCCGTCACATGCGCAGGAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAAACATGGCAGTCGATCCAAATATTTCCAGATGAGTGAAT 720
|||||
Db TGTGCGTTAATGTTGCTGGAAACATGGCAGTCGATCCAAATATTTCCAGATGAGTGAAT 720
QY 721 ACCACTCTGCACCTACGCTATCTATATAGAGATTAATTAATGGCCAAAGCCTGCTTA 780
|||||
Db ACCACTCTGCACCTACGCTATCTATATAGAGATTAATTAATGGCCAAAGCCTGCTTA 780
QY 781 TATGCTGCTGATTCGAATCAAAAACAGCATGGCCCTCACACCACTGTTACTTGCTGA 840
|||||
Db TATGCTGCTGATTCGAATCAAAAACAGCATGGCCCTCACACCACTGTTACTTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
|||||
Db CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGACGCTCTCATCTTGTGATATGTTGGATCGACAGATTA 960
|||||
Db CTGATATGATATGGAAGAGACGCTCTCATCTTGTGATATGTTGGATCGACAGATTA 960
QY 961 GTACAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCTCAAGATCTATCGACAGACG 1020
|||||
Db GTACAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCTCAAGATCTATCGACAGACG 1020
QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCANCATGTAATTTGCCAGTACTTTCGACTAC 1080
|||||
Db GCCAGAGAGTATGCTGTTTCTAGTCATCANCATGTAATTTGCCAGTACTTTCGACTAC 1080
QY 1081 AAAAAGAAAAAGATGCTTAATAAACTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
|||||
Db AAAAAGAAAAAGATGCTTAATAAACTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA 1200
|||||
Db CTGACATCAGAGAGAGTCTCAAAAGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAGAACACAGAAATTAATTAAGATGTTGATAGAGAGGTTGAAGAAATGAAG 1260
|||||
Db ATGTCTCAGAACACAGAAATTAATTAAGATGTTGATAGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTATTAATTTGGGATTAAGTAAACCTGACTAATGGTGTACTGCTGCGC 1320
|||||
Db AAGCATGAAGTATTAATTTGGGATTAAGTAAACCTGACTAATGGTGTACTGCTGCGC 1320
QY 1321 AATGCTATTAATGATTAATTTCTCTCAAAAGAGAGACAGAACCTGAAATAATCAGCAATTT 1380
|||||
Db AATGCTATTAATGATTAATTTCTCTCAAAAGAGAGACAGAACCTGAAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGACTATCACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
|||||
Db CCTGACAAACGAAAGTGAAGACTATCACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAAATCTCTTCTGAAAAACGCAACCCAGACAGACTTAAGCTGACA 1500
|||||
Db AAAACAGATGCCAAAATCTCTTCTGAAAAACGCAACCCAGACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGGAGAGTACAAAAGGCTTGAGGCGAGTGAATAATGSCCGCAGAGAGAAAAGATCT 1560
|||||
Db TCAGAGGAGAGTACAAAAGGCTTGAGGCGAGTGAATAATGSCCGCAGAGAGAAAAGATCT 1560

QY 1561 CAAAGACCAGAAATTAATTAAGATGTTGANTAGAGAGCTAGAAAAATTTTATGGCTATCGAA 1620
|||||
Db CAAAGACCAGAAATTAATTAAGATGTTGANTAGAGAGCTAGAAAAATTTTATGGCTATCGAA 1620
QY 1621 GAATTAAGAAAGCAGGAGATCTCATGTGCGATTTCCAGAAAACCTGACTAATGTGGCC 1680
|||||
Db GAATTAAGAAAGCAGGAGATCTCATGTGCGATTTCCAGAAAACCTGACTAATGTGGCC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTTCTCAAGAGAGACAGAACACCTGAAGC 1740
|||||
Db ACTGCTGGCAATGGTATGATGATTAATTTCTCAAGAGAGAGACAGAACACCTGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCACAGTGAAGCAAAATGATTAATCAG 1800
|||||
Db CAGCAATTTCTGACACTGAGATGAAGAGTATCACAGTGAAGCAAAATGATTAATCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACACGATGAGATTCTGATTCATGAA 1860
|||||
Db AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACACGATGAGATTCTGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAAGTGTGAAGAAAAATGAATTTCTGAGTTCTTCTAGTTGTAAGAA 1920
|||||
Db GAAAGCAGATAGAAGTGTGAAGAAAAATGAATTTCTGAGTTCTTCTAGTTGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGGGGAGAGAAATTCGATCTAAGACTG 1980
|||||
Db GAAAAAGACATCTTGCATGAAAAATAGTACGTTGGGGAGAGAAATTCGATCTAAGACTG 1980
QY 1981 GAGCTAGACAAATGAACATCAGAGCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040
|||||
Db GAGCTAGACAAATGAACATCAGAGCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040

RESULT 9
AAA06600
ID AAA06600 standard; cDNA; 2040 BP.
XX
AC AAA06600;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumor protein cDNA sequence SEQ ID NO:375.
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX immunogenic; cyostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
FN W0200004149-A2.
XX
PD 27-JAN-2000.
XX
PE 14-JUL-1999; 99WO-0515838.
XX
PR 14-JUL-1998; 98US-0115453.
XX 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
XX 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
XX 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein -
PS Claim 50; Page 223-224; 263pp; English.
XX

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06591 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention.

xx Sequence 2040 BP: 716 A; 393 C; 500 G; 431 T; 0 other:

Query Match 97.5%; Score 1989; DB 21; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 ATGGGTGTTGAGCTTGATTCATGCGCGCTGCCCTCTCTGTGAAGAAGCATTTGGTCTC 60
Db 1 ATGGGTGTTGAGCTTGATTCATGCGCGCTGCCCTCTCTGTGAAGAAGCATTTGGTCTC 60
OY 61 AGAGCAAGATGAGCAAGTGTGCTGCGCTTCCCTGCTGAGAGAGAGCGCAAG 120
Db 61 AGAGCAAGATGAGCAAGTGTGCTGCGCTTCCCTGCTGAGAGAGAGCGCAAG 120
OY 121 AGCAACGTGGGCACTTCTGGAGACACGACGACTGCTGTATGAAGACACTGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAGACACGACGACTGCTGTATGAAGACACTGAGCAAG 180
OY 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGAGAGAGAGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGAGAGAGAGCAAGCAAGCTG 240
OY 241 GCGCGTCTGAGACACGACGACTCTGCTATGAAGACACTGAGCAAGCAAGTGGGCAAG 300
Db 241 GCGCGTCTGAGACACGACGACTCTGCTATGAAGACACTGAGCAAGCAAGTGGGCAAG 300
OY 301 TGGTCTGCTGCTGCTTCCCTGCTGAGAGAGAGAGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCTGCTGCTTCCCTGCTGAGAGAGAGAGCAAGCAAGTGGGCGCTTGG 360
OY 361 GGAGACTGAGTACAGTGCCTTCTATGAGGCCAGGTACCAAGTCCGTTGGAGAAGATCG 420
Db 361 GGAGACTGAGTACAGTGCCTTCTATGAGGCCAGGTACCAAGTCCGTTGGAGAAGATCG 420
OY 421 GACAAAGTCCACAGAGTGCCTGTGTGGGTAAAGTCCCGAAGAAAGATCTCATCTCATG 480
Db 421 GACAAAGTCCACAGAGTGCCTGTGTGGGTAAAGTCCCGAAGAAAGATCTCATCTCATG 480
OY 481 CTCAGGGACACTGAGTGAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTGGGCC 540
Db 481 CTCAGGGACACTGAGTGAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTGGGCC 540
OY 541 TCTGCAATGGGAATTCAGAAAGTAAACACCTGCTGAGAGAGAGATGTAACCTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAAGTAAACACCTGCTGAGAGAGAGATGTAACCTTAAT 600
OY 601 GTCTTTGACAAACAAAAGAGAGACGCTGTATGAAGGCCGTACATGCGAGAGAAATGNA 660
Db 601 GTCTTTGACAAACAAAAGAGAGACGCTGTATGAAGGCCGTACATGCGAGAGAAATGNA 660
OY 661 TGTGCGTTAATGTTCGTGAGACATGGCACTGATCCAATATTCCAGATGAGTATGGAAT 720
Db 661 TGTGCGTTAATGTTCGTGAGACATGGCACTGATCCAATATTCCAGATGAGTATGGAAT 720
OY 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGGCAAGCACTGCTTGA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGGCAAGCACTGCTTGA 780
OY 781 TATGCTGCTGATATGAATCAAAAAAAGCATGCGCTCACACCACTGTTACTTGTGTA 840
```

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Db 781 TATGCTGCTGATATGAATCAAAAAAAGCATGCGCTCACACCACTGTTACTTGTGTA 840
OY 841 CATGAGCAAAAACACAGAGTGTGAATTTTATATCAAGAAAAAGCGAATTTAATATGA 900
Db 841 CATGAGCAAAAACACAGAGTGTGAATTTTATATCAAGAAAAAGCGAATTTAATATGA 900
OY 901 CTGATATGATATGAAGAGCTGCTCATCTGCTGTATGTTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAGAGCTGCTCATCTGCTGTATGTTGATCAGCAAGTATA 960
OY 961 GTACGCTTCTTACTGAGCAAAATATGATATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTACGCTTCTTACTGAGCAAAATATGATATCTTCAAGATCTATCTGAGACAGC 1020
OY 1021 GCCAGAGAGTATGCTGTTTCTATGATCATCATATGTAATTTGCCAGTACTTCTGAC 1080
Db 1021 GCCAGAGAGTATGCTGTTTCTATGATCATCATATGTAATTTGCCAGTACTTCTGAC 1080
OY 1081 AAGAAAAACAGATGCTAAATATCTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATATCTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
OY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAATAAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAATAAGCCAGCAGAGAA 1200
OY 1201 ATGCTCAAGAACCAAAATTAATTAAGATGCTATAGAGAGCTTGAAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATTAAGATGCTATAGAGAGCTTGAAAGAAATGAAG 1260
OY 1261 AAGCATGAAGATTAATATGTTGGATTTACTAGAAAACCTGATATGTTGCTGCTGGC 1320
Db 1261 AAGCATGAAGATTAATATGTTGGATTTACTAGAAAACCTGATATGTTGCTGCTGGC 1320
OY 1321 AATGTTGATTAATGATTAATTTCTCAAAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATTTCTCAAAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
OY 1381 CCTGACAAACGAAGTGAAGATATACAGATTTGCGAATTTGTTTCTGACATCAAGAA 1440
Db 1381 CCTGACAAACGAAGTGAAGATATACAGATTTGCGAATTTGTTTCTGACATCAAGAA 1440
OY 1441 AAGCAGATCCAAATATCTTCTGAAAACAGCAACCCGAAACAGACTTAAGCTGACA 1500
Db 1441 AAGCAGATCCAAATATCTTCTGAAAACAGCAACCCGAAACAGACTTAAGCTGACA 1500
OY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCACTGAAAATGCGCAGAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCACTGAAAATGCGCAGAGAGAAAGATCT 1560
OY 1561 CAAGAACCAAAATTAATTAAGAGTGTATAGAGCTTAGAAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCAAAATTAATTAAGAGTGTATAGAGCTTAGAAAATTTTATGCTATCGAA 1620
OY 1621 GAAATGAAGAAACAGGAAGTCTCATGCGGATTTCCAGAAAACCTGACTAATGGTGC 1680
Db 1621 GAAATGAAGAAACAGGAAGTCTCATGCGGATTTCCAGAAAACCTGACTAATGGTGC 1680
OY 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGAGAGACACCTAAAGC 1740
Db 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGAGAGACACCTAAAGC 1740
OY 1741 CAGCAATTTCTGACACTGAGATGAGATGATACAGTACAGTACGAACAAAATATATCTAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATACAGTACAGTACGAACAAAATATATCTAG 1800
OY 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATACAGATGAGATTTCTGATATGAA 1860
Db 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATACAGATGAGATTTCTGATATGAA 1860
OY 1861 GAAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGAGCTTCTTCTAGTTGAAGAA 1920
Db 1861 GAAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGAGCTTCTTCTAGTTGAAGAA 1920
```



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DB 1141 CTGACATGAGAGAGAGTACACAAAGGTTCAAGAGGAGTGAATAATAGCCAGCCAGAGAAA 1200
QY 1201 ATGCTCTAAGAACCAAAATTAATTAAGATGCTGATAGAGAGCTTGAGACAAATGAAG 1260
DB 1201 ATGCTCTAAGAACCAAAATTAATTAAGATGCTGATAGAGAGCTTGAGACAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
DB 1261 AAGCATGAAGATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
QY 1321 AATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
DB 1321 AATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
QY 1381 CCTGACAAACGAAAGTGAAGATATCAACAGATTTGGCAATTAATTAATTAATTAATTAATTAAT 1440
DB 1381 CCTGACAAACGAAAGTGAAGATATCAACAGATTTGGCAATTAATTAATTAATTAATTAATTAAT 1440
QY 1441 AAGCAGATGCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
DB 1441 AAGCAGATGCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
QY 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGAGGAGTGAATAATGAGCCAGAGAG 1551
DB 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGAGGAGTGAATAATGAGCCAGAGAG 1551
```

RESULT 11

```
AA167212
ID AA167212 standard; cDNA; 2000 BP.
```

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AC AA167212;
```

```
DT 11-FEB-2002 (first entry)
```

```
DE B305D Isoform C splice variant 2 encoding cDNA.
```

```
KW Genetic substructure: DNA microarray analysis; polymerase chain reaction:
   cancer; B305D; ss.
```

```
OS Homo sapiens.
```

```
FT Key Location/Qualifiers
```

```
FT CDS 1..1971
      /*tag= a
      /product= "B305D Isoform C splice variant"
```

```
PN WO200175171-A2.
```

```
PD 11-OCT-2001.
```

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PF 02-APR-2001; 2001WO-US10631.
```

```
PR 03-APR-2000; 2000US-194241P.
```

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PR 20-JUL-2000; 2000US-219862P.
```

```
PR 27-JUL-2000; 2000US-221300P.
```

```
PR 18-DEC-2000; 2000US-236592P.
```

```
XX (CORI-) CORIXA CORP.
```

```
XX Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
```

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XX WPI: 2001-626449/72.
```

```
XX P-PSDB: AAG65977.
```

```
XX Identifying tissue (tumour)-specific polynucleotides overexpressed in
XX tissue of interest as compared to control tissue, for detecting cancer
XX cells in patient, comprises DNA microarray analysis or quantitative
XX polymerase chain reaction -
XX Claim 4; Page 94; 127pp; English.
```

```
CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (S1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on S1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant.
```

```
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
```

```
Query Match 76.0%; Score 1551; DB 22; Length 2000;
```

```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ATGCTGCTTGAAGCTTGAATTCATGCCGGCTCTCTTCTGTAAGAGCCATTGGCTTC 60
DB 1 ATGCTGCTTGAAGCTTGAATTCATGCCGGCTCTCTTCTGTAAGAGCCATTGGCTTC 60
QY 61 AAGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTTGGTGGAGGAGCGGCAAG 120
DB 61 AAGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTTGGTGGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCACTTCTTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 240
DB 181 ATGGGCAAGTGGTGGGCACTTCTTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 240
QY 241 GGGGCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
DB 241 GGGGCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCTGACCTGCTTCCCTTCTGAGAGGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGACCTGCTTCCCTTCTGAGAGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCTGAGAGGAGCGGCAAGAGTGGGCGCTTGG 420
DB 361 GGAGACTACGATGACAGTGCCTTCTGAGAGGAGCGGCAAGAGTGGGCGCTTGG 420
QY 421 GACAGCTCCACAGAGCTGCTGAGAGGAGCGGCAAGAGTGGGCGCTTGG 480
DB 421 GACAGCTCCACAGAGCTGCTGAGAGGAGCGGCAAGAGTGGGCGCTTGG 480
QY 481 CTCAGGAGCACTGACGTGTAACAAGAGCAAGCAAGAGAGTGGTGGGCGG 540
DB 481 CTCAGGAGCACTGACGTGTAACAAGAGCAAGCAAGAGAGTGGTGGGCGG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTGAATAAATCTGCTGAGACAGAGTGAATTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTGAATAAATCTGCTGAGACAGAGTGAATTAAT 600
QY 601 GTGCTTGACAAACAAAGAGAGAGTCTGATTAAGAGCGGTCGAATGCCAGAGAGTGA 660
DB 601 GTGCTTGACAAACAAAGAGAGAGTCTGATTAAGAGCGGTCGAATGCCAGAGAGTGA 660
QY 661 TGTGCTTAATGTTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGAAT 720
DB 661 TGTGCTTAATGTTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
```


QY 781 TANGCTCTGATATCGAATCAAAAAACAGCATGCGCTCACACCACTGTTACTTGCTGA 840
 DB 781 TATGCTCTGATATCGAATCAAAAAACAGCATGCGCTCACACCACTGTTACTTGCTGA 840
 QY 841 CATGAGCAAAAAACAGCATGCTGAATTTTATCAAGAAAAAGCAATTTTAAAGCA 900
 DB 841 CATGAGCAAAAAACAGCATGCTGAATTTTATCAAGAAAAAGCAATTTTAAAGCA 900
 QY 901 CTGATAGATATGAGAGAGAGTCTCTCATCTTCTGATGTTGATGATGAGCAATATA 960
 DB 901 CTGATAGATATGAGAGAGAGTCTCTCATCTTCTGATGTTGATGATGAGCAATATA 960
 QY 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATGAGCAAGC 1020
 DB 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATGAGCAAGC 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATGATGATGATGATGATGATGATGATG 1080
 DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
 DB 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
 QY 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTGAATAGCCAGAGAAA 1200
 DB 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTGAATAGCCAGAGAAA 1200
 QY 1201 ATGCTCAAGAGAGAGAGTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAGGTTCA 1260
 DB 1201 ATGCTCAAGAGAGAGAGTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAGGTTCA 1260
 QY 1261 AAGCATGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 DB 1261 AAGCATGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 QY 1321 AATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 DB 1321 AATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 QY 1381 CCTGACACAGAGAGAGTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAGGTTCA 1440
 DB 1381 CCTGACACAGAGAGAGTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAGGTTCA 1440
 QY 1441 AAACAGATGCAAAATATCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAGCTGACA 1500
 DB 1441 AAACAGATGCAAAATATCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGAGAGAGTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAG 1551
 DB 1501 TCAGAGAGAGAGTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAGGTTCAAAAG 1551

RESULT 12
 AAS63808
 ID AAS63808 standard; cDNA; 2000 BP.
 XX
 AC AAS63808;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA clone B305D splice variant #9.
 XX
 KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001MO-US09919.

PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 DR WPI; 2001-639232/73.
 DR P-PSDB; AA069778.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 PS Claim 1; Page 349-350; 579pp; English.
 XX
 PS The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 XX
 SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 22; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTTGAGTGAATTCATGCGGCTGCTCTTGTGAAGAGCCATTGTGCTC 60
 DB 1 ATGTTGTTGAGTGAATTCATGCGGCTGCTCTTGTGAAGAGCCATTGTGCTC 60
 QY 61 AGAGCAAGATGGGCAAGTGGTCTGCTCCCTGCTGCAAGAGCGGCAAG 120
 DB 61 AGAGCAAGATGGGCAAGTGGTCTGCTCCCTGCTGCAAGAGCGGCAAG 120
 QY 121 AGCAAGTGGGCAATTTGTGAGACACAGACACTCTCTATGAAGACACAGAGCAAG 180
 DB 121 AGCAAGTGGGCAATTTGTGAGACACAGACACTCTCTATGAAGACACAGAGCAAG 180
 QY 181 ATGGCAAGTGGGCAATTTGTGAGACACAGACACTCTCTATGAAGACACAGAGCAAG 240
 DB 181 ATGGCAAGTGGGCAATTTGTGAGACACAGACACTCTCTATGAAGACACAGAGCAAG 240
 QY 241 GGGCTTCTGGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
 DB 241 GGGCTTCTGGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
 QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGAGGAGGCAAGAGCAAGTGGGCTGG 360
 DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGAGGAGGCAAGAGCAAGTGGGCTGG 360
 QY 361 GGAGACTAGCATGACATGCTTCTCATGAGAGCCAGGTACACAGTCCCTGGAGAGAGATCTG 420
 DB 361 GGAGACTAGCATGACATGCTTCTCATGAGAGCCAGGTACACAGTCCCTGGAGAGAGATCTG 420


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QY 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGCTGCAGGGGAGTGCAGAGCAAGCTG 240
    |||||
Db 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGCTGCAGGGGAGTGCAGAGCAAGCTG 240
QY 241 GGGCGTTTGGAGACGACGACTGCTATGAAGCACTCAGGAACAAGATGGGCAAG 300
    |||||
Db 241 GGGCGTTTGGAGACGACGACTGCTATGAAGCACTCAGGAACAAGATGGGCAAG 300
QY 301 TGGTGGTCCGACCTGCTTCCCTGCTGCAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
    |||||
Db 301 TGGTGGTCCGACCTGCTTCCCTGCTGCAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTCATGAGAGCCAGTACACGCTCGCTGGAGAAATCTG 420
    |||||
Db 361 GGAGACTACGATGACAGTGGCTTCATGAGAGCCAGTACACGCTCGCTGGAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
    |||||
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
QY 481 CTCAGGGACACTGACGTCGAACAAGAGGACAAAGAGGAGCTGCTCATCTGCGCC 540
    |||||
Db 481 CTCAGGGACACTGACGTCGAACAAGAGGACAAAGAGGAGCTGCTCATCTGCGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTAGTAAACCTCGCTGGACAGAGCTCAACTTAAT 600
    |||||
Db 541 TCTGCCAATGGGAATTCAGAACTAGTAAACCTCGCTGGACAGAGCTCAACTTAAT 600
QY 601 GTCCCTTGACACAACAAAAGAGGACGCTGTGATAAAGGCGCTACAACTCCAGGAAGTAA 660
    |||||
Db 601 GTCCCTTGACACAACAAAAGAGGACGCTGTGATAAAGGCGCTACAACTCCAGGAAGTAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGGCAGTCCAAATTTCCAGATGATGTAAT 720
    |||||
Db 661 TGTGCGTAAATGTTGCTGGAACATGGCAGTCCAAATTTCCAGATGATGTAAT 720
QY 721 ACCACTCTGCACCTACGCTATCTATATGAAGATAAATTAATGCGCAAGCAGCTCTTA 780
    |||||
Db 721 ACCACTCTGCACCTACGCTATCTATATGAAGATAAATTAATGCGCAAGCAGCTCTTA 780
QY 781 TATGGTCTATATTCGAATTAACAAACAGCATGGCTCACACCACTGTTACTTGGTGA 840
    |||||
Db 781 TATGGTCTATATTCGAATTAACAAACAGCATGGCTCACACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTGTGAATTTTATATCAAGAAAAAGGAAATTAATGCA 900
    |||||
Db 841 CATGAGCAAAAACAGCAAGCTGTGAATTTTATATCAAGAAAAAGGAAATTAATGCA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCATATCTGCTGATGTTGTGATCAGCAAGTATA 960
    |||||
Db 901 CTGGATAGATATGGAAGAGCTGCTCATATCTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTAGAGCTTACTGTAGGCAAAATATTGATGATCTTCTCAAGATCTATGTGGACACAG 1020
    |||||
Db 961 GTAGAGCTTACTGTAGGCAAAATATTGATGATCTTCTCAAGATCTATGTGGACACAG 1020
QY 1021 GCCAGAGAGTATGCTGTTTATGTCATCATGTAATTTGCCAGTACTTTCGATCTAC 1080
    |||||
Db 1021 GCCAGAGAGTATGCTGTTTATGTCATCATGTAATTTGCCAGTACTTTCGATCTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAACAGCAATCCAGAACAAAGATTAAAG 1140
    |||||
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAACAGCAATCCAGAACAAAGATTAAAG 1140
QY 1141 CTGACATCAGAGAGAGGTCACAAAGTTCAAAAGCAGTGAATAATAGCCAGAGAA 1200
    |||||
Db 1141 CTGACATCAGAGAGAGGTCACAAAGTTCAAAAGCAGTGAATAATAGCCAGAGAA 1200
QY 1201 ATGTCCTCAAGACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATGAAG 1260
    |||||
Db 1201 ATGTCCTCAAGACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATGAAG 1260
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```
QY 1261 AAGCATGAAGTAAATATGTGGGATTTACTAGAAAACCTGACTAATGTTGTCAGTGTGC 1320
    |||||
Db 1261 AAGCATGAAGTAAATATGTGGGATTTACTAGAAAACCTGACTAATGTTGTCAGTGTGC 1320
QY 1321 AATGCTGATTAATGATTTAATTCTCAAGAGAGACGAACACCTGAAATTCAGCAATTT 1380
    |||||
Db 1321 AATGCTGATTAATGATTTAATTCTCAAGAGAGACGAACACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCACGAATTTGGCAATTTAGTTTGTGACTCAAAAGAA 1440
    |||||
Db 1381 CCTGACAAAGAAAGTGAAGATATCACGAATTTGGCAATTTAGTTTGTGACTCAAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||||
Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAAGATCACAAGAGCTTGGAGGCAAGTGAATAATGGCCAGCCAGAG 1551
    |||||
Db 1501 TCAGAGGAAAGATCACAAGAGCTTGGAGGCAAGTGAATAATGGCCAGCCAGAG 1551

RESULT 14
AAH85029
ID AAH85029 standard; cDNA; 2000 BP.
XX
XX AAH85029;
XX
XX 25-SEP-2001 (first entry)
DE Human prostate-specific cDNA sequence B305D splice variant #9.
XX
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
KM prostate specific antigen; PSA; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200134802-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000MO-US30904.
XX
XX 12-NOV-1999; 99US-0439313.
XX
XX 18-NOV-1999; 99US-0443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
XX WPI; 2001-308785/32.
XX
XX
XX
XX Claim 31; Page 247-248; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
XX at least an immunogenic portion of a prostate-specific protein, or its
XX variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
XX (N1) have cytostatic activity and can be used in vaccine production.
XX The polypeptides, nucleic acids and antibodies from the present
XX invention are useful in the diagnosis and therapy of prostate cancer.
XX Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
XX in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
XX region. Prostate specific antigen (PSA) P501S was located on
XX chromosome 1. AAH84671 to AAH85143 and AA699000 to AAC99077 represent
XX polynucleotide and polypeptide sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
XX
XX
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Query Match 76.0%; Score 1551; DB 22; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 ATGGTGGTTGAGTGGATTCCATGCGCGCTGCTTCTTGTAAGAGCCATTGGTCTC 60
Db 1 ATGGTGGTTGAGTGGATTCCATGCGCGCTGCTTCTTGTAAGAGCCATTGGTCTC 60
Oy 61 AGGACAGATGGGCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGGACAGATGGGCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Oy 121 AGCAAGTGGGCACTTCTGAGACGACGACGACGACGACGACGACGACGACGACG 180
Db 121 AGCAAGTGGGCACTTCTGAGACGACGACGACGACGACGACGACGACGACGACG 180
Oy 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAC 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAC 240
Oy 241 GGGCGTTTGTGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
Db 241 GGGCGTTTGTGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
Oy 301 TGGTCTGCTCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGGAGTGGCGCTGG 360
Db 301 TGGTCTGCTCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGGAGTGGCGCTGG 360
Oy 361 GGAGACTACGATGACAGTGCCTTCTATGAGCCAGTACGACGTCGCTGGAGAGATCG 420
Db 361 GGAGACTACGATGACAGTGCCTTCTATGAGCCAGTACGACGTCGCTGGAGAGATCG 420
Oy 421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATG 480
Oy 481 CTCAGGACACTGACGTAACAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAGAA 540
Db 481 CTCAGGACACTGACGTAACAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAGAA 540
Oy 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGATGTCACCTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGATGTCACCTTAAT 600
Oy 601 GTCTTGACAAACAAAGAGACAGCTGATAAAGCCGTCATGCCAGAGATGAA 660
Db 601 GTCTTGACAAACAAAGAGACAGCTGATAAAGCCGTCATGCCAGAGATGAA 660
Oy 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTGCACTAGCTATCTATATGAAGTAAATTAATGAGCAAGCACTGCTTTA 780
Db 721 ACCACTGCACTAGCTATCTATATGAAGTAAATTAATGAGCAAGCACTGCTTTA 780
Oy 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGTGA 840
Db 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGA 900
Oy 901 CTGATATAGATGGAAGAGCTCTCATACTTGTATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATATAGATGGAAGAGCTCTCATACTTGTATGTTGTGATCAGCAAGTATA 960
Oy 961 GTCAGCCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
Db 961 GTCAGCCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG 1020

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Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGTAAGAACAGCAATCCAGAACAGTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGTAAGAACAGCAATCCAGAACAGTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAAGGACAGTGAATTAAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAAGGACAGTGAATTAAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGATGAATGATGAGTACTAGAAAACTGACTAATGTTGCTCACTGCTGCG 1320
Db 1261 AAGCATGAAGATGAATGATGAGTACTAGAAAACTGACTAATGTTGCTCACTGCTGCG 1320
Oy 1321 AATGTTGATTAATGATTAATTTCTCAAGAGAGACGACAGAACCTGAAATAGCAAAATT 1380
Db 1321 AATGTTGATTAATGATTAATTTCTCAAGAGAGACGACAGAACCTGAAATAGCAAAATT 1380
Oy 1381 CCTGACACGAAGTGAAGAGTATCAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACGAAGTGAAGAGTATCAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
Oy 1441 AAACAGATGCCAAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGATTCACAAAGGCTTGAGGGCACTGAAAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGATTCACAAAGGCTTGAGGGCACTGAAAAATGGCCAGCCAGAG 1551

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RESULT 15
 AAH02780
 ID AAH02780 standard; cDNA; 2000 BP.
 XX
 AC AAH02780;
 XX
 DT 14-JUN-2001 (first entry)
 XX
 DE prostate tumour antigen determined cDNA splice variant of B305D #9.
 XX
 KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200125272-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US27464.
 XX
 PR 04-OCT-1999; 99US-0157455.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Skelky YAM, Reed SG, Cheever MA;
 XX
 DR WP1; 2001-245062/25.
 XX
 DR P-PSDB; AAB74816.
 XX
 PT prostate specific protein and its encoding polynucleotide, useful for
 XX the treatment and diagnosis of prostate cancer -
 XX
 PS Claim 50; Page 232; 276bp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) comprising

at least an immunogenic portion of a prostate tumour antigen protein or its variant. (i), prostate tumour antigen polynucleotides, an antigen production cell (APC e.g. a dendritic cell) that expresses (i), and a pharmaceutical composition containing (i) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.

Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGAGTGGTTCATCCATCGCGCTCCCTCTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGGTGAGTGGTTCATCCATCGCGCTCCCTCTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGGAGCGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGGAGCGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACAGAGACTGCTGTGAAGACACACAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAGACACAGAGACTGCTGTGAAGACACACAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTCTGGAAACCAAGCAAGCTGCTGTATGAAGACATCAAGAAAGATGGGCAAG 300
DB 241 GGGGCTTCTGGAAACCAAGCAAGCTGCTGTATGAAGACATCAAGAAAGATGGGCAAG 300
QY 301 TGGTGTGACACTGCTTCCCTGCTGAGGAGGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGTGACACTGCTTCCCTGCTGAGGAGGAGCGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGGCTTCATGAGAGCCAGGTACACGCTCCGTGAGAGATCTG 420
DB 361 GGAAGCTACGATGACAGTGGCTTCATGAGAGCCAGGTACACGCTCCGTGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATCTGATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGAGACCTGACGTGAGCAAGAGGACAAAGGAGGAGTCTGCTACATCTGGCC 540
DB 481 CTCAGGAGACCTGACGTGAGCAAGAGGAGGAGGAGGAGTCTGCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTGCTGGACAGAGCATTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTGCTGGACAGAGCATTCAACTTAAT 600
QY 601 GTCTCTGACACAAAAAGAGGACAGCTGTGATTAAGGCGCTACAGTCCAGAGATGAA 660
DB 601 GTCTCTGACACAAAAAGAGGACAGCTGTGATTAAGGCGCTACAGTCCAGAGATGAA 660
QY 661 TGTGGGTTATGTTGGTGGAAATGGCAATGCAATTCCTGAGTGTGATGTAAT 720
DB 661 TGTGGGTTATGTTGGTGGAAATGGCAATGCAATTCCTGAGTGTGATGTAAT 720
QY 721 ACCACTCTGACATACGCTATCTATTAATGAAGATAAATTAAGGCCAAAGACAGCTCTTA 780
DB 721 ACCACTCTGACATACGCTATCTATTAATGAAGATAAATTAAGGCCAAAGACAGCTCTTA 780
QY 781 TATGTGTGATATCGAATCAAAAAACAGCATGGCTCACACACTGTTACTTGGTGTGA 840
DB 781 TATGTGTGATATCGAATCAAAAAACAGCATGGCTCACACACTGTTACTTGGTGTGA 840

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DB 781 TATGTGTGATATCGAATCAAAAAACAGCATGGCTCACACACTGTTACTTGGTGTGA 840
QY 841 CATGAGCAAAACAGCAAGTCTGAAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAACAGCAAGTCTGAAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGAGCTGCTTCATACCTTGCTGATATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGGAAGAGAGCTGCTTCATACCTTGCTGATATGTTGTGATCAGCAAGTATA 960
QY 961 GTACAGCTTCTACTGTAGCAAAATATGATGATCTCTCCCAATATCATATGTCAGCAGAG 1020
DB 961 GTACAGCTTCTACTGTAGCAAAATATGATGATCTCTCCCAATATCATATGTCAGCAGAG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAAGAGCAAGAGTCACAAAAGTTCAAAGGCGAGTAAATAGCCAGAGAGAAA 1200
DB 1141 CTGACATCAAGAGCAAGAGTCACAAAAGTTCAAAGGCGAGTAAATAGCCAGAGAGAAA 1200
QY 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATGATGATGAGAGGTTGAAAGAAATGTAAG 1260
DB 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATGATGATGAGAGGTTGAAAGAAATGTAAG 1260
QY 1261 AAGCATGAAAAGTAAATATGTTGGATTTACTAGAAAACCTGACTAATGCTGCTGCTG 1320
DB 1261 AAGCATGAAAAGTAAATATGTTGGATTTACTAGAAAACCTGACTAATGCTGCTGCTGCTG 1320
QY 1321 AATGCTGATATATGATTAATTTCTCAAAAGGAAGCAAGCAACCTGAAATTCAGCAATTT 1380
DB 1321 AATGCTGATATATGATTAATTTCTCAAAAGGAAGCAAGCAACCTGAAATTCAGCAATTT 1380
QY 1381 CTTGACAAACGAAGTGAAGAGTATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CTTGACAAACGAAGTGAAGAGTATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTTCTGAAACACGACCCAGAACAGACTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTTCTGAAACACGACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGGAGAGATGACAAAGGCTTGGAGGAGTGAAGAAATGGCCAGCCAGAG 1551
DB 1501 TCAGAGGAGAGATGACAAAGGCTTGGAGGAGTGAAGAAATGGCCAGCCAGAG 1551

RESULT 16
ABL95179
ID ABL95179 standard; cDNA; 2000 BP.
XX
AC ABL95179;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KM gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.

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PR 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-0030607.
 PR 14-JUL-1998; 98US-0115453.
 PR 23-SEP-1998; 98US-0159812.
 PR 15-JAN-1999; 99US-0232149.
 PR 09-APR-1999; 99US-0288946.
 PR 13-JUL-1999; 99US-0352616.
 PR 12-NOV-1999; 99US-0439313.
 PR 18-NOV-1999; 99US-0443686.
 PR 14-JAN-2000; 2000US-0483672.
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.

PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX WPI: 2002-255649/30.

PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer

PS Claim 1: SEQ ID NO 374; 87pp; English.

CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 24; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTATTCATGCCGGCTGCTTCTTGTGAAGAAGCCATTGGTCTC 60
 DB 1 ATGGTGGTGGAGTATTCATGCCGGCTGCTTCTTGTGAAGAAGCCATTGGTCTC 60
 QY AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCGTGAAGGAGGAGGCAAG 120
 DB AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCGTGAAGGAGGAGGCAAG 120
 QY 121 AGCAAGCTGGGCACTTCTGAGACCAAGAGACTGCTATGAAGAAGCACTCAGAGCAAG 180
 DB 121 ATGCTCAAGAACCAAGATTAATTAAGATGTGATAGAGAGGTGAAGAAGATGAAG 1260

DB 121 AGCAAGCTGGGCACTTCTGAGACCAAGAGACTGCTATGAAGAAGCACTCAGAGCAAG 180
 QY 181 ATGGCAAGTGGTGGCCCACTGCTCCCTGTGCGAGGGGAGTGGCAAGACCAAGT 240
 DB 181 ATGGCAAGTGGTGGCCCACTGCTCCCTGTGCGAGGGGAGTGGCAAGACCAAGT 240
 QY 241 GGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGACACTGAGCAAGATGGGCAAG 300
 DB 241 GGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGACACTGAGCAAGATGGGCAAG 300
 QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCGAGGGGAGGCGCAAGCAAGTGGGCTTGG 360
 DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCGAGGGGAGGCGCAAGCAAGTGGGCTTGG 360
 QY 361 GGAGACTAGATGACAGTGGCTTCATGAGGCCAGGTACACGCTCGTGGAGAAATCG 420
 DB 361 GGAGACTAGATGACAGTGGCTTCATGAGGCCAGGTACACGCTCGTGGAGAAATCG 420
 QY 421 GACAACTCCACAGAGCTGCTGGGGTAAAGTCCCGCAAGAGATCTCATCTCATG 480
 DB 421 GACAACTCCACAGAGCTGCTGGGGTAAAGTCCCGCAAGAGATCTCATCTCATG 480
 QY 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAGAGCTGCTCATCTGCGC 540
 DB 481 CTCAGGACACTGACGTGAACAAAGAGAGACAAAGAGAGCTGCTCATCTGCGC 540
 QY 541 TCTGCCAATGGGAATTCAGAAATGTAATTAATCTCTGACAGAGATGTAAT 600
 DB 541 TCTGCCAATGGGAATTCAGAAATGTAATTAATCTCTGACAGAGATGTAAT 600
 QY 601 GTGCTTGACAAACAAAGAGAGAGAGCTGATGAAGGCGGTACAAATGCCAGAAATGA 660
 DB 601 GTGCTTGACAAACAAAGAGAGAGAGCTGATGAAGGCGGTACAAATGCCAGAAATGA 660
 QY 661 TGTGCTTAATGTTGCTGGAACATGCGACTGATCCAAATTTCCAGATGATATGAAT 720
 DB 661 TGTGCTTAATGTTGCTGGAACATGCGACTGATCCAAATTTCCAGATGATATGAAT 720
 QY 721 ACCACTGCTGACCTGATCTATTAATGAAGATTAATTAATGCGCAAGAGCTGCTTA 780
 DB 721 ACCACTGCTGACCTGATCTATTAATGAAGATTAATTAATGCGCAAGAGCTGCTTA 780
 QY 781 TATGCTGCTGATATCAATCAAAACAAAGAGAGCTGCTGACAGAGTGTACTTGTGA 840
 DB 781 TATGCTGCTGATATCAATCAAAACAAAGAGAGCTGCTGACAGAGTGTACTTGTGA 840
 QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
 DB 841 CATGAGCAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGAGTGTCTCATCTGCTGATGTTGTGGATCAGCAATTA 960
 DB 901 CTGGATAGATATGGAAGAGAGTGTCTCATCTGCTGATGTTGTGGATCAGCAATTA 960
 QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATATCTTCAAGATCTATCTGAGACAG 1020
 DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATATCTTCAAGATCTATCTGAGACAG 1020
 QY 1021 GCCAGAGATGATGCTGTTCTAGTCATCATCATATTAATGCGAGTACTTCTGACTAC 1080
 DB 1021 GCCAGAGATGATGCTGTTCTAGTCATCATCATATTAATGCGAGTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAAGCAATCAAGAAAGCACTTAAG 1140
 DB 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAAGCAATCAAGAAAGCACTTAAG 1140
 QY 1141 CTGACATCAGAGGAAGTCAACAAAGTTCAAAGGAGTGAATATGCCAGAGAAAA 1200
 DB 1141 CTGACATCAGAGGAAGTCAACAAAGTTCAAAGGAGTGAATATGCCAGAGAAAA 1200
 QY 1201 ATGCTCAAGAACCAAGATTAATTAAGATGTGATAGAGAGGTGAAGAAGATGAAG 1260
 DB 1201 ATGCTCAAGAACCAAGATTAATTAAGATGTGATAGAGAGGTGAAGAAGATGAAG 1260

QY 1261 AAGCATGAAAGTAAATGTTGGATTACTAGAAAACTGACTAAATGTCCTGTCGGC 1320
DB 1261 AAGATGAAAGTAAATGTTGGATTACTAGAAAACTGACTAAATGTCCTGTCGGC 1320
QY 1321 AATGGTGAATGATTAATTCCTCAAGAGAGAGACAGACCTGAAATTCAGCAATTT 1380
DB 1321 AATGGTGAATGATTAATTCCTCAAGAGAGAGACAGACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAGAAAGTGAAGAGTATCACGAAATTTGCCAATAGTTTTCGACTACAAAGAA 1440
DB 1381 CCTGACAAGAAAGTGAAGAGTATCACGAAATTTGCCAATAGTTTTCGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCAGAAACAAGATTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCAGAAACAAGATTAAAGCTGACA 1500
QY 1501 TCAGAGGAAAGTCAACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
DB 1501 TCAGAGGAAAGTCAACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 17
AAS9858
ID AAS9858 standard; cDNA; 2000 BP.
AC AAS9858;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11a91 splice variant B11C-8.
XX
KW Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN WO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fridakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
DR WPI; 2002-089919/12.
XX
DR P-PSDB; AAU74378.
XX
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
XX
PS Claim 1; Page 224; 245pp; English.
XX
XX
CC The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.

XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
Query Match 76.0%; Score 1551; DB 24; Length 2000;
Best Local Similarity 100.0%; Pired.No.0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGGTGGTTGAGGTTGATTCATCGCGCTCCCTCTCTGTAAGAAAGCAATTTGTCCTC 60
DB 1 AATGGTGGTTGAGGTTGATTCATCGCGCTCCCTCTCTGTAAGAAAGCAATTTGTCCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTCTGCTCCGTTGCTTCCCTCTCGAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTCTGCTCCGTTGCTTCCCTCTCGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGAGACACTCTGTATGAAGACACTGAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACAGAGACACTCTGTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
QY 241 GGCGCTTCTGAGACACGACGACTCTGCTATGAAGACACTGAGACACAGATGGGCAAG 300
DB 241 GGCGCTTCTGAGACACGACGACTCTGCTATGAAGACACTGAGACACAGATGGGCAAG 300
QY 301 TGGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCTTGG 360
DB 301 TGGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTCCAGTCCGTGGAGAAATCTG 420
DB 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTCCAGTCCGTGGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGTCTATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGTCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGCAAGAAAGAGAGACTGCTCATCTGTGGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAGAGCAAGAAAGAGAGACTGCTCATCTGTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAGTAATAACTCTGCTGAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTAGTAATAACTCTGCTGAGACAGATGTCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGAGACTCTGATTAAGGCCGTACAAATGCCAGGAATGAA 660
DB 601 GTCTTGACAAACAAAAGAGAGAGACTCTGATTAAGGCCGTACAAATGCCAGGAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGACATGGGCACTGATCAAAATATTCAGATGATGAGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGACATGGGCACTGATCAAAATATTCAGATGATGAGAAAT 720
QY 721 ACCACTGCACTACGCTATCTATATATGAATGAATTAATGAGCAAGCAAGCACTGCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATATGAATGAATTAATGAGCAAGCAAGCACTGCTTA 780
QY 781 TATGGTGTGATATGCAATCAAAAAACAGATGGCTCACACCACTGTACTTGCTGTA 840
DB 781 TATGGTGTGATATGCAATCAAAAAACAGATGGCTCACACCACTGTACTTGCTGTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAGAAATTAATTAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAGAAATTAATTAATGCA 900
QY 901 CTGATATATATGGAAGAGCTCTCTCATACTCTGATGTTGATGATCGACAAGTATA 960
DB 901 CTGATATATATGGAAGAGCTCTCTCATACTCTGATGTTGATGATCGACAAGTATA 960
QY 961 GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020

Db	961	GTGAGCCTCTACTTGTAGCAAAATATGATGATCTCTCAAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATGATCCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC	1080
Db	1021	GCCAGAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG	1140
QY	1141	CTGACATCAGAGAAAGTCACAAAGGTTCAAGGACAGTAAATATGCGACCCAGAGAA	1200
Db	1141	CTGACATCAGAGAAAGTCACAAAGGTTCAAGGACAGTAAATATGCGACCCAGAGAA	1200
QY	1201	ATGCTTCAAGAACCCAGAAATTAATAAGATGGTGATAGAGAGTTGAAGAAATGAG	1260
Db	1201	ATGCTTCAAGAACCCAGAAATTAATAAGATGGTGATAGAGAGTTGAAGAAATGAG	1260
QY	1261	AAGCATGAAGTAAATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGC	1320
Db	1261	AAGCATGAAGTAAATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGC	1320
QY	1321	AATGATTAATGATTAATTCCTCAAGAGAGACAGAACCCGGAATAATCACAATTT	1380
Db	1321	AATGATTAATGATTAATTCCTCAAGAGAGACAGAACCCGGAATAATCACAATTT	1380
QY	1381	CCTGACAAAGAGTAAGAGTATCACAAATTTCCGAATTGTTCTGACTACAAAAGAA	1440
Db	1381	CCTGACAAAGAGTAAGAGTATCACAAATTTCCGAATTGTTCTGACTACAAAAGAA	1440
QY	1441	AAACAGATGCCAAAATATCTTCTGAAAACACAGAACCCGAAACAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATATCTTCTGAAAACACAGAACCCGAAACAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAAAGTCACAAAGGCTTGAGGGCAGTGAATAATGCCACCCAGAG	1551
Db	1501	TCAGAGAAAGTCACAAAGGCTTGAGGGCAGTGAATAATGCCACCCAGAG	1551

RESULT 18
AAA06599
ID AAA06599 standard; cDNA; 2000 BP.

DT 13-JUN-2000 (first entry)

DE	Human Immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.
...	

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
immunogenic; cytostatic; vaccine; ss.

OS Homo sapiens.

PN W0200004149-A2.

PD 27-JAN-2000.

PF 14-JUL-1999; 99WO-US15838.

PR 14-JUL-1998; 98US-0115453.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 99US-0232149.

PR 09-APR-1999; 99US-0288946.

PA (CORI-) CORIXA CORP.

PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

DR WPI; 2000-171268/15.

xx New polypeptide useful for treating and diagnosing prostate cancer
 pr comprises an immunogenic portion of prostate tumor protein -
 xx
 PS Claim 50; Page 222-223; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding in them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC or polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAM06241 to AAM06591 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention.

SQ Sequence 200 BP; 698 A; 387 C; 489 G; 426 T; 0 other;

Query Match	73.5%	Score	1500;	DB	21;	Length	2000;
Best Local Similarity	99.9%	Pred. No.	0;				
Matches 1550; Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;

1 ATGGTGGTTGAGGTTGATTCATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTGGTCTC 6

Db 1 ATGGTGGTGAAGTTGATTCATGCCGGCTGCCTTCTGTGAAGAAGCCATTGGTCTC 6

61 AGGAGCAAGATGGGCAAGTGGTCTGCCGTTGCTTCCCTGCTGCAGGGAGAGCGGCAAG 120

Db 61 AGGAGCAGATGGGCAAGTGGTGGCTGCCGTTGCTTCCCTGCTGCAGGGAGAGCGGCAAG 120

121 AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGGCTATGAAGACACTCAGGAGCAAG 180

Db 121 AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG 180

181 ATGGGCAAGTGGTGCCTTCCCTGCTGCAGGGGAGTGGCAAGAGCAACGTG 240

Db 181 ATGGGCAAGTGGTCCCGCCACTGCTTCCCTGCTGCAGGGGGAGTGGCAAGACGACGTG 240

241 GCGGCTTCTGGAGACCACGAGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300

Db 241 GCGGCTTCTGGAGACCACGAGACTCTGCTATGAGACACTCAGGAACAAGATGGCCAAG 300

301 TGGTCTGCCACTGCTTCCCCCTGCTGCAGGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360

Db 301 TGGTGTGCCACTGCTTCCCTGTGTCAGGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360

361 GGAGACTACGATGACAGTGCCTTCATGGAGCCACAGTACCACGTCCTGGAGAAGATCTG 420

Db 361 GGAGACTACGATGACAGTGCCTTCATGGAGCCCAAGTACCACGTCCTGGAGAGATCTG 420

421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCCAGAAAGGATCTCATGCTATG 480

Db 421 GACAAGCTCCACAGAGCTGCCCTGGTGGGTAAGTCCCCCAGAAAGGATTTCATCGTCATG 480

481 CTCAGGACACTGACGTGAACAAGAAGGACAAGCAAAGAGGACTGCTTACATCTGCC 540

Db 481 CTCAGGACACTGACGTGACACAGAGGACACAAGAGGACTGCTCTACATCTGGCC 540

541 TCTGCCAATGGGAATTCAGAAGTAGTAAACCTCCCTGCTGGACAGACGATGTCACCTTAAT 600

DB 541 TCTTGCCTAATGGGAATTCAGAACTAGTAAACCTCTCTGGACAGACGATGTCACCTTAAT 600

601 GTCTTGACACAAAGAGGACAGCTCTGATAAGGCCGTACAAATGCCAGGAGATGAA 660

D5 601 GTCCWGAACAAGAGGACAGCTCTGATTAAGGCCGTACCAATGCCAGGAGATGAA 660

661 TGTGGCTTAACTGTGGTGGACATGGCACCTGATCCAAATATCCAGATGAGTATGGAAAT / 20

DB 661 TGTGGCTTAATGTGGTGGACATGGCACCTGATCCAAATATCCAGATCAGTATGGAAAT / 20

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QY 721 ACCACTCTGCACCTAGCTATCTATATAGATATAATTAATGGCCAAAGCACTGCTCTTA 780
    |||||||
DB 721 ACCACTCTGCACCTAGCTATCTATATAGATATAATTAATGGCCAAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAAACAGAGATGGCCCTACACCACTCTTACTGGTGA 840
    |||||||
DB 781 TATGCTGCTGATATCGAATCAAAAAACAGAGATGGCCCTACACCACTCTTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTTAAATCA 900
    |||||||
DB 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTTAAATCA 900
QY 901 CTGATAGATATGAGAGAGACTGCTCTACACTCTCTATCTTGTGATTCAGACAATATA 960
    |||||||
DB 901 CTGATAGATATGAGAGAGACTGCTCTACACTCTCTATCTTGTGATTCAGACAATATA 960
QY 961 GTCAGCCTTCTACTTGGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGC 1020
    |||||||
DB 961 GTCAGCCTTCTACTTGGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTTCTTGACTAC 1080
    |||||||
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTTCTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
    |||||||
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATTCAGAGAGAGAGCTCCAAAGGTTCAAAAGCACTGAAATAGCCACCAGAGAAA 1200
    |||||||
DB 1141 CTGACATTCAGAGAGAGAGCTCCAAAGGTTCAAAAGCACTGAAATAGCCACCAGAGAAA 1200
QY 1201 ATGCTCTAAGAACAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAGAAATGAAG 1260
    |||||||
DB 1201 ATGCTCTAAGAACAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAATTAATGTTGGGATTAAGTAAAGCACTGACTGCTGCTGC 1320
    |||||||
DB 1261 AAGCATGAAAGTAATTAATGTTGGGATTAAGTAAAGCACTGACTGCTGCTGC 1320
QY 1321 AATGCTGATATGATTAATTCCTCAAAAGAGAGAGCAACACTGAAATACAGCAATTT 1380
    |||||||
DB 1321 AATGCTGATATGATTAATTCCTCAAAAGAGAGAGCAACACTGAAATACAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGAGTATCACAGATTTGCCAATTAAGTTTCTGACTACAAAGA 1440
    |||||||
DB 1381 CCTGACAAAGAAAGTGAAGAGTATCACAGATTTGCCAATTAAGTTTCTGACTACAAAGA 1440
QY 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||||||
DB 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCACAGAGAGAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
    |||||||
DB 1501 TCACAGAGAGAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 19
AAC81011
ID AAC81011 standard; cDNA; 1155 BP.
XX
AC AAC81011;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B11Ag1 antigen splice isoform B11C-15 cDNA.
XX
KW Human; breast tumour-specific antigen; cytosolic; vaccine;
KM breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
XX
OS Homo sapiens.
XX
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PN W0200061753-A2.
XX
XX 19-OCT-2000.
PD
XX
XX 07-APR-2000; 2000WO-US09312.
PF
XX
XX 09-APR-1999; 99US-0289198.
PR 28-OCT-1999; 99US-0429755.
PR 23-MAR-2000; 2000US-0534825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TM, Smith JM, Reed SG, Misher LE, Retter KM, Dillon DC;
PI
XX WPI: 2000-628403/60.
DR
DR P-PSDB: AAB28628.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX
XX Claim 4; Page 177; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.
XX
XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other:
XX
XX
XX Query Match 55.3%; Score 1128; DB 21; Length 1155;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGGATTTCATGCGCGCTCCTCTTCTGTAAGAAACCATTTGCTCTC 60
DB 1 ATGCTGTTGAGTGGATTTCATGCGCGCTCCTCTTCTGTAAGAAACCATTTGCTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
DB 61 AGGACCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACCCAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAGACCCAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGAACCTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGAACCTG 240
QY 241 GGGCTTCTGGAGACCCAGACGACTCTGCTATGAAGACACTCAGAGCAAGTGG 300
DB 241 GGGCTTCTGGAGACCCAGACGACTCTGCTATGAAGACACTCAGAGCAAGTGG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGCAAGTGGGCGCTGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGCAAGTGGGCGCTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTTCATGAGAGCCAGGTACCACTCCGTGGAAGAGATCG 420
DB 361 GGAGACTACGATGACAGTGGCTTTCATGAGAGCCAGGTACCACTCCGTGGAAGAGATCG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCCAGAAAAGATCTATGCTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCCAGAAAAGATCTATGCTCATG 480
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Db 421 GACAACTCCACAGAGCTCGTGGGGTAAAGTCCAGAAAAGATCTCATGTCATG 480
Oy 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGGCC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGAGATGTCATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGAGATGTCATTAAT 600
Oy 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCCGTACAAATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCCGTACAAATGCCAGAAATGAA 660
Oy 661 TGTGCTTATGTTGTGGAACATGACATGCAATATTCACATGATGATGTAAT 720
Db 661 TGTGCTTATGTTGTGGAACATGACATGCAATATTCACATGATGATGTAAT 720
Oy 721 ACCACTCTGACATGACCTATCTATTAATGAAGATTAATTAAGGCCAAGACATGCTCTTA 780
Db 721 ACCACTCTGACATGACCTATCTATTAATGAAGATTAATTAAGGCCAAGACATGCTCTTA 780
Oy 781 TATGCTGCTGATATGCAATCAAAAAAACAAGCATGGCCCTACACCATGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAAACAAGCATGGCCCTACACCATGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAACAGCAAGCTGTAATTTTAAATCAAGAAAAGCAATTAATTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGCTGTAATTTTAAATCAAGAAAAGCAATTAATTAATGCA 900
Oy 901 CTGGATAGATATGGAAGAGACTGCTCAATCTGCTGATGTTGTTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGGAAGAGACTGCTCAATCTGCTGATGTTGTTGGATCAGCAAGTATA 960
Oy 961 GTACAGCTTCTACTTACGACAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTACAGCTTCTACTTACGACAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGATGTAATTTGCCAGTTACTTCTGACTAC 1080
Oy 1081 AAAGAAAACAGATGCTAAAAATCTCTCTGAAAGACAGCAATCCAGAA 1128
Db 1081 AAAGAAAACAGATGCTAAAAATCTCTCTGAAAGACAGCAATCCAGAA 1128

RESULT 20
AAA06598
ID AAA06598 standard; cDNA; 1155 BP.
XX
AC AAA06598;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:373.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX
KW Immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
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PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (COR-) CORIXA CORP.
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX
PS comprises an immunogenic portion of prostate tumor protein -
XX
XX
XX Claim 50: Page 222; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (TRP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-Idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06591 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
XX
XX
Query Match 55.3%; Score 1128; DB 21; Length 1155;
Best local similarity .100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGGGTGTTGAGGTGATTCATGCGGGCTGCTTCTGTGAAGAAGCCATTGGTCTC 60
Db 1 ATGGGTGTTGAGGTGATTCATGCGGGCTGCTTCTGTGAAGAAGCCATTGGTCTC 60
Oy 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTGCTCCCTGTCGAGGGGAGTGGCAAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTGCTCCCTGTCGAGGGGAGTGGCAAGCGCAAG 120
Oy 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGTGTAAGACACTCAGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGTGTAAGACACTCAGAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Oy 241 GGGGCTTCTGGAGACCAAGCAAGCTGTGTAAGACACTCAGAGAGCAAGATGGGCAAG 300
Db 241 GGGGCTTCTGGAGACCAAGCAAGCTGTGTAAGACACTCAGAGAGCAAGATGGGCAAG 300
Oy 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTACAGATGACAGTGTGCTTATGAGACCCAGGTACCAAGTCCGTGAGAGATCTG 420
Db 361 GGAGACTACAGATGACAGTGTGCTTATGAGACCCAGGTACCAAGTCCGTGAGAGATCTG 420
Oy 421 GACAAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGAAAGGATTCATCGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGAAAGGATTCATCGTCATG 480
Oy 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGGCC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGAGATGTCATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGAGATGTCATTAAT 600
```

QY 601 GTCCCTGCAACAAAAGAGAGCAGCTCTGATAAAGCCGTACATGCCAGGAAGATGAA 660
 DB 601 GTCCCTGCAACAAAAGAGAGCAGCTCTGATAAAGCCGTACATGCCAGGAAGATGAA 660
 QY 661 TGTCCGTTAATGTTGCTGGGAACATGCACTGATCCAAATATTCCAGATGATGGAAT 720
 DB 661 TGTCCGTTAATGTTGCTGGGAACATGCACTGATCCAAATATTCCAGATGATGGAAT 720
 QY 721 ACCACTGCACTAGCGATCTATATGAATGAATTAATGAGCAAGCAGCTGCTCTTA 780
 DB 721 ACCACTGCACTAGCGATCTATATGAATGAATTAATGAGCAAGCAGCTGCTCTTA 780
 QY 781 TATGTCGTGATATGCAATCAAAAACAAAGCATGGCCCTCACACACAGTGTACTGGTGA 840
 DB 781 TATGTCGTGATATGCAATCAAAAACAAAGCATGGCCCTCACACACAGTGTACTGGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTAATCAAGAAAAAGCAATTTAATGCA 900
 DB 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTAATCAAGAAAAAGCAATTTAATGCA 900
 QY 901 CTGATGATATGAGAGAGCTGCTCTCATCTGCTGATGATGTTGGATCGACAAGTATA 960
 DB 901 CTGATGATATGAGAGAGCTGCTCTCATCTGCTGATGATGTTGGATCGACAAGTATA 960
 QY 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 DB 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTTGACTAC 1080
 DB 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACAGCAATCCAGAA 1128
 DB 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACAGCAATCCAGAA 1128
 RESULT 21
 AA167211
 ID AA167211 standard; cDNA; 1155 BP.
 AC AA167211;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE B305D isoform C splice variant 1 encoding cDNA.
 XX
 KW Genetic subfraction: DNA microarray analysis; polymerase chain reaction;
 KW cancer: B305D; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1155
 FT /*tag- a
 FT /product- "B305D isoform C splice variant"
 PN MO200175171-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 02-APR-2001; 2001MO-US10631.
 XX
 PR 03-APR-2000; 2000US-194241P.
 PR 20-JUL-2000; 2000US-219862P.
 PR 27-JUL-2000; 2000US-221300P.
 PR 18-DEC-2000; 2000US-256592P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;

DR WPI: 2001-626449/72.
 DR P-PSDB: AAG65976.
 XX
 PT Identifying tissue (tumour)-specific polynucleotides overexpressed in
 PT tissue of interest as compared to control tissue for detecting cancer
 PT cells in patient, comprises DNA microarray analysis or quantitative
 PT polymerase chain reaction
 XX
 PS Claim 4: Page 93-94; 127pp; English.
 XX
 CC The invention relates to identifying tissue-specific polynucleotides (P)
 CC that involves performing a genetic subtraction to identify pool of (P)
 CC from tissue of interest (TI), performing DNA microarray analysis to
 CC identify first subset of polynucleotides (SPI) at least 2-fold over
 CC expressed in TI, and performing quantitative polymerase chain reaction
 CC (PCR) analysis on SPI to identify second subset of (P). The method is
 CC useful for determining the presence or absence of a cancer cell in a
 CC patient, monitoring the progression of cancer in a patient using a
 CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
 CC urine or a tumour biopsy sample. The methods are useful for determining
 CC the presence or absence of or monitoring progression of prostate, breast,
 CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
 CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
 CC sequence represents a cDNA encoding a B305D isoform C splice variant.
 XX
 SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
 Query Match 55.3%; Score 1128; DB 22; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTGTTGAGTGGATTCCATGCCGCTCCCTCTCTGTGAAGAACCAATTGGTCTC 60
 DB 1 ATGCTGTTGAGTGGATTCCATGCCGCTCCCTCTCTGTGAAGAACCAATTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAATGCTGCTGCCGTTGCTTCCCTCTGCAAGGAGAGGGCAAG 120
 DB 61 AGGAGCAAGATGGGCAATGCTGCTGCCGTTGCTTCCCTCTGCAAGGAGAGGGCAAG 120
 QY 121 AGCAACGTGGGCACTTCTGGAGACACAGACAGCTCTGATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAACGTGGGCACTTCTGGAGACACAGACAGCTCTGATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGGTCCGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
 DB 181 ATGGGCAAGTGGTGGTCCGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
 QY 241 GCGGCTTCTGAGACACAGACAGCTCTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300
 DB 241 GCGGCTTCTGAGACACAGACAGCTCTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300
 QY 301 TGGTGTCCCACTGCTTCCCTGCTGACAGGGGAGGCAAGCAAGTGGGCGCTTGG 360
 DB 301 TGGTGTCCCACTGCTTCCCTGCTGACAGGGGAGGCAAGCAAGTGGGCGCTTGG 360
 QY 361 GGAGACTATGATGACAGTGCCTTCATGAGGCCAGGTACACAGTCCGGGAGGAAGATCG 420
 DB 361 GGAGACTATGATGACAGTGCCTTCATGAGGCCAGGTACACAGTCCGGGAGGAAGATCG 420
 QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGTTAAATGCCCAAAAGAGATCTATGTCATG 480
 DB 421 GACAAGCTCCACAGAGCTGCTGGTGGGTTAAATGCCCAAAAGAGATCTATGTCATG 480
 QY 481 CTGAGGGCACTGACGTGTAACAAGAGGACAAGCAAAAGAGAGCTGCTCATCTGGCC 540
 DB 481 CTGAGGGCACTGACGTGTAACAAGAGGACAAGCAAAAGAGAGCTGCTCATCTGGCC 540
 QY 541 TCTGCAATGGGAATTGAGAGTAGTAAACTCTGCTGACAGACAGATGTCAACTTAAT 600
 DB 541 TCTGCAATGGGAATTGAGAGTAGTAAACTCTGCTGACAGACAGATGTCAACTTAAT 600
 QY 601 GTCCCTGCAACAAAAGAGAGCAGCTCTGATAAAGCCGTACATGCCAGGAAGATGAA 660
 DB 601 GTCCCTGCAACAAAAGAGAGCAGCTCTGATAAAGCCGTACATGCCAGGAAGATGAA 660

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Db 601 GTCCCTTGACAAACAAAAAGAGACAGCTCTGATTAAGCCGCTACAAATGCCAGGAATGAA 660
Oy 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGAGTATGAAAT 720
Db 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGAGTATGAAAT 720
Oy 721 AACACTCTGCACTAGCTATCTATATATGAAATTAATTAATGATGCCAAAGCACTGCTTTA 780
Db 721 AACACTCTGCACTAGCTATCTATATGAAATTAATTAATGATGCCAAAGCACTGCTTTA 780
Oy 781 TATGGTCTGATATGCAATCAAAAAACAAGCATGGCCCTCACACCACTGTTACTGTGTA 840
Db 781 TATGGTCTGATATGCAATCAAAAAACAAGCATGGCCCTCACACCACTGTTACTGTGTA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCCAAATTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCCAAATTAATGCA 900
Oy 901 CTGATATGATATGAAAGAGACTGCTCAATCTGCTGATGTTGATGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAAGAGACTGCTCAATCTGCTGATGTTGATGATCAGCAAGTATA 960
Oy 961 GTCAAGCTTCTACTTGAGCAAAATATGATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTCAAGCTTCTACTTGAGCAAAATATGATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Oy 1021 GCCAAGAGATGATGCTGTTCTAGTATCATCATGTAATTTGGCACTTACTTCTGACTAC 1080
Db 1021 GCCAAGAGATGATGCTGTTCTAGTATCATCATGTAATTTGGCACTTACTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128

RESULT 22
AAS63807
ID AAS63807 standard; cDNA; 1155 BP.
XX
AC AAS63807;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #8.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0651279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Reller MW, Stoik JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
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DR P-PSDB; AAU69777.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 349; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
XX
Query Match 55.3%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGTGTTGAGTGGATTGCATGCCGGCTGCTTCTGTGAAGAAGCAATTTGGTCTC 60
Db 1 ATGTGTTGAGTGGATTGCATGCCGGCTGCTTCTGTGAAGAAGCAATTTGGTCTC 60
Oy 61 AGAGCAAGATGGCAAGTGTGCTGCTTCCCTGCTGAGGGAGAGTGGCAAGCAAGC 120
Db 61 AGAGCAAGATGGCAAGTGTGCTGCTTCCCTGCTGAGGGAGAGTGGCAAGCAAGC 120
Oy 121 AGCAAGTGGGCACTTCTGAGACACGACGAGCTGCTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACGACGAGCTGCTATGAAGACACTGAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGAGAGTGGCAAGCAAGC 240
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGAGAGTGGCAAGCAAGC 240
Oy 241 GGGCTTCTGAGACACGACGAGCTGCTATGAAGACACTGAGAGCAAGTGGCAAG 300
Db 241 GGGCTTCTGAGACACGACGAGCTGCTATGAAGACACTGAGAGCAAGTGGCAAG 300
Oy 241 GGGCTTCTGAGACACGACGAGCTGCTATGAAGACACTGAGAGCAAGTGGCAAG 300
Db 241 GGGCTTCTGAGACACGACGAGCTGCTATGAAGACACTGAGAGCAAGTGGCAAG 300
Oy 301 TGGTGTGCACTGCTTCCCTGCTGAGGGAGAGTGGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGGAGAGTGGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGAGAGTCTTCAATGAGCCAGGTACAGCTCCGTGAGAGATCTG 420
Db 361 GGAGACTACGATGAGAGTCTTCAATGAGCCAGGTACAGCTCCGTGAGAGATCTG 420
Oy 421 GACAAGCTTCACAGAGCTGCTGAGGGTAAAGTCCCAAGAAAGATCTCATCTG 480
Db 421 GACAAGCTTCACAGAGCTGCTGAGGGTAAAGTCCCAAGAAAGATCTCATCTG 480
Oy 481 CTCAGGACACTGAGCTGAGCAAGAAAGCAAGCAAGAAAGAGCTCTCAATCTGG 540
Db 481 CTCAGGACACTGAGCTGAGCAAGAAAGCAAGCAAGAAAGAGCTCTCAATCTGG 540
Oy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGAGAGATGCAACTTAAT 600
Oy 601 GTTCCTTGACAAACAAAAAGAGACAGCTGATGAAGAGCCGCTACATGCCAGAAATG 660
Db 601 GTTCCTTGACAAACAAAAAGAGAGACAGCTGATGAAGAGCCGCTACATGCCAGAAATG 660
Oy 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGAGTATGAAAT 720
Db 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGAGTATGAAAT 720
```

Db 661 TGTGCGTTAATGTTGCTGGACATGCGCATGATCCAAATATTCAGATGAGTATGAAAT 720
Qy 721 ACCACTGTGCATACGCTATCTATTAATGAATTAATTAATGAGCAAGCAAGCTGCTCTTA 780
Db 721 ACCACTGTGCATACGCTATCTATTAATGAATTAATTAATGAGCAAGCAAGCTGCTCTTA 780
Qy 781 TATGCTCTGATATCGAATCAAAAACAGCATGGCTCACACCACCTGTTACTTGGTGTGA 840
Db 781 TATGCTCTGATATCGAATCAAAAACAGCATGGCTCACACCACCTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCATGCTCTCATCTGCTGATGTTGGATGAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCATGCTCTCATCTGCTGATGTTGGATGAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTTGGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGAGCTTCTACTTGGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Qy 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGAGCTAC 1080
Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGAGCTAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 23

AAH93714 standard; cDNA; 1155 BP.

AAH93714;

04-OCT-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #8.

Human prostate cancer; prostate-specific; diagnosis; vaccine;

cytostatic; gene therapy; metastasis; ss.

Homo sapiens.

MO200151633-A2.

19-JUL-2001.

16-JAN-2001; 2001MO-US01574.

14-JAN-2000; 2000US-0483672.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,

PI Kalo J, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM,

Wang A, Meagher MJ;

WPI; 2001-425873/45.

New polynucleotide encoding a prostate-specific protein, for

diagnosis, monitoring and treating prostate cancer in a patient and

for use in vaccines -

Claim 1; Page 347; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode

prostate-specific proteins (II). (I) and (II) have cytostatic activity,

and can be used in vaccine production and gene therapy. (I), (II),

antibodies to (II), fusion proteins comprising (II), and isolated

T cells prepared using (I) or (II) are used treat cancer in a patient.

CC (I) and the antibodies are also used in the detection of cancer in a
CC prostate. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93714 to AAH93944 and AAH0115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 55.3%; Score 1128; DB 22; Length 1155;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTGATGAGTTGATTCATGCGCGGCTCTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTGATGAGTTGATTCATGCGCGGCTCTCTGTAAGAACCATTTGGTCTC 60
Qy 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGAGCGCAAG 120
Qy 121 AGCAACGTGGGCACTCTTGAGAACACAGACACTGCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTCTTGAGAACACAGACACTGCTATGAAGACATCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGACAGT 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGACAGT 240
Qy 241 GGGCTTCTGAGACACAGACGACTGCTATGAAGACACTCAGAAACAGATGGCAAG 300
Db 241 GGGCTTCTGAGACACAGACGACTGCTATGAAGACACTCAGAAACAGATGGCAAG 300
Qy 301 TGGTGTGCTGCACTGCTCCCTGCTGCAAGGAGGAGGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCTGCACTGCTCCCTGCTGCAAGGAGGAGGCAAGAGTGGGCGCTTGG 360
Qy 361 GGAGACTAGATGACATGCTGCTCATGAGCCAGGATGACAGTGGGAGAGATCTG 420
Db 361 GGAGACTAGATGACATGCTGCTCATGAGCCAGGATGACAGTGGGAGAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 481 CTCAGGACACTGACGCTGAACAGAGACAGCAAGAGAGAGTGGTCTGATCTGGCC 540
Db 481 CTCAGGACACTGACGCTGAACAGAGACAGCAAGAGAGAGAGTGGTCTGATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGAGAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGAGAGAGATGCAACTTAAT 600
Qy 601 GTCTTTCACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCTTTCACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTGTGCATACGCTATCTATTAATGAATTAATTAATGAGCAAGCAAGCTGCTTA 780
Db 721 ACCACTGTGCATACGCTATCTATTAATGAATTAATTAATGAGCAAGCAAGCTGCTTA 780
Qy 781 TATGCTCTGATATCGAATCAAAAACAGCATGGCTCACACCACCTGTTACTTGGTGTGA 840
Db 781 TATGCTCTGATATCGAATCAAAAACAGCATGGCTCACACCACCTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900

|||||
Db 841 CATGAGCAAAACAGCAGCTGTGAAATTTTAAATCAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATATATATGGAAGACACCTCTCATCTACTGTATATGTGGATCAGCAATATA 960
Db 901 CTGATATATATGGAAGACACCTCTCATCTACTGTATATGTGGATCAGCAATATA 960
Qy 961 GTCAAGCTTCTACTGTAGCAAAATATATGATGTATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAAGCTTCTACTGTAGCAAAATATATGATGTATCTTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATCTTAAAAATCTCTCTGTAAGAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATCTTAAAAATCTCTCTGTAAGAACAGCAATCCAGAA 1128

RESULT 24

AAH85028

ID AAH85028 standard; cDNA: 1155 BP.

AAH85028;

25-SEP-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #8.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
chromosome 22q11.2; prostate-specific protein; chromosome 1;
prostate specific antigen; PSA; ss.

Homo sapiens.

W0200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;

WPI: 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a
prostate-specific protein, useful in the diagnosis and therapy of
prostate cancer -

Claim 31; Page 246-247; 325pp; English.

The present invention describes an isolated polypeptide (P1) comprising
at least an immunogenic portion of a prostate-specific protein, or its
variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
(N1) have cytostatic activity and can be used in vaccine production.The polypeptides, nucleic acids and antibodies from the present
invention are useful in the diagnosis and therapy of prostate cancer.Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndromeregion. Prostate specific antigen (PSA) P501S was located on
chromosome 1. AAH84671 to AAH85143 and AAG9000 to AAG9077 representpolynucleotide and polypeptide sequences used in the exemplification
of the present invention.

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other:

Query Match 55.3%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTTGAGGTGATTCATGCCGGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
Db 1 ATGTGTGTTGAGGTGATTCATGCCGGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
Qy 61 AGGACCAAGATGGGCAAGGTGTCGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGCAAGGTGTCGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTTGAGACCAAGCAAGCACTGCTATGAAGCACTAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTTGAGACCAAGCAAGCACTGCTATGAAGCACTAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
Qy 241 GCGGCTTCTGAGACACAGCAAGCACTCTGCTATGAAGCACTAGAGCAAGTGGCAAG 300
Db 241 GCGGCTTCTGAGACACAGCAAGCACTCTGCTATGAAGCACTAGAGCAAGTGGCAAG 300
Qy 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
Qy 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACAGCTCCGTGGAGAAATCTG 420
Db 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACAGCTCCGTGGAGAAATCTG 420
Qy 421 GACAAGCTCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAGCTCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CTCAGGACACTGAGCTGTAAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Db 481 CTCAGGACACTGAGCTGTAAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 600
Qy 601 GTCTTGGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCTTGGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TGTGCTTAAATGTTGCTGTAAGATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCTTAAATGTTGCTGTAAGATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 780
Qy 781 TATGTGCTGATATGATGATCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 TATGTGCTGATATGATGATCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
Qy 901 CTGATATATATGGAAGACACCTCTCATCTACTGTATATGTGGATCAGCAATATA 960
Db 901 CTGATATATATGGAAGACACCTCTCATCTACTGTATATGTGGATCAGCAATATA 960
Qy 961 GTCAAGCTTCTACTGTAGCAAAATATATGATGTATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAAGCTTCTACTGTAGCAAAATATATGATGTATCTTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080

Db 1021 GCCAGAGATGATGTTTCTAGCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAATAATCTCTTGAAGAACAGCAATCCAGAA 1128
Db 1081 AAGAGAAAAAGATGCTAAATAATCTCTTGAAGAACAGCAATCCAGAA 1128
RESULT 25
AAH02779
ID AAH02779 standard; cDNA; 1155 BP.
XX AAH02779;
AC AAH02779;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined cDNA splice variant of B305D #8.
XX
KW Human: prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW Prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN W020012572-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PI (CORI-) CORIXA CORP.
XX
PI Xu J, Skeiky YAM, Reed SG, Cheever MA;
XX
DR WPI: 2001-245062/25.
DR P-PSDB: AAB74815.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 50: Page 231-232: 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Query Match 55.3%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 AGCAAGCTGGGCACTTCTGGAGACCACAGACACTCTCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGATGATGTCGCCCACTGCTCCCTGCTGACAGGGGAGATGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGATGATGTCGCCCACTGCTCCCTGCTGACAGGGGAGATGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGGAGACACAGAGACTCTGTATGAAGACACTCAGAACAAAGATGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGAGACTCTGTATGAAGACACTCAGAACAAAGATGGCAAG 300
QY 301 TGGTGTGCGCACTGCTTCCCTGCTGACAGGGGAGGGCAAGACAGATGGGCGTTGG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGACAGGGGAGGGCAAGACAGATGGGCGTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACCACTGCTCGTGAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACCACTGCTCGTGAAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCANTGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCANTGTCATG 480
QY 481 CTCAGGACACATGACGTGAACACAAAGACAAAGAAAGAGACTGCTTCATCATCTGGC 540
Db 481 CTCAGGACACATGACGTGAACACAAAGACAAAGAAAGAGACTGCTTCATCATCTGGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGACAGACAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGACAGACAGATGCAACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGACAGCTGTGATAAGGCCCTACAAATCCAGGAAGATGA 660
Db 601 GTCCCTGACAAACAAAAGAGAGACAGCTGTGATAAGGCCCTACAAATCCAGGAAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATTAAGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATTAAGCCAAAGCACTGCTCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAAACAACATGGCCTCACACACATGTAATCTGATGA 840
Db 781 TATGTCCTGATATGCAATCAAAAAACAACATGGCCTCACACACATGTAATCTGATGA 840
QY 841 CATGAGCAAAAAACGCAAGTCGTGAATTTTATTCAGAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACGCAAGTCGTGAATTTTATTCAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGACTGCTCATACTTCTGATGTTGTGATCAGCAAGATGA 960
Db 901 CTGATATGATATGGAAGAGACTGCTCATACTTCTGATGTTGTGATCAGCAAGATGA 960
QY 961 GTCAAGCTTCTACTTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTCAAGCTTCTACTTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAATAATCTCTTGAAGAACAGCAATCCAGAA 1128
Db 1081 AAGAGAAAAAGATGCTAAATAATCTCTTGAAGAACAGCAATCCAGAA 1128
RESULT 26
ABL95178
ID ABL95178 standard; cDNA; 1155 BP.
XX ABL95178;
AC ABL95178;
XX

DT 19-JUL-2002 (first entry)
XX Human B305D splice variant cDNA sequence SEQ ID NO 373.
DE Human, cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
KM Homo sapiens.
XX US2002022248-A1.
PN 21-FEB-2002.
PD 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-015453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler W, Henderson RA;
XX WPI: 2002-255649/30.
DR New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
PT
XX
PS Claim 1: SEQ ID NO 373; 87bp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX

SQL Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Query Match 55.3%; Score 1128; DB 24; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGTTGATTCATGCCGGCTGCTCTTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGTGTGTTGAGTTGATTCATGCCGGCTGCTCTTGTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCGTTCCTCCCTGCTGCAAGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCGTTCCTCCCTGCTGCAAGAGAGCGGCAAG 120
QY 121 ACCAAGGTGGGCACTTCTGGAACACGACGACTCTGCTATGAAGCACTCAGGAGCAAG 180
DB 121 ACCAAGGTGGGCACTTCTGGAACACGACGACTCTGCTATGAAGCACTCAGGAGCAAG 180
QY 181 ATGGGCAAGTGGTGCGGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGTGCGGCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAAGTGG 240
QY 241 GCGGCTTCTGAGACCAAGCAAGCACTCTGCTATGAACACTCAGAAAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGCAAGCACTCTGCTATGAAGCACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGAGGAGGCAAGCAAGTGGGCGCTTG 360
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGAGGAGGCAAGCAAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTGTCTTCATGAGCCAGGTACAGGTCCGTTGGAGAAATCTG 420
DB 361 GGAGACTACGATGACAGTGTCTTCATGAGCCAGGTACAGGTCCGTTGGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGGACACTGAGCTGTAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGGGACACTGAGCTGTAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAATCTCTGCTGAGCAAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAATAATCTCTGCTGAGCAAGATGTCAACTTAAT 600
QY 601 GTCTTGTGACCAAAAAAGAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
DB 601 GTCTTGTGACCAAAAAAGAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGTGTAACATGAGCACTGATCCAAATATTCAGATAGATGGAAT 720
DB 661 TGTGCGTTAATGTTGTGTAACATGAGCACTGATCCAAATATTCAGATAGATGGAAT 720
QY 721 ACCACTCTGCTACAGCTTCTATATGAAGTAATTAATGAGCCAAAGCAAGCTGCTTA 780
DB 721 ACCACTCTGCTACAGCTTCTATATGAAGTAATTAATGAGCCAAAGCAAGCTGCTTA 780
QY 781 TATGTGTGATATGTAATCAAAAAAAGCAAGTGGCGTCAACACTGTACTGTGTTGA 840
DB 781 TATGTGTGATATGTAATCAAAAAAAGCAAGTGGCGTCAACACTGTACTGTGTTGA 840
QY 841 CATGAGCAAAAAAGCAAGTGTGTAATTTTAATCAGAAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAAGCAAGTGTGTAATTTTAATCAGAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATATGATGGAAGAGCTGCTCATATCTGCTGTATGTTGGATCAGACAGATATA 960
DB 901 CTGGATATGATGGAAGAGCTGCTCATATCTGCTGTATGTTGGATCAGACAGATATA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAGAG 1020
DB 961 GTGAGCCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAGAG 1020

QY	1021	GCCACAGGATGATGCGTTTATGATCATCATCATGTAATTTGGCAGTTCCTTCTACATC	1080
Db	1021	GCCACAGGATGATGCGTTTATGATCATCATCATGTAATTTGGCAGTTCCTTCTACATC <td>1080</td>	1080
QY	1081	AAAGAAAAACAGATGCTAAATCTCTTGTGAAAAACAGCAATCCAGAA	1128
Db	1081	AAAGAAAAACAGATGCTAAATCTCTTGTGAAAAACAGCAATCCAGAA	1128
RESULT 27			
AAS99857			
ID	AAS99857	standard; cDNA; 1155 BP.	
XX			
AC	AAS99857;		
XX			
DT	12-MAR-2002	(first entry)	
XX			
DE	Breast tumour-specific DNA B11Agl splice variant B1C-15.		
KW	Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;		
KW	tumour; vaccine; immunogenic.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200190152-A2.		
PD			
XX	29-NOV-2001.		
FE	22-MAY-2001; 2001WO-US16776.		
XX			
PR	24-MAY-2000; 2000US-0577505.		
PR	08-JUN-2000; 2000US-0590583.		
PR	26-OCT-2000; 2000US-0699295.		
PR	16-MAR-2001; 2001US-0810936.		
XX			
PA	(CORI-) CORIXA CORP.		
PI	Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;		
PI	Wang A, Skelky YAW, Harlocker SL, Day CH;		
XX			
XX	WPI: 2002-089919/12.		
DR	P-PSDB; AAU74377.		
XX			
PT	New breast tumour proteins and polynucleotides encoding them, useful for		
PT	treating and/or preventing cancer, particularly breast cancer, and for		
PT	eliciting humoral and/or cellular immune response		
XX			
XX	Claim 1; Page 223; 245pp; English.		
CC			
CC	The invention relates to novel breast tumour polynucleotides and		
CC	polypeptides. The polypeptides and polynucleotides are useful in		
CC	pharmaceutical compositions for treating and/or preventing cancer,		
CC	particularly breast cancer, and for eliciting an immune response,		
CC	particularly humoral and/or cellular immune response. The polynucleotides		
CC	may be used as probes or primers for nucleic acid hybridisation. In the		
CC	design and preparation of ribozyme molecules for inhibiting expression of		
CC	tumour polypeptides and proteins, and in recombinant DNA molecules to		
CC	direct expression of a polypeptide in host cells. AAS99570-AAS99888		
CC	represent novel human breast cancer protein coding sequences and		
CC	PCR primers of the invention.		
XX			
XX	Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;		
SO			
Query Match	55.3%; Score 1128; DB 24; Length 1155;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1128; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGGTGTTGAGAGTTGATTCATCGCGGCTGCTTCTGTGAAGAAGCATTTGGTCTC	60
Db	1	ATGGTGTTGAGAGTTGATTCATCGCGGCTGCTTCTGTGAAGAAGCATTTGGTCTC	60
QY	61	AGGAGCAAGATGGCGAAGTGCTGCGCTTCCTCCCTGCTGAGAGAGCGGCAAG	120

Db	61	AGGACCAAGATGGGCAAGTGGTGGTGGCTGGCTTCCCTGCTGTCAGGGAGAGCGGGCAAG	120
Qy	121	AGCAACGTGGGCACTTTCTGGAGACCAACGACGACTCTGCTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTTCTGGAGACCAACGACGACTCTGCTATGAAGACACTCAGAGCAAG	180
Qy	181	ATGGGCAAGTGGTGGCGGCCACGTGCTTCCCTGCTGAGGGGAGTGGCAAGAGCAACGTG	240
Db	181	ATGGGCAAGTGGTGGCGGCCACGTGCTTCCCTGCTGAGGGGAGTGGCAAGAGCAACGTG	240
Qy	241	GGCGCTTCGGAGACACGACGACACTGCTGATGAAGACACTGAGCAACGATGGGCAAG	300
Db	241	GGCGCTTCGGAGACACGACGACACTGCTGATGAAGACACTGAGCAACGATGGGCAAG	300
Qy	301	TGGTCTGGCACTGCTTCCCTGCTGTCAGGGGAGCGGCAGACGAGTGGGCGCTTGG	360
Db	301	TGGTCTGGCACTGCTTCCCTGCTGTCAGGGGAGCGGCAGACGAGTGGGCGCTTGG	360
Qy	361	GGAGACTACGATGACAGTGGCTTCATGAGGAGCCAGGTACCACTCGTGGAGAAATCTG	420
Db	361	GGAGACTACGATGACAGTGGCTTCATGAGGAGCCAGGTACCACTCGTGGAGAAATCTG	420
Qy	421	GACAAGCTCCACAGAGCTGCTGATGGGGTAAAGTCCCCAGAAAGATCTATGTCATG	480
Db	421	GACAAGCTCCACAGAGCTGCTGATGGGGTAAAGTCCCCAGAAAGATCTATGTCATG	480
Qy	481	CTCAGGAGACACTGACGTGACAAGAAAGCAAGCAAGCAAGAGACATGCTACATCTGGCC	540
Db	481	CTCAGGAGACACTGACGTGACAAGAAAGCAAGCAAGCAAGAGACATGCTACATCTGGCC	540
Qy	541	TTGCGCAATGGGAATTACAGAAATGATTAACAATCTGCTGAGACAGACGATGCACCTTAAT	600
Db	541	TTGCGCAATGGGAATTACAGAAATGATTAACAATCTGCTGAGACAGACGATGCACCTTAAT	600
Qy	601	GTCCTTGACACAAAAAGAGAGCAGCTCTGATTAAGGCGCGTACAAATGCCAGAGATGAA	660
Db	601	GTCCTTGACACAAAAAGAGAGCAGCTCTGATTAAGGCGCGTACAAATGCCAGAGATGAA	660
Qy	661	TTGCGGTTAATGTTGCTGGAAATGAGCAATGGCAATGATTCGAAATTCGAGTATGGAAAT	720
Db	661	TTGCGGTTAATGTTGCTGGAAATGAGCAATGGCAATGATTCGAAATTCGAGTATGGAAAT	720
Qy	721	ACCACCTGTCACATAGCTATCTATATGAAATTAATTAATGAGCCCAAGCAGCTGCTTTA	780
Db	721	ACCACCTGTCACATAGCTATCTATATGAAATTAATTAATGAGCCCAAGCAGCTGCTTTA	780
Qy	781	TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTTCACACCACCTGTTACTTGGTGA	840
Db	781	TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTTCACACCACCTGTTACTTGGTGA	840
Qy	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCGAATTTAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCGAATTTAATGCA	900
Qy	901	CTGGATAGATATGAAGGACCTGCTCATACTTGGCTGATGTTGGTGGATCAGCAAGTATA	960
Db	901	CTGGATAGATATGAAGGACCTGCTCATACTTGGCTGATGTTGGTGGATCAGCAAGTATA	960
Qy	961	CTGACGCTTCTACTTGAGCAAAATATGATGATATCTTCTCAAGATCTATCTGGAACAGAG	1020
Db	961	CTGACGCTTCTACTTGAGCAAAATATGATGATATCTTCTCAAGATCTATCTGGAACAGAG	1020
Qy	1021	GCCAGAGATATGCTGTTTCTGATATATCAATCAATGTAATTTGCCAGTACTTCTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTGATATATCAATCAATGTAATTTGCCAGTACTTCTGACATAC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAA 1128	
Db	1081	AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAA 1128	

AAS9869
ID AAS9869 standard; DNA; 1590 BP.
AC AAS9869;
DT 12-MAR-2002 (first entry)
DE Breast tumour-specific gene B305D fusion construct.
XX
XX Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
XX Homo sapiens.
OS
PN W020190152-A2.
XX
XX 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US16776.
XX
XX 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
XX (CORI-) CORIXA CORP.
XX
PI Fridakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAW, Harlocker SL, Day CH;
XX
DR WPI; 2002-089919/12.
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
XX Example 8; Page 235; 245pp; English.
XX
PS The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
XX Sequence 1590 BP; 424 A; 403 C; 433 G; 329 T; 1 other:
SQ
Query Match 51.2%; Score 1044; DB 24; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 34 TCTTCTGTAAGAGCATTGTTGCTCAGAGCAAGATGGGCAAGTGGTCTCCGTTGC 93
DB 469 TCTTCTGTAAGAGCATTGTTGCTCAGAGCAAGATGGGCAAGTGGTCTCCGTTGC 528
QY 94 TTCCCTGCTGCGAGAGCGGCAAGAGCAACGTGGGCACTTGTGAGACGACGAC 153
DB 529 TTCCCTGCTGCGAGAGCGGCAAGAGCAACGTGGGCACTTGTGAGACGACGAC 588
QY 154 TCTGCTATGAAGACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 213
DB 589 TCTGCTATGAAGACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 648
QY 214 TCGAGGGGAGTGGCAAGCAAGCTGGGCGCTTCTGGAGACCAAGCACTCTGTATG 273
DB 649 TCGAGGGGAGTGGCAAGCAAGCTGGGCGCTTCTGGAGACCAAGCACTCTGTATG 708
QY 274 AAGACACTCAGAAAGATGGGCAAGTGGTGTGCACTGCTTCCCTCTCTCAAGGGG 333

DB 709 AAGACACTCAGAAAGATGGGCAAGTGGTGTGCACTGCTTCCCTCTCTCAAGGGG 768
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGATGACGTCCCTTCATGAGCCC 933
DB 769 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGATGACGTCCCTTCATGAGCCC 828
QY 394 AGGTACACGTCCTGAGAGATGTGAGCAAGCTCCACAGAGCTGCTGGGTAA 453
DB 829 AGGTACACGTCCTGAGAGATGTGAGCAAGCTCCACAGAGCTGCTGGGTAA 888
QY 454 GTCCCGAGAAAGATCTCATGTCATGCTCAGGAGACTGACGTGAACAAAGACAAAG 513
DB 889 GTCCCGAGAAAGATCTCATGTCATGCTCAGGAGACTGACGTGAACAAAGACAAAG 948
QY 514 CAAAAGAGACTGCTTACATCTGGGCTGCGCCAAATGGGAATTCAGAAAGTAAATC 573
DB 949 CAAAAGAGACTGCTTACATCTGGGCTGCGCCAAATGGGAATTCAGAAAGTAAATC 1008
QY 574 CTGCTGAGACAGATGTCACTTAATGTCCTGACAAACAAAAGAGACGCTGTATA 633
DB 1009 CTGCTGAGACAGATGTCACTTAATGTCCTGACAAACAAAAGAGACGCTGTATA 1068
QY 634 AAGCGGTACAAATGCCAGAGATGAATGTCCTTAATGTTGCTGGAACATGGCACTGAT 693
DB 1069 AAGCGGTACAAATGCCAGAGATGAATGTCCTTAATGTTGCTGGAACATGGCACTGAT 1128
QY 694 CCAATATTCAGATGATGGAATACCACCTGCTGACCTATCTAATGAAGAT 753
DB 1129 CCAATATTCAGATGATGGAATACCACCTGCTGACCTATCTAATGAAGAT 1188
QY 754 AATTAATGGCCAAAGACAGCTCTAATATGTCGATGTGAAATCAAAAACAAAGCAT 813
DB 1189 AATTAATGGCCAAAGACAGCTCTAATATGTCGATGTGAAATCAAAAACAAAGCAT 1248
QY 814 GGCTCACAACACTGTTACTTGGTGTACATGAGCAAAAACAGCAAGTGTGAATTTTA 873
DB 1249 GGCTCACAACACTGTTACTTGGTGTACATGAGCAAAAACAGCAAGTGTGAATTTTA 1308
QY 874 ATCAAGAAAAACGCAATTTAATGCACCTGATGATGATGGAAGAGCTGCTCATACTT 933
DB 1309 ATCAAGAAAAACGCAATTTAATGCACCTGATGATGATGGAAGAGCTGCTCATACTT 1368
QY 934 GCTGTAATGTTGATGATGAGCAAGATAGTACGCTTCTACTTGAACAAATATGATGTA 993
DB 1369 GCTGTAATGTTGATGATGAGCAAGATAGTACGCTTCTACTTGAACAAATATGATGTA 1428
QY 994 TCTTCTCAAGATCTATCTGGACAGAGCGCCAGAGATGCTGTTTCTACTCATATCAT 1053
DB 1429 TCTTCTCAAGATCTATCTGGACAGAGCGCCAGAGATGCTGTTTCTACTCATATCAT 1488
QY 1054 GTAATTTGCCAGTACTTCTGACTACAAAGAAAACAGATGCTTAATCTCTTGAA 1113
DB 1489 GTAATTTGCCAGTACTTCTGACTACAAAGAAAACAGATGCTTAATCTCTTGAA 1548
QY 1114 AAGCAATTCAGAA 1128
DB 1549 AAGCAATTCAGAA 1563
RESULT 29
AAS9872
ID AAS9872 standard; DNA; 1155 BP.
XX
XX AAS9872;
XX
XX 12-MAR-2002 (first entry)
XX
XX Breast tumour-specific gene B305D homologue #2.
DE Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX

OS Homo sapiens.
XX WO200190152-A2.
XX
XX
PD 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US16776.
XX
XX 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
XX (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
XX WPI; 2002-089919/12.
DR P-PSDB; AAU74390.
XX
XX New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
XX Claim 1; Page 239; 245pp; English.
XX
XX The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
XX Sequence 1155 BP; 346 A; 253 C; 296 G; 260 T; 0 other;
SQ
Query Match 47.88; Score 975; DB 24; Length 1155;
Best Local Similarity 99.78; Pred. No. 0;
Matches 1123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGCAAGTGTGCTGCTGCTTCCCTCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGCAAGTGTGCTGCTGCTTCCCTCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACACGACACTCTGTATGAAGACACTAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAGACACGACACTCTGTATGAAGACACTAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGACACGACGACTGTGCTATGAAGACACTAGAGCAAGATGGGCAAG 300
Db 241 GGGCTTCTGAGACACGACGACTGTGCTATGAAGACACTAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGAGACTACGATGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 GGAGACTACGATGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 CTCAGGAGACTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TCTGCCAATGGGAATTTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TCTGCCAATGGGAATTTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTCTTGAACAACAAAAGAGGACAGCTGTGATAAAGGCGTACATGCTGAGAGAGTAA 660
Db 601 GTCTTGAACAACAAAAGAGGACAGCTGTGATAAAGGCGTACATGCTGAGAGAGTAA 660
QY 661 TGTGCTTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TGTGCTTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 ACCACTGTGCACTACGCTATCTATATGAGTAAATTAATGAGCAAGCAAGCAAGCAAGCA 780
Db 721 ACCACTGTGCACTACGCTATCTATATGAGTAAATTAATGAGCAAGCAAGCAAGCAAGCA 780
QY 781 TATGCTGTGATATGCAATCAAAAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 TATGCTGTGATATGCAATCAAAAAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 CATGAGCAAAAACGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 CATGAGCAAAAACGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CTGATATATATGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 CTGATATATATGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GTGACCTTGTACCTGAGCAAAATATGATGTATCTCTCAAGATCTATCTGAGACAGC 1020
Db 961 GTGACCTTGTACCTGAGCAAAATATGATGTATCTCTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 GCCAGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 AAAGAAAACAGATCTATAAATCTCTCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAG 1128
Db 1081 AAAGAAAACAGATCTATAAATCTCTCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAG 1128
RESULT 30
AAV68995
ID AAV68995 standard; DNA; 1512 BP.
XX
AC AAV68995;
XX
XX 22-JAN-1999 (first entry)
XX
XX DNA molecule encoding a breast tumour specific polypeptide #187.
XX
XX Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW vaccine; epitope; endogenous; retroviral element; ss.
XX
XX Homo sapiens.
XX
XX WO9845328-A2.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98WO-US06939.
XX
XX 11-DEC-1997; 97US-0991789.
XX
XX 09-APR-1997; 97US-0838762.
XX

PA (CORI-) CORIXA CORP.
 XX Fridakis TN, Reed SG, Smith JM;
 XX WPI: 1998-557473/47.
 DR
 XX
 XX New DNA sequences isolated from endogenous human retroviral element
 PT - and related vectors, transformed cells, proteins and antibodies,
 PT useful for diagnosis, treatment and prevention of breast cancer
 XX
 PS Claim 1: Page 137-138; 173pp; English.
 XX
 XX AAV68800 to AAV68998 represent nucleotide sequences which encode human
 CC breast tumour specific polypeptides. Detection or measurement of
 CC human breast tumour specific polypeptides and nucleotide sequences,
 CC or the corresponding RNA in a sample, is used for diagnosis and
 CC monitoring of breast cancer. Human breast tumour specific polypeptides
 CC and nucleotide sequences, and the vectors containing the DNAs, are also
 CC useful in vaccines for inhibiting development (for prevention or
 CC therapy) of breast cancer. The polypeptides may also be used to
 CC raise monoclonal antibodies, used as immunoassay reagents.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
 Query Match 24.1%; Score 491; DB 19; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 6.4e-180;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 34 TCTTGTGAGAGAGCCATTGCTCTCAGAGACCAAGTGGGAGTGTGCGCTTGC 93
 DB 256 TCTTGTGAGAGAGCCATTGCTCTCAGAGACCAAGTGGGAGTGTGCGCTTGC 315
 OY 94 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGACCTTGGAGACCAAGAGC 153
 DB 316 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGACCTTGGAGACCAAGAGC 375
 OY 154 TCTGCTATGAGACACTCAGAGAGCAAGATGGGAGTGGGCGGACACTTCCCTGC 213
 DB 376 TCTGCTATGAGACACTCAGAGAGCAAGATGGGAGTGGGCGGACACTTCCCTGC 435
 OY 214 TGCAGGGGAGTGGCAAGACAGCTGGGCGCTTGTGAGACCAAGAGCAAGCTGTATG 273
 DB 436 TGCAGGGGAGTGGCAAGACAGCTGGGCGCTTGTGAGACCAAGAGCAAGCTGTATG 495
 OY 274 AAGACACTCAGAGAAACAATGGGCAAGTGTGCTGCCACTGCTTCCCTGCGAGGGG 333
 DB 496 AAGACACTCAGAGAAACAATGGGCAAGTGTGCTGCCACTGCTTCCCTGCGAGGGG 555
 OY 334 AGCGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGAGTGCCTTCATGGAGCCC 393
 DB 556 AGCRCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGAGTGCCTTCATGGAGCCC 615
 OY 394 AGGTACACGCTCGTGGAGAAAGTGGACAAGCTCCACAGAGCTGCCCTGTGGGTAAA 453
 DB 616 AGGTACACGCTCGTGGAGAAAGTGGACAAGCTCCACAGAGCTGCCCTGTGGGTAAA 675
 OY 454 GTCCCAAGAAAGAGATCTCATGCTGCTCAGGAGACACTGAGTGAACAAGAGCAAG 513
 DB 676 GTCCCAAGAAAGAGATCTCATGCTGCTCAGGAGACACTGAGTGAACAAGAGCAAG 735
 OY 514 CAAAGAGGAGACTGCTCATGCTGCTGCTGCAATGGGAATTGAGAAATAGTAAACATC 573
 DB 736 CAAAGAGGAGACTGCTCATGCTGCTGCTGCAATGGGAATTGAGAAATAGTAAACATC 795
 OY 574 CTGCTGAGACAGAGATGTCACCTTAATGTCTTGACAAACAAAGAGAGACAGCTGTGATA 633
 DB 796 STGCTGAGACAGAGATGTCACCTTAATGTCTTGACAAACAAAGAGAGACAGCTGTGATA 855
 OY 634 AAGGCGGTACATGGCAGAGAAATGATGTGGTTAATTTCTGTGAAATGCGACTGAT 693
 DB 856 AAGGCGGTACATGGCAGAGAAATGATGTGGTTAATTTCTGTGAAATGCGACTGAT 915
 OY 694 CCAATATTTCCAGATGAGTATGGAATAACACTCT 728

DB 916 CCAATATTTCCAGATGAGTATGGAATAACACTCT 950
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 31
 AAC81006
 ID AAC81006 standard; cDNA; 1512 BP.
 XX
 AC AAC81006;
 XX
 XX 13-FEB-2001 (first entry)
 DT
 XX Human B11a91 antigen protein coding exon cDNA SEQ ID NO: 294.
 XX
 DE Human; breast tumour-specific antigen; cytostatic; vaccine;
 XX breast cancer; B11a91; B11a91; B15a91; ss.
 KM
 XX Home sapiens.
 OS
 XX WO20061753-A2.
 PN
 XX 19-OCT-2000.
 PD
 XX 07-APR-2000; 2000WO-US09312.
 PF
 XX 09-APR-1999; 99US-0289198.
 PR 28-OCT-1999; 99US-0429755.
 PR 23-MAR-2000; 2000US-0534825.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 PI Fridakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
 DR WPI: 2000-628403/60.
 XX
 XX An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -
 PT
 PS Claim 4; Page 172; 187pp; English.
 XX
 XX The present sequence is given in a specification relating to compositions
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
 CC sequences that are preferentially expressed in breast tumour tissue, and
 CC the polypeptides encoded by such nucleotide sequences, are used in
 CC compositions and vaccines to inhibit the development of cancer,
 CC especially breast cancer. The progression of a cancer may be monitored by
 CC carrying out detection of tumour-specific antigens at subsequent time
 CC points and comparing the results from the different time points.
 CC CD4+ and/or CD8+ T-cells isolated from the cancer patient may be treated
 CC with tumour-specific polypeptides, polynucleotides encoding the
 CC polypeptides or antigen presenting cells expressing the polypeptides. The
 CC cells are then administered to the patient to inhibit development of
 CC cancer.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
 Query Match 24.1%; Score 491; DB 21; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 6.4e-180;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 34 TCTTGTGAGAGAGCCATTGCTCTCAGAGACCAAGTGGGAGTGTGCGCTTGC 93
 DB 256 TCTTGTGAGAGAGCCATTGCTCTCAGAGACCAAGTGGGAGTGTGCGCTTGC 315
 OY 94 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGACCTTGGAGACCAAGAGC 153
 DB 316 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGACCTTGGAGACCAAGAGC 375
 OY 154 TCTGCTATGAGACACTCAGAGAGCAAGATGGGAGTGGGCGGACACTGCTTCCCTGC 213
 DB 376 TCTGCTATGAGACACTCAGAGAGCAAGATGGGAGTGGGCGGACACTGCTTCCCTGC 435

QY 214 TGCAGGGGAGTGCGAAGCAAGCTGGGCGCTTCTGAGACGACGACTGTGCTATG 273
DB 436 TGCAGGGGAGTGCGAAGCAAGCTGGGCGCTTCTGAGACGACGACTGTGCTATG 495
QY 274 AAGCACTCAGGAACAGATGGGCAAGTGGTGGCCACGCTTCCCTGCTGAGGGG 333
DB 496 AAGCACTCAGGAACAGATGGGCAAGTGGTGGCCACGCTTCCCTGCTGAGGGG 555
QY 334 AGCGGCAAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGGCTTCATGGAGCC 393
DB 556 AGCGGCAAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGGCTTCATGGAGCC 615
QY 394 AGGTACCACTCGGTGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGTAA 453
DB 616 AGGTACCACTCGGTGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGTAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGCTCAGGGACACTGACGTAACAAGAGAGAG 513
DB 676 GTCCCGAAGAAAGATCTCATGCTGCTCAGGGACACTGACGTAACAAGAGAGAG 735
QY 514 CAAAAGAGAGCTGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
DB 736 CAAAAGAGAGCTGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
QY 574 CTGCTGACAGAGAGATCTCACTTAATGCTCTTGACACAAAAAGAGACAGCTGTATA 633
DB 796 STGCTGACAGAGAGATCTCACTTAATGCTCTTGACACAAAAAGAGACAGCTGTATA 855
QY 634 AAGCCCTTACAAATGCCAGAAAGATGTCGTTAATGTTGCGGAACATGGACATGAT 693
DB 856 AAGCCCTTACAAATGCCAGAAAGATGTCGTTAATGTTGCGGAACATGGACATGAT 915
QY 694 CCAATATTCAGATGATGGAATGGAATACCACTCT 728
DB 916 CCAATATTCAGATGATGGAATGGAATACCACTCT 950
RESULT 32
AAA06593
ID AAA06593 standard; cDNA; 1512 BP.
XX
AC AAA06593;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:368.
XX
KM Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX
KM Immunogenic; cytosolic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99MO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0232880.
XX
XX (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 50; Page 219; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AY82000 to AY82020 represent sequences used in the exemplification of
CC the present invention.

XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 21; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGCTCTCAGGAGCAAGATGGGCAAGTGGCTGCTGCTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGCTCTCAGGAGCAAGATGGGCAAGTGGCTGCTGCTGC 315
QY 94 TTCCCTGCTGCGAGGAGAGCGGCAAGCAAGCTGGGCACTTGTGAGACACGACAGC 153
DB 316 TTCCCTGCTGCGAGGAGAGCGGCAAGCAAGCTGGGCACTTGTGAGACACGACAGC 375
QY 154 TCTGCTATGAAGACATCTCAGAGAGCAAGATGGGCAAGTGGTGGCCCACTGCTCCCTGC 213
DB 376 TCTGCTATGAAGACATCTCAGAGAGCAAGATGGGCAAGTGGTGGCCCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGCGAAGCAAGCTGGGCGCTTCTGAGACGACGACACTGTGCTATG 273
DB 436 TGCAGGGGAGTGCGAAGCAAGCTGGGCGCTTCTGAGACGACGACACTGTGCTATG 495
QY 274 AAGCACTCAGGAACAGATGGGCAAGTGGTGGCCACGCTTCCCTGCTGAGGGG 333
DB 496 AAGCACTCAGGAACAGATGGGCAAGTGGTGGCCACGCTTCCCTGCTGAGGGG 555
QY 334 AGCGGCAAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGGCTTCATGGAGCC 393
DB 556 AGCGGCAAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGGCTTCATGGAGCC 615
QY 394 AGGTACCACTCGGTGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGTAA 453
DB 616 AGGTACCACTCGGTGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGTAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGCTCAGGGACACTGACGTAACAAGAGAGAG 513
DB 676 GTCCCGAAGAAAGATCTCATGCTGCTCAGGGACACTGACGTAACAAGAGAGAG 735
QY 514 CAAAAGAGAGCTGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
DB 736 CAAAAGAGAGCTGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
QY 574 CTGCTGACAGAGAGATCTCACTTAATGCTCTTGACACAAAAAGAGACAGCTGTATA 633
DB 796 STGCTGACAGAGAGATCTCACTTAATGCTCTTGACACAAAAAGAGACAGCTGTATA 855
QY 634 AAGCCCTTACAAATGCCAGAAAGATGTCGTTAATGTTGCGGAACATGGACATGAT 693
DB 856 AAGCCCTTACAAATGCCAGAAAGATGTCGTTAATGTTGCGGAACATGGACATGAT 915
QY 694 CCAATATTCAGATGATGGAATGGAATACCACTCT 728
DB 916 CCAATATTCAGATGATGGAATGGAATACCACTCT 950

Query Match	24.1%	Score 491	DB 22	Length 1512
Best Local Similarity	99.4%	Pred. NO. 6.4e-180		
Matches 691	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Sequence 1512 BP	406 A	301 C	393 G	399 T
13 other:				
Query Match	24.1% <td>Score 491 <td>DB 22 <td>Length 1512</td> </td></td>	Score 491 <td>DB 22 <td>Length 1512</td> </td>	DB 22 <td>Length 1512</td>	Length 1512
Best Local Similarity	99.4% <td>Pred. NO. 6.4e-180</td> <td></td> <td></td>	Pred. NO. 6.4e-180		
Matches 691	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Sequence 1512 BP	406 A	301 C	393 G	399 T
13 other:				

Db	376	TTCTGCTATTGAAGACACTCTAGAGGCAAGATGGGCAAGTGTGTCGCCCACTGCTTCCCTGC	435
Oy	214	TGCAAGGGGAGTGGCCAAAGCAACGTTGGGCGCTTCTGTGAGACCAAGCACTCTGCTATG	273
Db	436	TGCAAGGGGAGTGGCCAAAGCAACGTTGGGCGCTTCTGTGAGACCAAGCAAGATGCTGATG	495
Oy	274	AAGACACTCTAGGAACACAGATGGGCAAGTGTGTGCCACTGTCTTCCCTGTGTCAGGGGG	333
Db	496	AAGACACTCAGGAACACAGATGGGCAAGTGTGTGCCACTGTCTTCCCTGTGTCAGGGGG	555
Oy	334	AGCGCCAGAGCAAGGTGGGGGCTTGGGGACATACATGACATGACGTGCTTCATGAGACCC	393
Db	556	AGCGCCAGAGCAAGGTGGGGGCTTGGGGACATACATGACATGACATGCTTCATGAGACCC	615
Oy	394	AGGTCCACAGTCCGGGAGAGATCTGTGACAAAGCTCCACAGAGTGCCTGGTGGGGTAAA	453
Db	616	AGGTCCACAGTCCGGGAGAGATCTGTGACAAAGCTCCACAGAGTGCCTGGTGGGGTAAA	675
Oy	454	GTGCCCAAGAAAGATCTCATCTGTCATGCTCAGGGACACTGACGTGAACAGAGAGACAG	513
Db	676	GTGCCCAAGAAAGATCTCATCTGTCATGCTCAGGGACACTGACGTGAACAGAGAGACAG	735
Oy	514	CAAAAGAGAGCTGCTCTCATCTGTGGCCCTCTCCCAATGGGAATTCAGAAATGTAATTAATC	573
Db	736	CAAAAGAGAGCTGCTCTCATCTGTGGCCCTCTCCCAATGGGAATTCAGAAATGTAATTAATC	795
Oy	574	CTGCTGGACAGACGATGTCACTTAATGTCCCTGACAAACAAAAGAGAGACAGCTCTGATA	633
Db	796	STGCTGGACAGACGATGTCACTTAATGTCCCTGACAAACAAAAGAGAGACAGCTCTGATA	855
Oy	634	AAGGCCGTACAAATGCGCAGGAAGATGAATGTGCGTTAATGTTGTGTGAACATGCGCATGAT	693
Db	856	AAGGCCGTACAAATGCGCAGGAAGATGAATGTGCGTTAATGTTGTGTGAACATGCGCATGAT	915
Oy	694	CCAAATATTCCAGATGATATGGAATTCACACTCT	728
Db	916	CCAAATATTCCAGATGATGGAATTCACACTCT	950
RESULT 34			
AAH93709			
ID	AAH93709	standard; cDNA: 1512 BP.	
XX	AC		
XX	AAH93709;		
DT	04-OCT-2001	(first entry)	
XX	XX		
DE	XX	Human prostate-specific cDNA sequence B305D splice variant #3.	
XX	XX		
KM	XX	Human: prostate cancer; prostate-specific; diagnosis; vaccine;	
KW	XX	cytostatic; gene therapy; metastasis; ss.	
XX	OS	Homo sapiens.	
XX	PN	WO200151633-A2.	
XX	PD	19-JUL-2001.	
XX	PF	16-JAN-2001; 2001WO-US01574.	
XX	PR	14-JAN-2000; 2000US-0483672.	
XX	PA	(CORI-) CORIXA CORP.	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;		
PI	Kalos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelky YAW,		
PI	Wang A, Meagher MJ;		
XX	WPI: 2001-425873/45.		
PT	New polynucleotide encoding a prostate-specific protein, for		
PT	diagnosing, monitoring and treating prostate cancer in a patient and		

PT for use in vaccines -

XX PS Claim 1; Page 343-344; 543pp; English.

XX CC The present invention describes polynucleotide sequences (I) which encode
XX CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX CC and can be used in vaccine production and gene therapy. (I), (II),
XX CC antibodies to (II), fusion proteins comprising (II), and isolated
XX CC T cells prepared using (I) or (II) are used treat cancer in a patient.
XX CC (I) and the antibodies are also used in the detection of cancer in a
XX CC patient. The cancer that is diagnosed or treated is particularly
XX CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX CC (I) can be used for monitoring the progression of cancer in a patient.
XX CC (I) and (II) can also be used to improve diagnostic and therapeutic
XX CC methods for prostate cancer. They can indicate the level of metastasis
XX CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
XX CC AAH01318 represent polynucleotide and amino acid sequences used in the
XX CC exemplification of the present invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180; Mismatches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 34 TCTTCTGTGAAGAACCATTTGTTCTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTGC 93
XX 256 TCTTCTGTGAAGAACCATTTGTTCTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTGC 315
XX 94 TTCCCTGCTCCAGGAGAGGCGGCAAGACAGTGGGCACTTCTTGAGACACGACGAC 153
XX 316 TTCCCTGCTCCAGGAGAGGCGGCAAGACAGTGGGCACTTCTTGAGACACGACGAC 375
XX 154 TCTGCTATGAAGACACTCAGGAGCAAGTGGGCAAGTGGTCCGCGCACTGCTCCCTGC 213
XX 376 TCTGCTATGAAGACACTCAGGAGCAAGTGGGCAAGTGGTCCGCGCACTGCTCCCTGC 435
XX 214 TGCAGGGGGAGTGGCAAGACAGTGGGCGCTTCTGAGACCAAGAGTCTGCTATG 273
XX 436 TGCAGGGGGAGTGGCAAGACAGTGGGCGCTTCTGAGACCAAGAGTCTGCTATG 495
XX 274 AAGCACTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTGCTGCAAGGGG 333
XX 496 AAGCACTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTGCTGCAAGGGG 555
XX 334 AGCGGCAAGCAAGTGGGCGCTTGGGAGACTACAGTACAGTGGCTTCATGAGGCC 393
XX 556 AGCGCAAGCAAGTGGGCGCTTGGGAGACTACAGTACAGTGGCTTCATGAGGCC 615
XX 394 AGTACCAAGTGGTGGAGAAATCTGAGACAAGCTCCACAGAGCTGCTGGGTAA 453
XX 616 AGTACCAAGTGGTGGAGAAATCTGAGACAAGCTCCACAGAGCTGCTGGGTAA 675
XX 454 GTCCCGAAGAAAGTCTCATCTGTCATGCTCAGGAGCACTGACGTGAACAGAGACAAG 513
XX 676 GTCCCGAAGAAAGTCTCATCTGTCATGCTCAGGAGCACTGACGTGAACAGAGACAAG 735
XX 514 CAAAAGAGAGTGGTCTACATCTGGCTGCGCAATGGGAATTAGAGAGTAAACTC 573
XX 736 CAAAAGAGAGTGGTCTACATCTGGCTGCGCAATGGGAATTAGAGAGTAAACTC 795
XX 574 CTGCTGACAGAGAGTGTCAACTTAATGCTCTTGACAACAAAAGAGAGAGCTGTATA 633
XX 796 STGCTGACAGAGAGTGTCAACTTAATGCTCTTGACAACAAAAGAGAGAGCTGTATA 855
XX 634 AAGGCGCTTACAAATGCCAGGAAGATGATGTCGTTAATGTTCTGCGAATGGCAGTAT 693
XX 856 AAGGCGCTTACAAATGCCAGGAAGATGATGTCGTTAATGTTCTGCGAATGGCAGTAT 915
XX 694 CCAAAATATTCAGATGATGATGAAATACCACTCT 728
XX 916 CCAAAATATTCAGATGATGATGAAATACCACTCT 950

RESULT 35

AAH85023 ID AAH85023 standard; cDNA; 1512 BP.

XX AC AAH85023;

XX DT 25-SEP-2001 (first entry)

XX DE Human prostate-specific cDNA sequence B305D splice variant #3.

XX KW Human: prostate cancer; therapy; diagnosis; cat eye syndrome;

XX KW chromosome 22q11.2; prostate-specific protein; chromosome 1;

XX KW prostate specific antigen; PSA; ss.

XX OS Homo sapiens.

XX PN W0200134802-A2.

XX PD 17-MAY-2001.

XX PF 09-NOV-2000; 2000WC-US30904.

XX PR 12-NOV-1999; 99US-0439313.

XX PR 18-NOV-1999; 99US-0443686.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

XX PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;

XX WP1; 2001-308785/32.

XX PS Claim 31; Page 243-244; 325pp; English.

XX CC The present invention describes an isolated polypeptide (P1) comprising
XX CC at least an immunogenic portion of a prostate-specific protein, or its
XX CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
XX CC (N1) have cytostatic activity and can be used in vaccine production.
XX CC The polypeptides, nucleic acids and antibodies from the present
XX CC invention are useful in the diagnosis and therapy of prostate cancer.
XX CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
XX CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
XX CC region. Prostate specific antigen (PSA) P501S was located on
XX CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
XX CC polynucleotide and polypeptide sequences used in the exemplification
XX CC of the present invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180; Mismatches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 34 TCTTCTGTGAAGAACCATTTGTTCTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTGC 93
XX 256 TCTTCTGTGAAGAACCATTTGTTCTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTGC 315
XX 94 TTCCCTGCTCCAGGAGAGGCGGCAAGACAGTGGGCACTTCTTGAGACACGACGAC 375
XX 316 TTCCCTGCTCCAGGAGAGGCGGCAAGACAGTGGGCACTTCTTGAGACACGACGAC 435
XX 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCGCACTGCTCCCTGC 213
XX 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCGCACTGCTCCCTGC 435
XX 214 TGCAGGGGGAGTGGCAAGACAGTGGGCGCTTCTTGAGACCAAGACAGTCTGCTATG 273
XX 436 TGCAGGGGGAGTGGCAAGACAGTGGGCGCTTCTTGAGACCAAGACAGTCTGCTATG 495

OY	274	AAGACACTCAGAAACAAGATGGGCAAGGGGCGCCACAGCTCCCTCCCTCCTCAGAGGGG	3333
Db	496	AAGACACTCAGAAACAAGATGGGCAAGGGGCGCCACAGCTCCCTCCCTCCTCAGAGGGG	5555
OY	334	AGCGGCAAGACCAAGGTGGGCGCTTGGGGAGACTACATGCATGACATGCCTTCATGAGACC	3939
Db	556	AGCRGCAAGACCAAGGTGGGCGCTTGGGGAGACTACATGCATGACATGCCTTCATGAGACC	6151
OY	394	AGGTAACCACTGCTCGTGGAGAAAGATCTGGACAACTCCACAGAGCTGCTCGTGGGGTTAA	4535
Db	616	AGGTAACCACTGCTCGTGGAGAAAGATCTGGACAAAGTCCACAGAGTGGCTCGTGGGGTTAA	6757
OY	454	GTCCGCAAGAAAGATCTCATGCTATGCTCGAGGACACTGACGTGACCAAGAAAGAACAG	5131
Db	676	GTCCGCAAGAAAGATCTCATGCTATGCTCGAGGACACTGACGTGACCAAGAAAGAACAG	7355
OY	514	CAAAAAGAGACTGCTCTACATCTGGGCGCTCTGCCAATGGGAATTCAGAGTAGTAAACCTC	5737
Db	736	CAAAAAGAGACTGCTCTACATCTGGGCGCTCTGCCAATGGGAATTCAGAGTAGTAAACCTC	7959
OY	574	CTGCTGGACACAGCATGTCACACTTAATGTCTCTTACACAACAAAAAGAGACAGCTGTATA	6333
Db	796	STGCTGGACACAGCATGTCACACTTAATGTCTCTTACACAACAAAAAGAGACAGCTGTATA	8555
OY	634	AAGCGCTACAAATCCCAAGGAAGATGAATGTGCGTTAATGTGTGCGAACAATGGCACTGAT	6939
Db	856	AAGCGCTACAAATCCCAAGGAAGATGAATGTGCGTTAATGTGTGCGAACAATGGCACTGAT	9151
OY	694	CCAAATATTCAGATGAGTAGAAGAAATACCACTCT 728	
Db	916	CCAAATATTCAGATGAGTAGAAGAAATACCACTCT 950	

CC	AAH02774	standard; cDNA; 1512 BP.
CC	AAH02774	
CC	AAH02774	
CC	14-JUN-2001	(first entry)
CC	Prostate tumour antigen determined cDNA splice variant of B305D #3.	
CC	Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;	
CC	prostate cancer; immunogenic; cytosolic; vaccine; ss.	
CC	Homo sapiens.	
CC	MO200125272-A2.	
CC	12-APR-2001.	
CC	04-OCT-2000; 2000MO-US27464.	
CC	04-OCT-1999; 99US-0157455.	
CC	(CORI-) CORIXA CORP.	
CC	Xu J, Skeiky YAM, Reed SG, Cheever MA;	
CC	WPI; 2001-245062/25.	
CC	Prostate specific protein and its encoding polynucleotide, useful for	
CC	the treatment and diagnosis of prostate cancer -	
CC	Claim 50; Page 229; 276pp; English.	

CC Pharmaceutical composition containing (i) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AB574798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match	24.18;	Score 491;	DB 82;	Length 1512;
Best Local Similarity	99.48;	Pred. No. 6.4e-180;		
Matches 691; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

OY	34	TCCTCTGGAAGAAAGCCATTGGTCTCAGAGGCAAGATGGGCAAGTGTGCTGCGCTTGC	93
Dd	256	TCCTTGTGGAAGAAAGCCATTGGTCTCAGAGGCAAGATGGGCAAGTGTGCTGCGCTTGC	31.5
OY	94	TTCCCTCTCTCTCAGAGGAGCGGCAAGAGCAACGTGGGCACTTCTTGAGACACAGAGAC	15.3
Dd	316	TTCCCTCTCTCAGAGGAGCGGCAAGAGCAACGTGGGCACTTCTTGAGACACAGAGAC	37.5
OY	134	TCTGCTATGAAGAACCTCAGAGGCAAGATGGGCAAGTGTGCGGCCACTGCTTCCCTGC	21.3
Dd	376	TCTGCTATGAAGAACCTCAGAGGCAAGATGGGCAAGTGTGCGGCCACTGCTTCCCTGC	43.5
OY	214	TGCAGGGGAGTGGCAGAGCAAGTGGGGCTTCTGAGAGCCAGCAGACTGCTGATG	27.3
Dd	436	TGCAGGGGAGTGGCAGAGCAAGTGGGGCTTCTGAGAGCCAGCAGACTGCTGATG	49.5
OY	274	AAGACATCTCAGAGAACAGATGGGCAAGTGTGTGCTGCCACTGCTTCCCTCTGAGGGG	33.3
Dd	496	AAGACATCTCAGAGAACAGATGGGCAAGTGTGTGCTGCCACTGCTTCCCTCTGAGGGG	55.5
OY	334	AGCGGCAAGAGCAAGTGTGGCGCTTTGGGGAGACTACATGACAGTGCCTTCATGAGACC	39.3
Dd	556	AGCGGCAAGAGCAAGTGTGGCGCTTTGGGGAGACTACATGACAGTGCCTTCATGAGACC	61.5
OY	394	AGGTCCACAGTCCGGGGAGGAAGATCTGGACAAAGCTCCACAGAGTGCCTGGTGGGTTAA	45.3
Dd	616	AGGTCCACAGTCCGGGGAGGAAGATCTGGACAAAGCTCCACAGAGTGCCTGGTGGGTTAA	67.5
OY	454	GTCCCCAGAAAGGATCTCATGCTGCTCAGGGACACTGACGTGAACAAGAGAGACAG	51.3
Dd	676	GTCCCCAGAAAGGATCTCATGCTGCTCAGGGACACTGACGTGAACAAGAGAGACAG	73.5
OY	514	CAAAAGAGGACTGCTTACATCTGGCCTCTGCCAAATGGGAATTCAGAAATGTTAAACTC	57.3
Dd	736	CAAAAGAGGACTGCTTACATCTGGCCTCTGCCAAATGGGAATTCAGAAATGTTAAACTC	79.5
OY	574	CTGCTGGACAGACGATGTCACCTTAATGTCTCTACAACAAAAAAGAGACAGCTGTGTA	63.3
Dd	796	CTGCTGGACAGACGATGTCACCTTAATGTCTCTACAACAAAAAAGAGACAGCTGTGTA	85.5
OY	634	AAGGCCGTACATGCCAGGAAGATGAATGTGCGTTAATGTGTGTCGGAACATGGCAGTAT	69.3
Dd	856	AAGGCCGTACATGCCAGGAAGATGAATGTGCGTTAATGTGTGTCGGAACATGGCAGTAT	91.5
OY	694	CCAAATATTCCAGATGAGTATGGAATATCCACTCT	728
Dd	916	CCAAATATTCCAGATGAGTATGGAATATCCACTCT	950
RESULT 37			
ABL95173			
ID	ABL95173	standard; cDNA: 1512 BP.	
XX	ABL95173;		
XX	19-JUN-2002	(first entry)	
DE	Human B305D splice variant cDNA sequence SEQ ID NO 368.		

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
XX US2002022248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
XX 01-AUG-1997; 97US-0904804.
XX 09-FEB-1998; 98US-0020956.
XX 25-FEB-1998; 98US-0030607.
XX 14-JUL-1998; 98US-0115453.
XX 23-SEP-1998; 98US-0159812.
XX 15-JAN-1999; 99US-0232149.
XX 09-APR-1999; 99US-0288946.
XX 13-JUL-1999; 99US-0352616.
XX 12-NOV-1999; 99US-0439313.
XX 18-NOV-1999; 99US-0443686.
XX 14-JAN-2000; 2000US-0483672.
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PI XU J, DILLON DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX Claim 1: SEQ ID NO 368; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;
SO Query Match 24.1%; Score 491; DB 24; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 34 TCTTCGTGAAGAACCATTTGGCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGC 93
|||
Db 256 TCTTCGTGAAGAACCATTTGGCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGC 315
OY 94 TTCCTCTGTCAGAGGAGACCGGCACAGACCACTTCTGAGACCAAGACAGAC 153
|||
Db 316 TTCCTCTGTCAGAGGAGACCGGCACAGACCACTTCTGAGACCAAGACAGAC 375
OY 154 TCTGCTATGAAGACACCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGC 213
|||
Db 376 TCTGCTATGAAGACACCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGC 435
OY 214 TGCAGGGGAGTGGCAAGACCAAGTGGGCTTCTGAGACCAAGACAGTGTGATG 273
|||
Db 436 TGCAGGGGAGTGGCAAGACCAAGTGGGCTTCTGAGACCAAGACAGTGTGATG 495
OY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCTCCACTTCCCTGTCAGAGGGG 333
|||
Db 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCTCCACTTCCCTGTCAGAGGGG 555
OY 334 AGCGGCAGAGCAAGTGGGCGCTTGGGGAGACTAGCATGCTGCTTCAATGAGGCC 393
|||
Db 556 AGCGGCAGAGCAAGTGGGCGCTTGGGGAGACTAGCATGCTGCTTCAATGAGGCC 615
OY 394 AGGTACACGCTCGTGAGAGAGATCTGACACAGTCCACAGACTGCTGGGGTAA 453
|||
Db 616 AGGTACACGCTCGTGAGAGAGATCTGACACAGTCCACAGACTGCTGGGGTAA 675
OY 454 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGACTAGCATGCTGCTGAGAGCAAG 513
|||
Db 676 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGACTAGCATGCTGCTGAGAGCAAG 735
OY 514 CAAAAGAGAGCTGCTACATCTGCGCTTGGCCCAATGGGAATTCAGAAAGTAAACTC 573
|||
Db 736 CAAAAGAGAGCTGCTACATCTGCGCTTGGCCCAATGGGAATTCAGAAAGTAAACTC 795
OY 574 CTGCTGACAGAGATGTCACCTTAATGTCCTGACACAAAGAGAGACAGCTGTGATA 633
|||
Db 796 STGCTGACAGAGATGTCACCTTAATGTCCTGACACAAAGAGAGACAGCTGTGATA 855
OY 634 AAGGCCGTACAAATGCCAGAAATGAATGCGTTAATGTTGCTGAAACATGGCACTGAT 693
|||
Db 856 AAGGCCGTACAAATGCCAGAAATGAATGCGTTAATGTTGCTGAAACATGGCACTGAT 915
OY 694 CCAAAATTTCCAGATGATGTAATGGAATACCACTCT 728
|||
Db 916 CCAAAATTTCCAGATGATGTAATGGAATACCACTCT 950
RESULT 38
ABK46896
ID ABK46896 standard; DNA: 1512 BP.
XX
XX ABK46896;
XX
XX 05-JUN-2002 (first entry)
XX
XX Human breast tumour-specific DNA B11a91, protein coding exon #3.
XX
XX Human; breast tumour-specific protein; vaccine; breast cancer;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX US6344550-B1.
XX
XX 05-FEB-2002.
PD
XX 17-APR-1998; 98US-0062451.
XX

PR 01-JAN-1996; 96US-0585392.
PR 20-AUG-1996; 96US-0700014.
PR 10-JAN-1997; 97WO-US00485.
PR 09-APR-1997; 97US-0838762.
PR 11-DEC-1997; 97US-0991789.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG;
XX
XX WPI: 2002-215084/27.
XX
XX Polynucleotide encoding breast-specific tumour polypeptides useful as
XX vaccine for preventing and treating breast cancer in a subject -
XX
PS Claim 1; Column 211-213; 128pp; English.
XX
XX The invention relates to an isolated DNA molecule (I) encoding breast-
XX tumour-specific polypeptides. (I) is useful as a vaccine for preventing
XX and treating breast cancer in a subject. The polypeptide encoded by (I)
XX is used for production of compounds such as antibodies useful in
XX diagnosing and monitoring the progression of breast cancer. ABR46614-
XX ABR46899 represent human breast tumour-specific coding sequences and
XX related PCR primers of the invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 24; Length 1512;
Best Local Similarity 99.4%; Pred. No. 6.4e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTCTGTGAAGAACCCATTGCTCTCAGAGCAGATGGGCAAGTGGTGCCTGCTGC 93
DB 256 TCTTCTGTGAAGAACCCATTGCTCTCAGAGCAGATGGGCAAGTGGTGCCTGCTGC 315
OY 94 TTCCCTCTGCGAGGAGAGCGGCAAGCAACGTGGGCACTTCTGAGACGACGACGAC 153
DB 316 TTCCCTCTGCGAGGAGAGCGGCAAGCAACGTGGGCACTTCTGAGACGACGACGAC 375
OY 154 TCTGTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGCCTGCTGCCTGCTGC 213
DB 376 TCTGTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGCCTGCTGCCTGCTGC 435
OY 214 TGCAGGGGAGTGGCAAGCAAGCTGGGCGCTTCTGAGACACGACGACGACGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGCTGGGCGCTTCTGAGACACGACGACGACGCTATG 495
OY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGCCTGCTGCCTGCTGCCTGCTGC 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGCCTGCTGCCTGCTGCCTGCTGC 555
OY 334 AGCGGCAAGCAAGATGGGCGCTTGGGCAACTACGATGACAGTGCCTTCAATGAGCCC 393
DB 556 AGCGGCAAGCAAGATGGGCGCTTGGGCAACTACGATGACAGTGCCTTCAATGAGCCC 615
OY 394 AGGTACCAAGTCCGTGGGAAGATCTGGCAAGCTCCACAGAGTGCCTGGGGGTTAA 453
DB 616 AGGTACCAAGTCCGTGGGAAGATCTGGCAAGCTCCACAGAGTGCCTGGGGGTTAA 675
OY 454 GTCCCCAGAAAGATCTCATCTGTCATGCTCAGGAGCACTGACGTGAACAAGAGCAAG 513
DB 676 GTCCCCAGAAAGATCTCATCTGTCATGCTCAGGAGCACTGACGTGAACAAGAGCAAG 735
OY 514 CAAAAGAGAGCTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAGTAAACTC 573
DB 736 CAAAAGAGAGCTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAGTAAACTC 795
OY 574 CTGTGACAGACAGATGCACTTAATGCTTGAACAACAAAGAGGACACTCTGATA 633
DB 796 STGCTGGACAGACAGATGCACTTAATGCTTGAACAACAAAGAGGACACTCTGATA 855
OY 634 AAGGCGGTACAAATGCGCAGGAAGATGAATGTGCTTAATGCTGGAACATGGCACTGAT 693
|||||

DB 856 AAGGCGGTACAAATGCGCAGGAAGATGAATGTGCTTAATGCTGGAACATGGCACTGAT 915
OY 694 CCAATATTCCAGATGAGTGAATAATACACTCT 728
DB 916 CCAATATTCCAGATGAGTGAATAATACACTCT 950

RESULT 39
AAS99852
ID AAS99852 standard; cDNA; 1512 BP.
XX
XX AAS99852;
XX
XX 12-MAR-2002 (first entry)
XX
XX Breast tumour-specific DNA #225.
DE

KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
XX Homo sapiens.
OS
XX WO200190152-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 22-MAY-2001; 2001WO-US16776.
PF
XX
XX 24-MAY-2000; 2000US-0577505.
PR
XX 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
XX (CORI-) CORIXA CORP.

PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
XX WPI: 2002-089919/12.
DR
XX
XX New breast tumour proteins and polynucleotides encoding them, useful for
XX treating and/or preventing cancer, particularly breast cancer, and for
XX eliciting humoral and/or cellular immune response -
XX
PS Claim 1; Page 219; 245pp; English.

XX The invention relates to novel breast tumour polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response,
XX particularly humoral and/or cellular immune response. The polynucleotides
XX may be used as probes or primers for nucleic acid hybridisation. In the
XX design and preparation of ribozyme molecules for inhibiting expression of
XX tumour polypeptides and proteins, and in recombinant DNA molecules to
XX direct expression of a polypeptide in host cells. AAS9570-AAS9888
XX represent novel human breast cancer protein coding sequences and
XX PCR primers of the invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 24; Length 1512;
Best Local Similarity 99.4%; Pred. No. 6.4e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTCTGTGAAGAACCCATTGCTCTCAGAGCAGATGGGCAAGTGGTGCCTGCTGC 93
DB 256 TCTTCTGTGAAGAACCCATTGCTCTCAGAGCAGATGGGCAAGTGGTGCCTGCTGC 315
OY 94 TTCCCTCTGCGAGGAGAGCGGCAAGCAACGTGGGCACTTCTGAGACGACGACGAC 153
DB 316 TTCCCTCTGCGAGGAGAGCGGCAAGCAACGTGGGCACTTCTGAGACGACGACGAC 375
OY 154 TCTGTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGCCTGCTGCCTGCTGC 213
|||||

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Db 376 TCTGCTATGAGACACACAGAGAGCAGATGGGCAAGTGGGCCCCCTCTCTCCCTGC 435
QY 214 TGCAGGGGAGGTGGCAAGACAGCTGGGGCTTCTGAGAGCCAGACGATGCTATG 273
Db 436 TGCAGGGGAGGTGGCAAGACAGCTGGGGCTTCTGAGAGCCAGACGATGCTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 333
Db 496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 555
QY 334 AGCGGCAGAGCAAGTGGGGCGCTTGGGGAGACTACAGTACAGTGGCTTCATGGAGCC 393
Db 556 AGCGGCAGAGCAAGTGGGGCGCTTGGGGAGACTACAGTACAGTGGCTTCATGGAGCC 615
QY 394 AGTACCACTCCGTGGAGAGATCTGAGACAGCTCCAGAGAGCTGGCTGGGGGTAA 453
Db 616 AGTACCACTCCGTGGAGAGATCTGAGACAGCTCCAGAGAGCTGGCTGGGGGTAA 675
QY 454 GTCCCCGAAAAGATCTCATCTCATGCTCAGGACACTGACGTGAACAAGAGACAG 513
Db 676 GTCCCCGAAAAGATCTCATCTCATGCTCAGGACACTGACGTGAACAAGAGACAG 735
QY 514 CAAAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAAACTC 573
Db 736 CAAAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAAACTC 795
QY 574 CTCTGGACAGAGAGTGTCAATTAATGTCTTGACAAACAAAAGAGACAGCTGTAT 633
Db 796 STCTGGACAGAGAGTGTCAATTAATGTCTTGACAAACAAAAGAGACAGCTGTAT 855
QY 634 AAGCCGCTACAAATGCCAGAGATGAATGTCCGTTAATGTCTGTAACATGGCAGTAT 693
Db 856 AAGCCGCTACAAATGCCAGAGATGAATGTCCGTTAATGTCTGTAACATGGCAGTAT 915
QY 694 CCAAAATATCCAGATGATGTAATGAAATACACACT 728
Db 916 CCAAAATATCCAGATGATGTAATGAAATACACACT 950

RESULT 40
AAV68996
ID AAV68996 standard; DNA; 1853 BP.
XX
AC AAV68996;
XX
DT 22-JAN-1999 (first entry)
XX
DE DNA molecule encoding a breast tumour specific polypeptide #188.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
XX vaccine; epitope; endogenous; retroviral element; ss.
XX
OS Homo sapiens.
XX
PN WO9845328-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98MO-US06939.
XX
PR 11-DEC-1997; 97US-0991789.
XX
PR 09-APR-1997; 97US-0838762.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM;
XX
DR WPI: 1998-557473/47.
XX
PT New DNA sequences isolated from endogenous human retroviral element
PT - and related vectors, transformed cells, proteins and antibodies,
PT useful for diagnosis, treatment and prevention of breast cancer
```

```

XX
PS Claim 1; Page 138-139; 173pp; English.
CC AAV68800 to AAV68998 represent nucleotide sequences which encode human
CC breast tumour specific polypeptides. Detection or measurement of
CC human breast tumour specific polypeptides and nucleotide sequences,
CC or the corresponding RNA in a sample, is used for diagnosis and
CC monitoring of breast cancer. Human breast tumour specific polypeptides
CC and nucleotide sequences, and the vectors containing the DNAs, are also
CC useful in vaccines for inhibiting development (for prevention or
CC therapy) of breast cancer. The polypeptides may also be used to
CC raise monoclonal antibodies, used as immunoassay reagents.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
XX
Query Match 12.4%; Score 252; DB 19; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCCGTTGC 93
Db 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCCGTTGC 315
QY 94 TTCCCTCTGCTGCAGGAGAGACGGCAAGCAAGTGGGCACTTCTGAGACACAGAGAC 153
Db 316 TTCCCTCTGCTGCAGGAGAGACGGCAAGCAAGTGGGCACTTCTGAGACACAGAGAC 375
QY 154 TCTGCTATGAAAGACACTCAGAGACAGATGGGCAAGTGGGCGCCACTCTCCCTGC 213
Db 376 TCTGCTATGAAAGACACTCAGAGACAGATGGGCAAGTGGGCGCCACTCTCCCTGC 435
QY 214 TGCAGGGGAGGTGGCAAGACCAAGTGGGCGCTTCTGAGACCAAGCAAGCACTGTATG 273
Db 436 TGCAGGGGAGGTGGCAAGACCAAGTGGGCGCTTCTGAGACCAAGCAAGCACTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 333
Db 496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 555
QY 334 AGC 336
Db 556 AGC 558

RESULT 41
AAC81007
ID AAC81007 standard; cDNA; 1853 BP.
XX
AC AAC81007;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B1Agl antigen protein coding exon cDNA seq ID NO: 295.
XX
KW Human; breast tumour-specific antigen; cytostatic; vaccine;
XX breast cancer; B1Agl1; B1Agl1; B15Agl1; ss.
XX
OS Homo sapiens.
XX
PN WO200061753-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000MO-US09312.
XX
PR 09-APR-1999; 99US-0289198.
XX
PR 28-OCT-1999; 99US-0429755.
XX
PR 23-MAR-2000; 2000US-0534825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX
```

DR WPI: 2000-628403/60.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX
XX
PS Claim 4; Page 172-173; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
XX
Query Match 12.4%; Score 252; DB 21; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 34 TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGC 93
DB 256 TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGC 315
XX
QY 94 TTCCCTCTGTCAGAGGAGCGCGCAAGAGCAAGTGTGCTTGTGAACACGACGAC 153
DB 316 TTCCCTCTGTCAGAGGAGCGCGCAAGAGCAAGTGTGCTTGTGAACACGACGAC 375
XX
QY 154 TCTGTATGAACACTCTGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGCCTTGC 213
DB 376 TCTGTATGAACACTCTGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGCCTTGC 435
XX
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGTGCTTGTGAAGACGACGACGACTGTCTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGTGCTTGTGAAGACGACGACGACTGTCTATG 495
XX
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGTGCTGCTCTTCCCTGTGCAAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGTGCTGCTCTTCCCTGTGCAAGGGG 555
XX
QY 334 AGC 336
DB 556 AGC 558
XX
RESULT 42
AAA06594
ID AAA06594 standard; cDNA; 1853 BP.
XX
XX AAA06594;
XX
XX 13-JUN-2000 (first entry)
XX
XX Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:369.
XX
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX
XX Immunogenic; cytostatic; vaccine; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200004149-A2.
XX
XX PD 27-JAN-2000.
XX
XX 14-JUL-1999; 99WO-US15838.
XX
PF

XX
XX 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
XX WPI: 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
PS Claim 50; Page 219-220; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AAA82000 to AAA82020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
XX
Query Match 12.4%; Score 252; DB 21; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 34 TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGC 93
DB 256 TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGC 315
XX
QY 94 TTCCCTCTGTCAGAGGAGCGCGCAAGAGCAAGTGTGCTTGTGAACACGACGAC 153
DB 316 TTCCCTCTGTCAGAGGAGCGCGCAAGAGCAAGTGTGCTTGTGAACACGACGAC 375
XX
QY 154 TCTGTATGAACACTCTGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGCCTTGC 213
DB 376 TCTGTATGAACACTCTGAGAGCAAGATGGGCAAGTGTGCTGCCCTTGCCTTGC 435
XX
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGTGCTTGTGAAGACGACGACGACTGTCTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGTGCTTGTGAAGACGACGACGACTGTCTATG 495
XX
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGTGCTGCTCTTCCCTGTGCAAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGTGCTGCTCTTCCCTGTGCAAGGGG 555
XX
QY 334 AGC 336
DB 556 AGC 558
XX
RESULT 43
AAS63803
ID AAS63803 standard; cDNA; 1853 BP.
XX
XX AAS63803;
XX
XX 29-JAN-2002 (first entry)
XX
XX

DE Human prostate cDNA clone B305D splice variant #4.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001MO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR MPI; 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 346-347; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 22; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCGCCGTTCG 93
DB 256 TCTTCTGTGAAGAAGCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCGCCGTTCG 315

QY 94 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 153
DB 316 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 375

QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGCCGTTCGCGCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGCCGTTCGCGCTGC 435

QY 214 TGGAGGGGGGAGGCAAGCAACGTGGGCGCTTCTGGAACACAGCAAGCACTGTGATG 273
DB 436 TGGAGGGGGGAGGCAAGCAACGTGGGCGCTTCTGGAACACAGCAAGCACTGTGATG 495

QY 274 AAGACACTGAGAAACAAGATGGGCAAGTGTGCGCACTGTCCCTCTCAGAGGGG 333

DB 496 AAGACACTGAGAAACAAGATGGGCAAGTGTGCGCACTGTCCCTCTCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 44
AAH93710
ID AAH93710 standard; cDNA; 1853 BP.
XX
AC AAH93710;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #4.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001MO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX
DR MPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 344-345; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 22; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCGCCGTTCG 93
DB 256 TCTTCTGTGAAGAAGCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCGCCGTTCG 315

QY 94 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 153
DB 316 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 375

QY 154 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGACACTCTCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGACACTCTCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 45
AAH85024
ID AAH85024 standard; cDNA: 1853 BP.
XX
AC AAH85024;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #4.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Keltner MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
DR WPI: 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 31; Page 244; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 22; Length 1853;
Best Local Similarity 99.7%; Pred. NO. 8.9e-88;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAACCAATTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTGC 93
DB 256 TCTTCTGTAAGAACCAATTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTGC 315
QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACACAGCAGCAGC 153
DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACACAGCAGCAGC 375
QY 154 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGACACTCTCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGACACTCTCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

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OM nucleic - nucleic search, using sw model

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Searched: 2185239 seqs, 112599159 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2000	100.0	2000	21 AAC81012	Human B1Agl1 antiIg
2	2000	100.0	2000	22 AA167212	B305D isoform C sp
3	2000	100.0	2000	22 AAS63808	Human prostate CDN
4	2000	100.0	2000	22 AAH93715	Human prostate-spe
5	2000	100.0	2000	22 AAH85029	Human prostate-spe
6	2000	100.0	2000	22 AAB02780	Prostate tumour an
7	2000	100.0	2000	24 ABL95179	Human B305D splice
8	2000	100.0	2000	24 AAS99858	Breast tumour-spec
9	1949	97.5	2000	21 AAA06599	Human immunogenic

10	1551	77.5	2040	21 AAC81013	Human B1Agl1 antiIg
11	1551	77.5	2040	22 AA167213	B305D isoform C sp
12	1551	77.5	2040	22 AAS63809	Human prostate CDN
13	1551	77.5	2040	22 AAH93716	Human prostate-spe
14	1551	77.5	2040	22 AAH85030	Human prostate-spe
15	1551	77.5	2040	22 AAH02781	Prostate tumour an
16	1551	77.5	2040	24 ABL95180	Human B305D splice
17	1551	77.5	2040	24 AAS99859	Breast tumour-spec
18	1500	75.0	2040	21 AAA06600	Human immunogenic
19	1128	56.4	1155	21 AAC81011	Human B1Agl1 antiIg
20	1128	56.4	1155	21 AAA06598	Human immunogenic
21	1128	56.4	1155	22 AA167211	B305D isoform C sp
22	1128	56.4	1155	22 AAS63807	Human prostate CDN
23	1128	56.4	1155	22 AAH93714	Human prostate-spe
24	1128	56.4	1155	22 AAH85028	Human prostate-spe
25	1128	56.4	1155	22 AAH02779	Prostate tumour an
26	1128	56.4	1155	24 ABL95178	Human B305D splice
27	1128	56.4	1155	24 AAS99857	Breast tumour-spec
28	1044	52.2	1590	24 AAS99869	Breast tumour-spec
29	975	48.8	1155	24 AAS99872	Breast tumour-spec
30	491	24.6	1512	19 AAV68995	DNA molecule encod
31	491	24.6	1512	21 AAC81006	Human B1Agl1 antiIg
32	491	24.6	1512	21 AAA06593	Human immunogenic
33	491	24.6	1512	22 AAS63802	Human prostate CDN
34	491	24.6	1512	22 AAH93709	Human prostate-spe
35	491	24.6	1512	22 AAH85023	Human prostate-spe
36	491	24.6	1512	22 AAH02774	Prostate tumour an
37	491	24.6	1512	24 ABL95173	Human B305D splice
38	491	24.6	1512	24 ABL95173	Human breast tumou
39	491	24.6	1512	24 AAS99852	Breast tumour-spec
40	252	12.6	1853	19 AAV68996	DNA molecule encod
41	252	12.6	1853	21 AAC81007	Human B1Agl1 antiIg
42	252	12.6	1853	21 AAA06594	Human immunogenic
43	252	12.6	1853	22 AAS63803	Human prostate CDN
44	252	12.6	1853	22 AAH93710	Human prostate-spe
45	252	12.6	1853	22 AAH85024	Human prostate-spe

ALIGNMENTS

RESULT 1					
ID	AAC81012	strand:	CDNA: 2000 BP.		
AC	AAC81012:				
DT	13-FEB-2001	(first entry)			
DE	Human B1Agl1 antigen splice isoform B1C-8 CDNA.				
KW	Human; breast tumour-specific antigen; cytosolic; vaccine;				
KW	breast cancer; B1Agl1; B1Agl1; B1Agl1; ss.				
OS	Homo sapiens.				
PN	WO200061753-A2.				
PD	19-OCT-2000.				
PF	07-APR-2000; 2000WO-US09312.				
PR	09-APR-1999; 990US-0288198.				
PR	28-OCT-1999; 990US-0429755.				
PR	23-MAR-2000; 2000US-0534825.				
PA	(CORI-) CORIXA CORP.				
PI	Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MM, Dillon DC;				
PI	WPI; 2000-628403/60.				
DR	P-PSDB; AAB28629.				
XX					

PR An isolated polypeptide comprising an immunogenic portion of a breast
 PR tumor protein used for inhibiting the development of cancer, especially
 PR breast cancer, and monitoring cancer progression in a patient -
 XX
 PS Claim 4; Page 177-178; 187pp; English.

CC The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4⁺ and/or CD8⁺ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.

SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match	100.0%	Score 2000	DB 21	Length 2000
Best Local Similarity	100.0%	Pred. NC	0	
Matches 2000, Conservative	0	Mismatches	0	Gaps 0

OY	1	ATGTGTTGAGGTTGATTCATCCATCCCGGCTCCCTTCTGTGAAGAAGCAATTTGGTCTC	60
Dp	1	ATGGTGTTTGAGGTTGATTCATCCATCCCGGCTCCCTTCTGTGAAGAAGCAATTTGGTCTC	60
OY	61	AGGAGCAAGATGGGCAAGTGGTGGCGCTGGCTTCCCTCGTCGACGAGAGGCGGCAAG	120
Dp	61	AGGAGCAAGATGGGCAAGTGGTGGCGCTGGCTTCCCTCGTCGACGAGAGGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTGAGAGACAGACGACACTCTGCTATGAAGACACACAGAGCAAG	180
Dp	121	AGCAACGTGGGCACTTCTGAGAGACAGACGACACTCTGCTATGAAGACACACAGAGCAAG	180
OY	181	ATGGGCAAGTGGTCCGCGCACTCTTCCCTCGTCGACAGGGGAGTGGCAAGCAACGTG	240
Dp	181	ATGGGCAAGTGGTCCGCGCACTCTTCCCTCGTCGACAGGGGAGTGGCAAGCAACGTG	240
OY	241	GAGCGTTCTGGAGACACAGACACTCTGCTATGAAGACACACAGCAAGATGGGCAAG	300
Dp	241	GAGCGTTCTGGAGACACAGACACTCTGCTATGAAGACACACAGCAAGATGGGCAAG	300
OY	301	TGTGTCTTCCCACTGCTTCCCTCGCTGCAAGGGGAGAGCGGCAAGACAGTGGGCGCTTGG	360
Dp	301	TGTGTCTTCCCACTGCTTCCCTCGCTGCAAGGGGAGAGCGGCAAGACAGTGGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCGAGTACACACGTCCGTGGAGAAGATCTG	420
Dp	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCGAGTACACACGTCCGTGGAGAAGATCTG	420
OY	421	GACAAGCTCCACAGAGTGCCTTGGTGGGTTAAATCCCCAGAAAGATCTCATCTGTCATG	480
Dp	421	GACAAGCTCCACAGAGTGCCTTGGTGGGTTAAATCCCCAGAAAGATCTCATCTGTCATG	480
OY	481	CTCAGGCACTGCAGCTGTAACAACAAGACAGCAAGAAAGAGATGCTGTACATCTGGCC	540
Dp	481	CTCAGGCACTGCAGCTGTAACAACAAGACAGCAAGAAAGAGATGCTGTACATCTGGCC	540
OY	541	TCTGCCATGTGGGAATTGCAAGATGTGTAAAACTCTGCTGACAGACGATGTCAACTTAAT	600
Dp	541	TCTGCCATGTGGGAATTGCAAGATGTGTAAAACTCTGCTGACAGACGATGTCAACTTAAT	600
OY	601	GTCCTTGACAAACAAAAGAGGACAGCTCTGTGATTAAGGCCGTACATGCCAGGAATGAA	660
Dp	601	GTCCTTGACAAACAAAAGAGGACAGCTCTGTGATTAAGGCCGTACATGCCAGGAATGAA	660
OY	661	TGTGCGTTAAATGTTGTGTGGAACATGGGACATGATCCAAATATTCACATGTAGTATGAAAT	720
Dp	661	TGTGCGTTAAATGTTGTGTGGAACATGGGACATGATCCAAATATTCACATGTAGTATGAAAT	720

QY	721	ACCACTGCACTACGCTATCTATATGAAGATAAATTAAATGGCCAAAGCACTGCTTTA	780
Db	721	ACCACTGCACTACGCTATCTATATGAAGATAAATTAAATGGCCAAAGCACTGCTTTA	780
QY	781	TATGGTGTGATATCGAATCAAAAAACAACATGGGCTCACACACTGTACTGTGTGA	840
Db	781	TATGGTGTGATATCGAATCAAAAAACAACATGGGCTCACACACTGTACTGTGTGA	840
QY	841	CATGAGCAAAAAACAGCAAGTCGTGAATTTTTTATCAAGAAAAAAGCGAATTTAAATCA	900
Db	841	CATGAGCAAAAAACAGCAAGTCGTGAATTTTTTATCAAGAAAAAAGCGAATTTAAATCA	900
QY	901	CTGGATAGATATATGGAAGACTGCTCTCATACTTGGCTATATTGTGGATCAGCAAGTATA	960
Db	901	CTGGATAGATATATGGAAGACTGCTCTCATACTTGGCTATATTGTGGATCAGCAAGTATA	960
QY	961	GTCAGCCCTTACTATGAGCAAAATATATGATGTATCTTCAAGATCTATCTGACAGAGC	1020
Db	961	GTCAGCCCTTACTATGAGCAAAATATATGATGTATCTTCAAGATCTATCTGACAGAGC	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGGCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGGCAGTTACTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACACGAATTCAGACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACACGAATTCAGACAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAAGTCCAAAGGTTCCAAAGGAGGAAATATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTCCAAAGGTTCCAAAGGAGGAAATATAGCCAGCCAGAGAA	1200
QY	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGGATGTGATAGAGAGGTTGAAGAAAGTAAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGGATGTGATAGAGAGGTTGAAGAAAGTAAG	1260
QY	1261	AAGCATGAAGTAAATTAATGTGGGATTACTTAGAAAACCTGACTAAATGTGTCACTGTGC	1320
Db	1261	AAGCATGAAGTAAATTAATGTGGGATTACTTAGAAAACCTGACTAAATGTGTCACTGTGC	1320
QY	1321	AATGGTGAATATGATTAATTTCCTCAAAGGACAGAGAAACCTGAAAATCAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTTCCTCAAAGGACAGAGAAACCTGAAAATCAGCAATTT	1380
QY	1381	CCTGACAAACGAAGTGAAGATATCAACGAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAGTGAAGATATCAACGAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTCTTGAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTCTTGAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGGTACAAAGGCTTGAGGGCAGTGAAGAAATGGGCACGACAGCTAAGAAAT	1560
Db	1501	TCAGAGGAAGGTACAAAGGCTTGAGGGCAGTGAAGAAATGGGCACGACAGCTAAGAAAT	1560
QY	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAACGGAATCTCATGTGCGATTTCCACAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAACGGAATCTCATGTGCGATTTCCACAGAAAC	1620
QY	1621	CTGACTAATGGTGCACTGCTGGCAATGGGATGATGATTAATTTCTTCCAAAGAAAGC	1680
Db	1621	CTGACTAATGGTGCACTGCTGGCAATGGGATGATGATTAATTTCTTCCAAAGAAAGC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTGCAGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTGCAGAA	1740
QY	1741	CAAAATGATATCTCGAAGCAATTTTGTGAAGAACAGAACTCGGAATATACAGATAG	1800
Db	1741	CAAAATGATATCTCGAAGCAATTTTGTGAAGAACAGAACTCGGAATATACAGATAG	1800

OY	1061	AAAGAAAACAGATGCTAAAAAATCTCTCTGAAAACAGCAATCTCAGAACAAACCTAAAG	11400
Db	1081	AAAGAAAACAGATGCTAAAAAATCTCTCTGAAAACAGCAATCTCAGAACAAACCTAAAG	11400
OY	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGCAAGAAAATAGCAGCCACAGAAA	12000
Db	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGCAAGAAAATAGCAGCCACAGAAA	12000
OY	1201	ATGCTCTCAAGAACCCAGAAATPAATTAAGGATGCTGATAGAGGTTGAACAGAAATTAAG	12600
Db	1201	ATGCTCTCAAGAACCCAGAAATPAATTAAGGATGCTGATAGAGGTTGAACAGAAATTAAG	12600
OY	1261	AAGCATGAAGACTATATATGTGGGATTACTATGAAAACCTGACTAAATGTCTCACTCTGGC	13200
Db	1261	AAGCATGAAGACTATATATGTGGGATTACTATGAAAACCTGACTAAATGTCTCACTCTGGC	13200
OY	1321	AATGGTGTATATGATTTAATTTCTCTCAAAAGGAGACAGACAACCTGAAAATACGAATTT	13800
Db	1321	AATGGTGTATATGATTTAATTTCTCTCAAAAGGAGACAGACAACCTGAAAATACGAATTT	13800
OY	1381	CCTGACCAACGAAAGTGAAGAGTATCACAGAAATTTGGGATTTAGTTTCTGACTACCAAAA	14400
Db	1381	CCTGACCAACGAAAGTGAAGAGTATCACAGAAATTTGGGATTTAGTTTCTGACTACCAAAA	14400
OY	1441	AAACAGATGCCAAATATCTCTCTGAAAACAGCAACCCAGAACAGACTTAAGCTGCACA	15000
Db	1441	AAACAGATGCCAAATATCTCTCTGAAAACAGCAACCCAGAACAGACTTAAGCTGCACA	15000
OY	1501	TCAGAGGAAGAGTCACAAAGGCTTTGAGGGCACTGAAAATGSCCAGCCAGACTAGAAAT	15600
Db	1501	TCAGAGGAAGAGTCACAAAGGCTTTGAGGGCACTGAAAATGSCCAGCCAGACTAGAAAT	15600
OY	1561	TTTATGGCTATTCGAAGAAATGAAGAAGCAACGGAAATCAATGTGGGATTTCCACAAAAC	16200
Db	1561	TTTATGGCTATTCGAAGAAATGAAGAAGCAACGGAAATCAATGTGGGATTTCCACAAAAC	16200
OY	1621	CTGACTATATGGTGGCACTGCTGGCAATGTGATGATGATTAATTTCTCTCAAGGAAGAGC	16800
Db	1621	CTGACTATATGGTGGCACTGCTGGCAATGTGATGATGATTAATTTCTCTCAAGGAAGAGC	16800
OY	1681	AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAGATATCACAGTGACGA	17400
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAGATATCACAGTGACGA	17400
OY	1741	CAAAATATATCTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATTAATACAGATAG	18000
Db	1741	CAAAATATATCTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATTAATACAGATAG	18000

QY 1801 ATCTGATCATGAAAGAAAGCAGATAGAGTGTGAAATTAATGATTCGAGCTTCT 1860
DB 1801 ATCTGATCATGAAAGAAAGCAGATAGAGTGTGAAATTAATGATTCGAGCTTCT 1860
QY 1861 CTTACTGTGAAAGAAAGAAAGCAGATCTTCGATGAAATAGTACGTGGCGGAGAAATT 1920
DB 1861 CTTACTGTGAAAGAAAGAAAGCAGATCTTCGATGAAATAGTACGTGGCGGAGAAATT 1920
QY 1921 GCCATGCTAAGAGCTGAGCTAGACACAAATGAACATCAGAGCGAGCTAAATTAATTAATTA 1980
DB 1921 GCCATGCTAAGAGCTGAGCTAGACACAAATGAACATCAGAGCGAGCTAAATTAATTAATTA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
AA167212
ID AA167212 standard; cDNA; 2000 BP.
XX
AC AA167212;
XX
DI 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 2 encoding cDNA.
XX
KM Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
KM cancer; B305D; ss.
OS Homo sapiens.
FH Key 1.1971
FT CDS /tag= a
FT /product= "B305D isoform C splice variant"
PN WO200175171-A2.
XX 11-OCT-2001.
XX 02-APR-2001; 2001WO-US10631.
XX 03-APR-2000; 2000US-194241P.
PR 20-JUL-2000; 2000US-219862P.
PR 27-JUL-2000; 2000US-221300P.
PR 18-DEC-2000; 2000US-256592P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RL, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH;
XX WPI: 2001-626649/72.
DR P-PSDB; AAG65977.
XX
XX Identifying tissue (tumour)-specific polynucleotides overexpressed in
PT tissue of interest as compared to control tissue, for detecting cancer
PT cells in patient, comprises DNA microarray analysis or quantitative
PT polymerase chain reaction -
XX
PS Claim 4; Page 94; 127pp; English.
XX
XX The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SP1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SP1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,

CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other:

Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best local similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGTGCTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCCGCTGCTCCCTGCGAGGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTCCGCTGCTCCCTGCGAGGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACACAGACGACTGCTATGAAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAGACACAGAGACTGCTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
QY 241 GCGGCTTCTGGAGACACAGACGACTGCTATGAAAGCACTCAGAAAGATGGGCAAG 300
DB 241 GCGGCTTCTGGAGACACAGACGACTGCTATGAAAGCACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGGCAAGCAAGGAGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGGCAAGCAAGGAGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACACGCTCGTGAGAGATCTG 420
DB 361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACACGCTCGTGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTCGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
DB 421 GACAACTCCACAGAGCTCGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
QY 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAGAGCTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAGAGCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTGTAAGTCTGCTGGACAGAGATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAACTGTAAGTCTGCTGGACAGAGATGTCACTTAAT 600
QY 601 GTCCCTTGAAACAAAAGAGAGACGCTCGATTAAGGCGCTTACATGCCAGAAATGGA 660
DB 601 GTCCCTTGAAACAAAAGAGAGACGCTCGATTAAGGCGCTTACATGCCAGAAATGGA 660
QY 661 TGTGCGTGAATGTGCTGGAACATGCGACTGATCCAAATATTCAGATGATGAAT 720
DB 661 TGTGCGTGAATGTGCTGGAACATGCGACTGATCCAAATATTCAGATGATGAAT 720
QY 721 ACCACTCTGCTAGCGCTATCTATAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTCTGCTAGCGCTATCTATAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTCGTGATATGAAATCAAAAAAGCAATGGCTCACACCACTGTTACTGGTGA 840
DB 781 TATGTCGTGATATGAAATCAAAAAAGCAATGGCTCACACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAATCAAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAATCAAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATTAAGGAAGAGCTGCTCATATGCTGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATTAAGGAAGAGCTGCTCATATGCTGTATGTTGTGATCAGCAAGTATA 960

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QY 961 GTCAGCCTCTACTTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTCAGCCTCTACTTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAGAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAAGCAGTGAATAATAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAAGCAGTGAATAATAGCCAGAGAGAA 1200
QY 1201 ATGCTCTCAAGACAGAAATAAATTAAGATGCTGATAGAGAGTTGAAGAAAGAAATGAG 1260
Db 1201 ATGCTCTCAAGACAGAAATAAATTAAGATGCTGATAGAGAGTTGAAGAAAGAAATGAG 1260
QY 1261 AAGCATAAAGTATATATGTTGGGATTACTAGAAAACCTGACTAATGGTGTCTGCTGCC 1320
Db 1261 AAGCATAAAGTATATATGTTGGGATTACTAGAAAACCTGACTAATGGTGTCTGCTGCC 1320
QY 1321 AATGCTATATGATTAATTTCTCAAGAGAGAGACAGACACCTGAAATCAGCAATTT 1380
Db 1321 AATGCTATATGATTAATTTCTCAAGAGAGAGACAGACACCTGAAATCAGCAATTT 1380
QY 1381 CTTGACACAGCAAGAGTATCAGAGATTTGCGAATTAATTTCTGACTACAGAGAA 1440
Db 1381 CTTGACACAGCAAGAGTATCAGAGATTTGCGAATTAATTTCTGACTACAGAGAA 1440
QY 1441 AAACAGATGCGAAATCTCTTCTGAAAACAGCAACCCAGAACAGCTTAAACCTGACA 1500
Db 1441 AAACAGATGCGAAATCTCTTCTGAAAACAGCAACCCAGAACAGCTTAAACCTGACA 1500
QY 1501 TCAGAGAGAGAGTGCACAAAGGCTTGAGGAGAGTGAATAATGGCCAGCCAGAGCTGAAAT 1560
Db 1501 TCAGAGAGAGAGTGCACAAAGGCTTGAGGAGAGTGAATAATGGCCAGCCAGAGCTGAAAT 1560
QY 1561 TTTATGCTCTTCCAGAAATGAGAGACACGGAATCTCATGTCGATTTCCAGAAAAC 1620
Db 1561 TTTATGCTCTTCCAGAAATGAGAGACACGGAATCTCATGTCGATTTCCAGAAAAC 1620
QY 1621 CTGACTAATGCTGCTGCTGCAATGCTGATGATGATTAATTTCTCCAGAGAAAGC 1680
Db 1621 CTGACTAATGCTGCTGCTGCAATGCTGATGATGATTAATTTCTCCAGAGAAAGC 1680
QY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAAGTTCACAGTACGAA 1740
Db 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAAGTTCACAGTACGAA 1740
QY 1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACACGATGAG 1800
Db 1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACACGATGAG 1800
QY 1801 ATTTCTGATTTATGAAAGAGAGATGAAAGTGTGTAATAAATGATTTCTGAGCTTTCT 1860
Db 1801 ATTTCTGATTTATGAAAGAGAGATGAAAGTGTGTAATAAATGATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAAATAGTAGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAAATAGTAGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACACAATGAATCAAGAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACTGAGAGCTAGACACAATGAATCAAGAGCCAGCTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 3
AAS63808
ID AAS63808 standard; cDNA; 2000 BP.
XX
AC AAS63808;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #9.
XX
KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WC-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657219.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX
DR WPI: 2001-639232/73.
XX
DR P-PSDB; AA069778.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 349-350; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
XX
Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTGTTGAGTGTGATTCATCCGCGTCCCTTCTGTGAAGAGCAATTTGCTCTC 60
Db 1 ATGTTGTTGAGTGTGATTCATCCGCGTCCCTTCTGTGAAGAGCAATTTGCTCTC 60
QY 61 AGAGCAAGATGGCAAGTGGTCTGCTTCCCTGCTGACAGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGGTCTGCTTCCCTGCTGACAGAGAGCGCAAG 120

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QY	121	AGCAGCTGGGCACTTCTGGAGACACGACGACACTGCTGTATGAGACACTAGAGCAAG	180
Db	121	AGCAACCTGGGCACTTCTGGAGACACGACGACACTGCTGTATGAGACACTAGAGCAAG	180
QY	181	ATGGGCAAGAGTGGCCGCACTCTCCCTGCTGTGAGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCCCACTCTCTCCCTGCTGTGAGGGGAGTGGCAAGCAAGCTG	240
QY	241	GGCGCTTCTGGAGACACGACGACACTGCTATGAAACACTGAGAACAAAGTGGGCAAG	300
Db	241	GGCGCTTCTGGAGACACGACGACACTGCTATGAAAGACTGAGAACAAAGTGGGCAAG	300
QY	301	TGGTGGTGGCCAGTCTCCCTCTCTGTCAGGGGGAGGGGCAAGCAAGTGGGCGCTTGG	360
Db	301	TGGTGGTGGCCAGTCTCCCTCTCTGTCAGGGGGAGGGGCAAGCAAGTGGGCGCTTGG	360
QY	361	GGAGACTACGANTACAGTGGCTTCATGAGAGCCAGGTACACGTCCTGTGAGAAAGATGTG	420
Db	361	GGAGACTACGATGACAGTGGCTTCATGAGAGCCAGGTACACGTCCTGTGAGAAAGATGTG	420
QY	421	GACAGCTCCACAGAGCTGGCTGTGGGGTAAAGTCCCAAGAGATCTATGCTATG	480
Db	421	GACAGCTCCACAGAGCTGGCTGTGGGGTAAAGTCCCAAGAAAGATCTATGCTATG	480
QY	481	CTCAGGAGACACTACGAGGAACAGAAAGGAGCAAGCAAAAGAGACTGCTTCATGTGCC	540
Db	481	CTCAGGAGACACTACGAGGAACAGAAAGGAGCAAGCAAAAGAGACTGCTTCATGTGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGTGACAGACGATGTCAACTTAAT	600
Db	541	TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGTGACAGACGATGTCAACTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGAGAGTGTGATPAAAGCCGTACATGGCAGGAAGATGAA	660
Db	601	GTCCTTGACAAACAAAAGAGAGAGTGTGATPAAAGCCGTACATGGCAGGAAGATGAA	660
QY	661	TGTGCGTTAATGTTGCTGGAACATGCGACTGTATCCAAATATTCAGATGAGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACATGCGACTGTATCCAAATATTCAGATGAGATGGAAT	720
QY	721	ACCACTGTGACATACGCTATCTTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGTGACATACGCTATCTTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
QY	781	TATGTCGTATATTCGATCAAAAAACAAGCATGGCGCTCACACCACTGTTACTGGTGA	840
Db	781	TATGTCGTATATTCGATCAAAAAACAAGCATGGCGCTCACACCACTGTTACTGGTGA	840
QY	841	CATAGCAAAAACAGCAAGTCTGTAATTTTATCAGAAAAAANGCAATTTAAATGCA	900
Db	841	CATAGCAAAAACAGCAAGTCTGTAATTTTATCAGAAAAAANGCAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGGATGCTGCTCAATACCTGCTATGTTGGAGTACAGCAAGTGA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCAATACCTGCTATGTTGGATCAGCAAGTGA	960
QY	961	GTCAGCTTACTTGACGCAAAATATTTGATGTATCTTCCAGAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCTTACTTGACGCAAAATATTTGATGTATCTTCCAGAGATCTATCTGGACAGAG	1020
QY	1021	GGCAGAGATGCTGTTTCTATCTATCATCATGATTAATTTGGCAATTTACTTCTTACATAC	1080
Db	1021	GGCAGAGATGCTGTTTCTATCTATCATCATGATTAATTTGGCAATTTACTTCTTACATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAAACTCTTGTGAAAACAGCAATCCAGAAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAAACTCTTGTGAAAACAGCAATCCAGAAACAGACTTAAAG	1140
QY	1141	CTGACATACAGAGAGATGACAAAGGCTTCAAAAGGAGTGAAGAAATAGCCAGCCAGAGAAA	1200
Db	1141	CTGACATACAGAGAAAGTGTACAAAGGCTTCAAAAGGAGTGAAGAAATAGCCAGCCAGAGAAA	1200

OY	1201	ATGCTCAAGACACAGAAATATAATTAAGATGGTGATAGAGAGGTGAAGAAATGAAG	1260
Db	1201	ATGTCTCAAGAACCGAAAAATAATTAAGATGGTGATAGAGAGGTGAAGAAATGAAG	1260
OY	1261	AAGATGAAGATATATATGGGATTAATAGAAAACCTACATAATGGTGCTACGTGGC	1320
Db	1261	AAGATGAAGATATATATGGGATTAATAGAAAACCTACATAATGGTGCTACGTGGC	1320
OY	1321	AATGGTATATATGGATTAATCTCCAAAGAGAGCGAAGACACCTGAAATTCAGCAATT	1380
Db	1321	AATGGTATATATGGATTAATCTCCAAAGAGAGCGAAGACACCTGAAATTCAGCAATT	1380
OY	1381	CTGTACAACGGAAGTGAAGAGTTCACAGATTTGCCAATTGTGTTCTGTACTACAAGAA	1440
Db	1381	CTGTACAACGGAAGTGAAGAGTTCACAGATTTGCCAATTGTGTTCTGTACTACAAGAA	1440
OY	1441	AAACAGATGCCAAATATCTCTTGAAAAACGACACCCGAACCAAGACTTAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTGAAAAACGACACCCGAACCAAGACTTAAGCTGACA	1500
OY	1501	TCAGAGGAAGAGTCAACAAGGCTTGGAGGCGATGAAAATGGCCAGCCAGAGCTAGAAT	1560
Db	1501	TCAGAGGAAGAGTCAACAAGGCTTGGAGGCGATGAAAATGGCCAGCCAGAGCTAGAAT	1560
OY	1561	TTTATGGCTATCGAAGAAATGAAGAAACGACGGAATCTCATCTGCGATTCCACAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAACGACGGAATCTCATCTGCGATTCCACAGAAAC	1620
OY	1621	CTGACTAATGGTGGCCTGCTGGCCANTGGATGATGATTAATTCTCCAAAGAAAGAC	1680
Db	1621	CTGACTAATGGTGGCCTGCTGGCCANTGGATGATGATTAATTCTCCAAAGAAAGAC	1680
OY	1681	AGAACACCTGGAAGCCAGCAATTTCCGTGACACTGAGAAATGAAGAGTATCACAGTACGAA	1740
Db	1681	AGAACACCTGGAAGCCAGCAATTTCCGTGACACTGAGAAATGAAGAGTATCACAGTACGAA	1740
OY	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACACGATGAG	1800
Db	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACACGATGAG	1800
OY	1801	ATTCTGANTCTGGAAGAAAGCAGATRGAAGTGGTGAAGAAATGAATTCGAGTTTCT	1860
Db	1801	ATTCTGANTCTGGAAGAAAGCAGATRGAAGTGGTGAAGAAATGAATTCGAGTTTCT	1860
OY	1861	CTTAGTGTATGAAGAAAGAGACATCTTGCATGAATAATAGTACGTGGCGGAAGAAAT	1920
Db	1861	CTTAGTGTATGAAGAAAGAGACATCTTGCATGAATAATAGTACGTGGCGGAAGAAAT	1920
OY	1921	GCCATGCTAAGACTGAGAGTACAGACAAATGAACATCAGAGCCAGCTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGAGTACAGACAAATGAACATCAGAGCCAGCTAAAAA	1980
OY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	
RESULT 4			
AAH93715			
ID	AAH93715 standard; cDNA; 2000 BP.		
XX	AAH93715;		
XX	04-Oct-2001 (first entry)		
XX	Human prostate-specific cDNA sequence B305D splice variant #9.		
XX	Human: prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cyclostatic; gene therapy; metastasis; ss.		
XX	Homo sapiens.		
OS			
PN	WO200151633-A2.		

QY	1561	TTTTGGCTATCGAAGAAATGAAAGAAAGCAGGAACTACTCATGTGCGATTTCCCGAATAAC	1620
Dp	1561	TTTTATGGCTATCGAAGAAATGAAAGAAAGCAGGAACTACTCATGTGCGATTTCCCGAATAAC	1620
QY	1621	CTGACTAATGTGGCCACTCTGGCAATGGTGTGATGGAATTAATTCCTCCAGAGAGAGC	1680
Dp	1621	CTGACTAATGTGGCCACTCTGGCAATGGTGTGATGGAATTAATTCCTCCAGAGAGAGC	1680
QY	1681	AGAAACACTGAAAGCCAGCAATTTCTGTACTGTGAATGAAGAGTATCACAGTGACGAA	1740
Dp	1681	AGAAACACTGAAAGCCAGCAATTTCTGTACTGTGAATGAAGAGTATCACAGTGACGAA	1740
QY	1741	CAAAATGATCTCAGAGCAATTTTGTGAAAGAACAGAACTCTGGAATTTTACAGATGAG	1800
Dp	1741	CAAAATGATCTCAGAGCAATTTTGTGAAAGAACAGAACTCTGGAATTTTACAGATGAG	1800
QY	1801	ATTCTGATTCATGACAGAAAGCAGATAGAAAGTGTTGAAAAAATGAATTCTGAGCTTTC	1860
Dp	1801	ATTCTGATTCATGACAGAAAGCAGATAGAAAGTGTTGAAAAAATGAATTCTGAGCTTTC	1860
QY	1861	CTTAGTGTGTAGAAAGAAAGACACTCTGCATGGAATATGACTTCGGGAGGAATTT	1920
Dp	1861	CTTAGTGTGTAGAAAGAAAGACACTCTGCATGGAATATGACTTCGGGAGGAATTT	1920
QY	1921	GCCATGCTAAGACTGGAGCTAGACACAAATGAACACATCGAGCGAGCTAAAAAAGAAAAA	1980
Dp	1921	GCCATGCTAAGACTGGAGCTAGACACAAATGAACACATCGAGCGAGCTAAAAAAGAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Dp	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

[illegible]

CC variant. Also described are polynucleotides (N1) encoding (P1), (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305P are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84571 to AAH55143 and AAG90000 to AAG90777 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX Sequence 2000 BP; 658 A; 388 C; 489 G; 425 T; 0 other;

[illegible]

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QY 841 CATGAGCAAAAACGCAAGTCGTGAAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
    |||||
Db 841 CATGAGCAAAAACGCAAGTCGTGAAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATGATGAAAGACAGTCTCTCATCTCTGTATGTGTGTGATCAGCAAGATTA 960
    |||||
Db 901 CTGATGATGATGAAAGACAGTCTCTCATCTCTGTATGTGTGTGATCAGCAAGATTA 960
QY 961 GTCAGCCTTCTACTGAGCAAAAATATGATGATCTCTCAAGATCTATCTGGACACAGC 1020
    |||||
Db 961 GTCAGCCTTCTACTGAGCAAAAATATGATGATCTCTCAAGATCTATCTGGACACAGC 1020
QY 1021 GCCAGAGAGATAGCTGTTCTTCTAGTCATCATCAGTAATTTGCCAGTTACTTCTGACTAC 1080
    |||||
Db 1021 GCCAGAGAGATAGCTGTTCTTCTAGTCATCATCAGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTTAAAAATCTCTTGTGAAAACAGCAATCCAGAAACAGACTTAAAG 1140
    |||||
Db 1081 AAAGAAAAACAGATGCTTAAAAATCTCTTGTGAAAACAGCAATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGAGTCACAAAAGGTTCAAAAGCAGTGAATATACCCAGCCAGAGAAA 1200
    |||||
Db 1141 CTGACATCAGAGAAAGAGTCACAAAAGGTTCAAAAGCAGTGAATATACCCAGCCAGAGAAA 1200
QY 1201 ATGCTCTCAAGAACCCAGAAATTAATTAAGGATGATGATAGAGAGTTGAAGAAATGAG 1260
    |||||
Db 1201 ATGCTCTCAAGAACCCAGAAATTAATTAAGGATGATGATAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAGTAAATATGAGGATTTACTGAAAACCTGACTATAGTGTGCACAGCTGGC 1320
    |||||
Db 1261 AAGCATGAAGTAAATATGAGGATTTACTGAAAACCTGACTATAGTGTGCACAGCTGGC 1320
QY 1321 AATGATGATGATGATTAATTTCTTCAAGAGAAAGAGCAAGCACTGAAAATCAGCAATTT 1380
    |||||
Db 1321 AATGATGATGATGATTAATTTCTTCAAGAGAAAGAGCAAGCACTGAAAATCAGCAATTT 1380
QY 1381 CTGACACAGCAAGATGAAAGATATCACAGAAATTTGCGAATTAATTTCTGACTACAAAAGAA 1440
    |||||
Db 1381 CTGACACAGCAAGATGAAAGATATCACAGAAATTTGCGAATTAATTTCTGACTACAAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTTGTGAAAACAGCAACCCAGAAACAGCTTAAACCTGACA 1500
    |||||
Db 1441 AAACAGATGCAAAATCTCTTGTGAAAACAGCAACCCAGAAACAGCTTAAACCTGACA 1500
QY 1501 TCAGAGAGAAAGTCTACAAAGGCTTGAGGCGAGTGAATGCGCCAGACAGCTGAAAT 1560
    |||||
Db 1501 TCAGAGAGAAAGTCTACAAAGGCTTGAGGCGAGTGAATGCGCCAGACAGCTGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAACACGGAAGTACTCATGTGCGATTCCCGAAGAAC 1620
    |||||
Db 1561 TTTATGCTATCGAAGAAATGAAGAACACGGAAGTACTCATGTGCGATTCCCGAAGAAC 1620
QY 1621 CTGACTAATGCTGCAATGCTGCGCAATGATGATGATGATTAATTCCTCCAGAAAGAGC 1680
    |||||
Db 1621 CTGACTAATGCTGCAATGCTGCGCAATGATGATGATGATTAATTCCTCCAGAAAGAGC 1680
QY 1681 AGAACACCTGAAGCCAGCAATTTCTGACACAGTGAATGAAGTATCAACAGTACGAA 1740
    |||||
Db 1681 AGAACACCTGAAGCCAGCAATTTCTGACACAGTGAATGAAGTATCAACAGTACGAA 1740
QY 1741 CAAAATATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
    |||||
Db 1741 CAAAATATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
QY 1801 ATTCTGATGATGAAAGAAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
    |||||
Db 1801 ATTCTGATGATGAAAGAAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CTTAGTTTGAAGAAAGAAAGACATCTTCATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
    |||||
Db 1861 CTTAGTTTGAAGAAAGAAAGACATCTTCATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGCTAGACACAATGAATGAACATCAGAGCCAGCTTAAAAA 1980
    |||||

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Db 1921 GCCATGCTAAGACTGAGCTAGACACAATGAATGAAATCATCAGAGCCAGCTTAAAAA 1980
    |||||
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||

RESULT 6
AAH02780
ID AAH02780 standard; cDNA; 2000 BP.
XX
XX AAH02780;
AC
XX
XX 14-JUN-2001 (first entry)
DT
XX
DE Prostate tumour antigen determined cDNA splice variant of B305D #9.
XX
XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KM prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
XX W0200125272-A2.
XX
XX 12-APR-2001.
PD
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
XX 04-OCT-1999; 99US-0157455.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Skeiky YAM, Reed SG, Cheever MA;
PI
XX WPI; 2001-245062/25.
XX
XX P-PSDB; AAB74816.
DR
XX
XX Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
PS
XX
XX Claim 50; Page 232; 276pp; English.
XX
XX
XX The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTGAATTCATGCCGCGCCCTCTGTGAAAGAACCATTTGCTC 60
    |||||
Db 1 ATGGTGGTGAAGTGAATTCATGCCGCGCCCTCTGTGAAAGAACCATTTGCTC 60
    |||||
QY 61 AGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGACAGGAGAGCGCAAG 120
    |||||
Db 61 AGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGACAGGAGAGCGCAAG 120
    |||||
QY 61 AGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGACAGGAGAGCGCAAG 120
    |||||
Db 61 AGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGACAGGAGAGCGCAAG 120
    |||||
QY 121 AGCAGCTGGGCACTTGTGAGACACAGACGCTCTCTATGAAGACACTCAGAGCAAG 180
    |||||

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Db 121 AGCAACGTGGGCACCTTGTGAGACCAAGCAAGCTCTGTATGTAAGACACTCAGAGCAAG 180
Oy 181 ATGGCAAGTGTGGCGCCACTGTTCCCTGCTGAGGGGGAGTGGCAAGCAAGCG 240
Db 181 ATGGCAAGTGTGGCGCCACTGTTCCCTGCTGAGGGGGAGTGGCAAGCAAGCG 240
Oy 241 GCGGCTTGTGAGACACAGACACTCTGCTATGAAGACACTCAGCAAGTGGGCAAG 300
Db 241 GCGGCTTGTGAGACACAGACACTCTGCTATGAAGACACTCAGCAAGTGGGCAAG 300
Oy 301 TGTGCTGCCACTGCTCCCTGCTGTCAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGTGCTGCCACTGCTCCCTGCTGTCAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTAGATGACAGTGCCTTCATGGAGCCAGGTACCAAGTCCGCTGAGCAAGTCCG 420
Db 361 GGAGACTAGATGACAGTGCCTTCATGGAGCCAGGTACCAAGTCCGCTGAGCAAGTCCG 420
Oy 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
Oy 481 CTCAGGAGACACTGACGTGAACAAGACAAAGAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAATGATAAACCTGCTGTCAGAGAGATGCAACTTAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATAAACCTGCTGTCAGAGAGATGCAACTTAT 600
Oy 601 GTCTTTGACAAACAAAAGAGACAGCTGTATAAAGCCGCTCAATGCCAGAGATGAA 660
Db 601 GTCTTTGACAAACAAAAGAGAGACAGCTGTATAAAGCCGCTCAATGCCAGAGATGAA 660
Oy 661 TGTGGCTTATATGTCTGGAACATGGCACTGATCCAAATTTCCAGATGATGGAAT 720
Db 661 TGTGGCTTATATGTCTGGAACATGGCACTGATCCAAATTTCCAGATGATGGAAT 720
Oy 721 ACCACTCTGCACTAGCCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTA 780
Db 721 ACCACTCTGCACTAGCCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTA 780
Oy 781 TATGCTGTGATATGAATCAAAAAACAAGATGGCTCACAACCTGTTACTTGGTGA 840
Db 781 TATGCTGTGATATGAATCAAAAAACAAGATGGCTCACAACCTGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
Oy 901 CTGGATATGATGAAGAGCTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGGATATGATGAAGAGCTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
Oy 961 GTCAAGCTTCTACTTGTAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAAGCTTCTACTTGTAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
Oy 1021 GCCAAGAGATGATGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAAGAGATGATGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Oy 1081 AAGAAAAACAGATGCTAAATCTCTGTAAGAACAGAAATCCAGAACAAAGCTTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATCTCTGTAAGAACAGAAATCCAGAACAAAGCTTTAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGCAAGTGAAGTCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTCAAGGCAAGTGAAGTCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260

Oy 1261 AAGCATGAAGATTAATATGTGGATTAATCTAGAAAAACCTGACATAATGTGTCACCTGGC 1320
Db 1261 AAGCATGAAGATTAATATGTGGATTAATCTAGAAAAACCTGACATAATGTGTCACCTGGC 1320
Oy 1321 AATGGATTAATGGATTAATTCCTCAAAAGAGAGCAGAACACCTGAAAAATGCAAAATT 1380
Db 1321 AATGGATTAATGGATTAATTCCTCAAAAGAGAGCAGAACACCTGAAAAATGCAAAATT 1380
Oy 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
Oy 1441 AAACAGATGCCAAATATCTCTGTAAGAACAGAACCCAGAACAAACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTCTGTAAGAACAGAACCCAGAACAAACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGATTCACAAAGGCTTGAAGGCGAGTGAATAATGGCCAGCAGAGTGAATAAT 1560
Db 1501 TCAGAGGAAGATTCACAAAGGCTTGAAGGCGAGTGAATAATGGCCAGCAGAGTGAATAAT 1560
Oy 1561 TTTATGCTATGAGAAATGAAGAAACGACGAGTACTCATGTGCGATTCCAGAAAC 1620
Db 1561 TTTATGCTATGAGAAATGAAGAAACGACGAGTACTCATGTGCGATTCCAGAAAC 1620
Oy 1621 CTGACTAATGGGCCACTGCTGCAATGGTGAATGATGATTAATTCCTCCAGGAAGAGC 1680
Db 1621 CTGACTAATGGGCCACTGCTGCAATGGTGAATGATGATTAATTCCTCCAGGAAGAGC 1680
Oy 1681 AGAACACCTGAAGAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
Db 1681 AGAACACCTGAAGAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
Oy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACACTGGAATTTACACGATGAG 1800
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACACTGGAATTTACACGATGAG 1800
Oy 1801 AATCTGATTCATGAAGAAAGCAGATGAAGTGTGAAGAAATGAATCTGAGCTTCT 1860
Db 1801 AATCTGATTCATGAAGAAAGCAGATGAAGTGTGAAGAAATGAATCTGAGCTTCT 1860
Oy 1861 CTTAGTTGTAGAAAGAAAGACATCTGATGAATAATGATGCTTGGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAGAAAGAAAGACATCTGATGAATAATGATGCTTGGGGAAGAAAT 1920
Oy 1921 GCCATGCTAAGACTGAGCTAGACACATGAATCAATCAGAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAATCAATCAGAGCCAGCTAAAAAAGAAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
ABL95179
ID ABL95179 standard: cDNA; 2000 BP.
XX ABL95179;
XX
DE Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
XX
KW Human; cancer; prostate cancer; vaccine; cytosolic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX

PF 12-JAN-2001; 2001US-0759143.
 XX 25-FEB-1997; 97US-0806099.
 PR 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-0030607.
 PR 14-JUL-1998; 98US-0115453.
 PR 23-SEP-1998; 98US-0159812.
 PR 15-JAN-1999; 99US-0232149.
 PR 09-APR-1999; 99US-0288946.
 PR 13-JUL-1999; 99US-0352616.
 PR 18-NOV-1999; 99US-0439313.
 PR 18-NOV-1999; 99US-0443686.
 PR 14-JAN-2000; 2000US-0483672.
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593783.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 XX Xu J, Dillon DC, Mitcham JT, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX WPI: 2002-255649/30.
 XX New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer -
 XX
 PS Claim 1; SEQ ID NO 374; 87bp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 XX
 SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
 Query Match 100.0%; Score 2000; DB 24; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AGCAGCTGGGCACTTCTGGAGACCAGACACTCTGCTATGAAGACATCAGAGCAAG 180
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 Db 121 AGCAACGTGGGCACTTCTGGAGACCAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGTCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGTG 240
 |||||||
 Db 181 ATGGGCAAGTGTGTCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGTG 240
 QY 241 GGGCTTCTGGAGACACAGACACTGCTGTGAAGACACTCAGAAACAAGATGGGCAAG 300
 |||||||
 Db 241 GGGCTTCTGGAGACACAGACACTGCTGTGAAGACACTCAGAAACAAGATGGGCAAG 300
 QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
 |||||||
 Db 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
 QY 361 GGAGACTACGATGACAGTGCCTTATGAGAGCCAGGTACACAGTCCCTGGAGAAAGATCTG 420
 |||||||
 Db 361 GGAGACTACGATGACAGTGCCTTATGAGAGCCAGGTACACAGTCCCTGGAGAAAGATCTG 420
 QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
 |||||||
 Db 421 GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
 QY 481 CTCAGGACACTGACGTGAACAGAGAGACAGAAAGAGAGACTGCTACATCTGACC 540
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 Db 481 CTCAGGACACTGACGTGAACAGAGAGAGACAGAAAGAGAGACTGCTACATCTGACC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTAACTCCTGCTGCAAGACAGATGCAACTTAAT 600
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 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTAACTCCTGCTGCAAGACAGATGCAACTTAAT 600
 QY 601 GTCCCTTGACAAACAAAG 660
 |||||||
 Db 601 GTCCCTTGACAAACAAAG 660
 QY 661 TGTGCTGAATGTTGCTGGAACATGGAACATGGAACATGGAACATGGAACATGGAACAT 720
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 Db 661 TGTGCTGAATGTTGCTGGAACATGGAACATGGAACATGGAACATGGAACATGGAACAT 720
 QY 721 ACCACTGTGCACTACGCTATATATGAAGATGAATGAATGAATGAATGAATGAATGAAT 780
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 Db 721 ACCACTGTGCACTACGCTATATATGAAGATGAATGAATGAATGAATGAATGAATGAAT 780
 QY 781 TATGCTGCTGATATGATGATCAAAAACAGCATGAGCTCACACCACTGTTACTGGTGTGA 840
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 Db 781 TATGCTGCTGATATGATGATCAAAAACAGCATGAGCTCACACCACTGTTACTGGTGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTGTGAAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
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 Db 841 CATGAGCAAAAACAGCAAGTGTGAAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
 QY 901 CTGATATGATATGAGAGAGACTGCTCTCATACTTCTGTATGTGTGATCAGCAAGTATA 960
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 Db 901 CTGATATGATATGAGAGAGACTGCTCTCATACTTCTGTATGTGTGATCAGCAAGTATA 960
 QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATATCTTCTCAAGATCTATCTGCAAGACG 1020
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 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTTTCCAGTTACTTCTGACTAC 1080
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 Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTTTCCAGTTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAAATATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
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 Db 1081 AAAGAAAAACAGATGCTAAAATATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAATAATACCGCCAGAGAAA 1200
 |||||||
 Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAATAATACCGCCAGAGAAA 1200


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Oy 1201 ATGTCACAGAACGAGATAATTAAGATGCTGATAGAGGTTGAGAGAAATGAAG 1260
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Db 1201 ATGTCACAGAACGAGATAATTAAGATGCTGATAGAGAGTTGAGAGAAATGAAG 1260
Oy 1261 AAGCATGAAAGTAATTAATGTGGGATTAAGAAAACCTGACTTAATGTGTCACCTGCGC 1320
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Db 1261 AAGCATGAAAGTAATTAATGTGGGATTAAGAAAACCTGACTTAATGTGTCACCTGCGC 1320
Oy 1321 AATGCTGAATTAATGATTAATTCCTCAAGAGAGACAGAACCTGAAATATGACAAATT 1380
    |||||||
Db 1321 AATGCTGAATTAATGATTAATTCCTCAAGAGAGACAGAACCTGAAATATGACAAATT 1380
Oy 1381 CCTGACACGAGAAAGTAAGATATCACAGATTTTGGCAATTTAGTTTCTGACTACAAAGAA 1440
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Oy 1441 AAACAGATGCCAAAATTAATCTTTCTGAAAACAGCCAGAACCAAGACTTAAAGCTGACA 1500
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Db 1441 AAACAGATGCCAAAATTAATCTTTCTGAAAACAGCCAGAACCAAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAAAGTACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGAGCTAGAAAAT 1560
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Db 1501 TCAGAGAGAAAGTACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGAGCTAGAAAAT 1560
Oy 1561 TTTATGCGTATCGAAGAAATGAAGAACGACGAGATCTGATGCGGATTTCCAGAAAAC 1620
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Db 1561 TTTATGCGTATCGAAGAAATGAAGAACGACGAGATCTGATGCGGATTTCCAGAAAAC 1620
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Db 1681 AAGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGAA 1740
Oy 1741 CAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATTTACACGATGAG 1800
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Db 1741 CAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATTTACACGATGAG 1800
Oy 1801 AATTCGATTCATGAGAAAGACAGATAGAGATGATGATGATTAATTCCTGAGCTTTCT 1860
    |||||||
Db 1801 AATTCGATTCATGAGAAAGACAGATAGAGATGATGATGATTAATTCCTGAGCTTTCT 1860
Oy 1861 CTTAGCTTGAAGAAAGAAAGAAAGCAATCTTGCAATGAAATATGATACGTTGGGGAAAGAA 1920
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Db 1861 CTTAGCTTGAAGAAAGAAAGAAAGCAATCTTGCAATGAAATATGATACGTTGGGGAAAGAA 1920
Oy 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAGAAAAA 1980
    |||||||
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAGAAAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 8
AAS9858
ID AAS9858 standard; cDNA; 2000 BP.
AC AAS9858;
XX

DT 12-MAR-2002 (first entry)
XX

DE Breast tumour-specific DNA B11a1 splice variant B11c-8.
XX

KW Human: breast cancer. PCR primer; ss; cytosolic; immunostimulant;
XX

KW tumour; vaccine; immunogenic.
XX

OS Homo sapiens.
XX

PN WO200190152-A2.
XX

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XX 29-NOV-2001.
PD 22-MAY-2001; 2001WO-US16776.
XX 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX (CORI-) CORIXA CORP.
PA
XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX WPI: 2002-089919/12.
DR P-PSDB; AA074378.
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response -
XX
PS Claim 1; page 224; 245pp; English.
XX
CC The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response.
CC CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other:
XX
Query Match 100.0%; Score 2000; DB 24; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AATGCTGTTGAGGTTGATTCATGCGGCTGCTTCTGTGTAAGAACCATTTGGTCTC 60
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Db 1 AATGCTGTTGAGGTTGATTCATGCGGCTGCTTCTGTGTAAGAACCATTTGGTCTC 60
Oy 61 AGGAGCAAGATGGGCAAGTGTGCTCCCTGCTTCCCTGCTGCAAGGAGAGACGGCAAG 120
    |||||||
Db 61 AGGAGCAAGATGGGCAAGTGTGCTCCCTGCTTCCCTGCTGCAAGGAGAGACGGCAAG 120
Oy 121 AGCAAGCTGGGCACTTCTGGAAGCAAGCAAGCACTGCTATGTAAGCACTCAGAGACAG 180
    |||||||
Db 121 AGCAAGCTGGGCACTTCTGGAAGCAAGCAAGCACTGCTATGTAAGCACTCAGAGACAG 180
Oy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGTTG 240
    |||||||
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGTTG 240
Oy 241 GGGGCTTGTGAGACACGACGACTGCTGTANGAAGCACTCAGAAACAAGATGGGCAAG 300
    |||||||
Db 241 GGGGCTTGTGAGACACGACGACTGCTGTANGAAGCACTCAGAAACAAGATGGGCAAG 300
Oy 301 TGGTGTGCGCACGTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGGTGGGCGCTTG 360
    |||||||
Db 301 TGGTGTGCGCACGTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGGTGGGCGCTTG 360
Oy 361 GGAGCTACGATGACAGTGTGCTTCCCTGCTGCAAGGAGGAGGCAAGGTGGGCAAGTCTG 420
    |||||||
Db 361 GGAGCTACGATGACAGTGTGCTTCCCTGCTGCAAGGAGGAGGCAAGGTGGGCAAGTCTG 420
Oy 421 GACAAAGCTCCACAGAGCTGCTGTTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
    |||||||
Db 421 GACAAAGCTCCACAGAGCTGCTGTTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480

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QY 481 CTCAGGGACACTGACGTGAACAAGAMGACAAAGAGAGACTGCTTACATCTGGCC 540
| | | | |
Db 481 CTCAGGGACACTGACGTGAACAAGAMGACAAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTATGTAATAACTCTGCTGCAGACAGCATCTCAACTTAAT 600
| | | | |
Db 541 TCTGCCAATGGGAATTCAGAAAGTATGTAATAACTCTGCTGCAGACAGCATCTCAACTTAAT 600
QY 601 GTCCTTGCACAAACAAAAGAGAGACAGCTCTGATTAAGGCGCTTACAAATGCTCAGGAAGATGAA 660
| | | | |
Db 601 GTCCTTGCACAAACAAAAGAGAGACAGCTCTGATTAAGGCGCTTACAAATGCTCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCGACATGCCAAATATTCAGATGAGTATGAAAT 720
| | | | |
Db 661 TGTGCGTTAATGTTGCTGGAACATGCGACATGCCAAATATTCAGATGAGTATGAAAT 720
QY 721 ACCAGCTCTGCATACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGACACTGCTCTTA 780
| | | | |
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Db 841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
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Db 901 CTGGATGATATGAAGAGACTGCTCTCATCTGCTGATGTTGTGATCAGCAAGATTA 960
QY 961 GTCAGCCTTCTACTGTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGCAGACAGC 1020
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Db 961 GTCAGCCTTCTACTGTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGCAGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1081 AAAGAAAAAAGATGCTAAAAATCTCTCTGAAAAACGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGCGAGTAAAAATATACGCCAGAGAA 1200
| | | | |
Db 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGCGAGTAAAAATATACGCCAGAGAA 1200
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| | | | |
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGCGGATTAAGAAAACCTGACTAATGGTGTCTGCTGCTGCGC 1320
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Db 1261 AAGCATGAAGATTAATTAATGCGGATTAAGAAAACCTGACTAATGGTGTCTGCTGCTGCGC 1320
QY 1321 AATGTGATATGATTAATTTCTCTCAAAAGAGAGCAAGACACTGTAATAATTCAGCAATTT 1380
| | | | |
Db 1321 AATGTGATATGATTAATTTCTCTCAAAAGAGAGCAAGACACTGTAATAATTCAGCAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTACAAAGAA 1440
| | | | |
Db 1381 CCTGACAAACGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGAACCCAGAACAGACTTAAAGCTGACA 1500
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Db 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATAATGCCAGCCAGAGCTAGAAAT 1560
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Db 1501 TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATAATGCCAGCCAGAGCTAGAAAT 1560

QY 1561 TTTATGGCTATCGAAGAATGAAGAACACAGGAAGTACTCATGCTGGATTTCCAGAAAC 1620
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Db 1561 TTTATGGCTATCGAAGAATGAAGAACACAGGAAGTACTCATGCTGGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGGTGCACATCTGCGCAATGTCATGATGATGATTAATTCCTCCAGGAAGAGC 1680
| | | | |
Db 1621 CTGACTAATGGTGCACATCTGCGCAATGTCATGATGATGATTAATTCCTCCAGGAAGAGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACATGAGAAATGAAGATATCACAGTACGAA 1740
| | | | |
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Db 1741 CAAAATGATCTCAGAAACAAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAG 1800
QY 1801 ATTCTGATCATGAAGAAAGCAGATGAGTGGTTGTAATAAATGATTTCTGAGCTTCT 1860
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Db 1801 ATTCTGATCATGAAGAAAGCAGATGAGTGGTTGTAATAAATGATTTCTGAGCTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATATGATGTTCCGGGAAAGAAAT 1920
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Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATATGATGTTCCGGGAAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGCTAGACACAATGAACATCAGACCCAGCTTAAAAA 1980
| | | | |
Db 1921 GCCATGCTAAGACTGAGCTAGACACAATGAACATCAGACCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
| | | | |
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 9

AAA06599

ID AAA06599 standard; cDNA; 2000 BP.

AC AAA06599;

DT 13-JUN-2000 (first entry)

XX

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.

XX

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

KW immunogenic; cytosolic; vaccine; ss.

XX

OS Homo sapiens.

XX

PN WO200004149-A2.

PD

XX 27-JAN-2000.

XX

PF 14-JUL-1999; 99NC-US15838.

XX

PR 14-JUL-1998; 98US-0115453.

XX

PR 14-JUL-1998; 98US-0116134.

XX

PR 23-SEP-1998; 98US-0159812.

XX

PR 23-SEP-1998; 98US-0159822.

XX

PR 15-JAN-1999; 99US-0232149.

XX

PR 15-JAN-1999; 99US-0232880.

XX

PR 09-APR-1999; 99US-0288946.

XX

PA (CORI-) CORIXA CORP.

XX

PI Dillion DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

XX

DR MPI; 2000-171268/15.

XX

PT New polypeptide useful for treating and diagnosing prostate cancer

XX

XX comprises an immunogenic portion of prostate tumor protein -

XX

XX Claim 50; Page 222-223; 263pp; English.

XX

CC The present invention describes isolated polypeptides, comprising an
 CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express
 CC the polypeptides, antibodies against the polypeptides and vaccines
 CC comprising them can be used for inhibiting the development of prostate
 CC cancer in a patient. The polypeptides can be used to generate antibodies
 CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
 CC the polynucleotides encoding the polypeptides can be used as a probe or
 CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
 CC AA08200 to AA08200 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 2000 Bp: 698 A: 387 C: 489 G: 426 T: 0 other:

Query Match 97.5%; Score 1949; DB 21; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGGGTGAGGTGATTCATGCGGGCTGCTTCTGTGAAGAAGCATTTGGTCTC 60
 DB 1 ATGGGTGAGGTGATTCATGCGGGCTGCTTCTGTGAAGAAGCATTTGGTCTC 60
 OY 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGCAAGAGCGGCAAG 120
 DB 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGCAAGAGCGGCAAG 120
 OY 121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGTGCTATGAAGACTCAGAGCAAG 180
 DB 121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGTGCTATGAAGACTCAGAGCAAG 180
 OY 181 ATGGGGAAGTGGGCGGCGGCTGCTCCCTGCTGAGGGGGAGTGGCAAGCAACGCTG 240
 DB 181 ATGGGGAAGTGGGCGGCGGCTGCTCCCTGCTGAGGGGGAGTGGCAAGCAACGCTG 240
 OY 241 GGGGCTTCTGAGACCAAGAGACTGTGCTATGAAGACTCAGAGCAAGAGTGGGCAAG 300
 DB 241 GGGGCTTCTGAGACCAAGAGACTGTGCTATGAAGACTCAGAGCAAGAGTGGGCAAG 300
 OY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGGAGCGGCAAGCAAGTGGGCTTGG 360
 DB 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGGAGCGGCAAGCAAGTGGGCTTGG 360
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 DB 361 GGAGACTAGAGTACAGTGCCTCATGAGGCCAGGTACAGTCCGTGAGAGAAAGTCTG 420
 OY 421 GACAACTCCACAGAGCTGCTGCTGAGGGTAAAGTCCCGCAAGAAAGTCTCATGCTCATG 480
 DB 421 GACAACTCCACAGAGCTGCTGCTGAGGGTAAAGTCCCGCAAGAAAGTCTCATGCTCATG 480
 OY 481 CTGAGGAGACTGAGTGAACAAAGAGACCAAAAGAGACTGCTTACATCTGGCC 540
 DB 481 CTGAGGAGACTGAGTGAACAAAGAGACCAAAAGAGAGTCTTACATCTGGCC 540
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 DB 601 GTGCTTGACAAACAAAAGAGAGAGCTGTGATAAAGCCCTTACATGCGCAGAAATGAA 660
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 DB 661 TGTGCTTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
 OY 721 ACCACCTGACTAGAGTATCTAATGAAGATAAATTAATGGCAAGAGAGCTCTTA 780
 DB 721 ACCACCTGACTAGAGTATCTAATGAAGATAAATTAATGGCAAGAGAGCTCTTA 780
 OY 781 TATGTGTGATATGCAATCAAAAACAAAGCATGGCTCAGACCACTGTTACTTGTGTA 840

DB 781 TATGTGTGATATGCAATCAAAAACAAAGCATGGCTCAGACCACTGTTACTTGTGTA 840
 OY 841 CATGACAAAACAGCAAGCTGGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 DB 841 CATGACAAAACAGCAAGCTGGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 OY 901 CTGATAGATATGGAAGAGTGTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
 DB 901 CTGATAGATATGGAAGAGTGTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
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 DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAGC 1020
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 DB 1021 GCCAGAGATATCTGTTTCTAGTATCATCATGATATTTTCCAGTTACTTCTGACTAC 1080
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 OY 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCCAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
 DB 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCCAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
 OY 1201 ATGTCTCAGAACCCAGCAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
 DB 1201 ATGTCTCAGAACCCAGCAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
 OY 1261 AAGCATGAAGTATTAATGAGGATTAATGAGAAACCTGATATGCTGCTGCTGGC 1320
 DB 1261 AAGCATGAAGTATTAATGAGGATTAATGAGAAACCTGATATGCTGCTGCTGGC 1320
 OY 1321 AATGTGATTAATGATTAATTTCTCAAAAGAGAGCAACACCTGAAATCAGCAATTT 1380
 DB 1321 AATGTGATTAATGATTAATTTCTCAAAAGAGAGCAACACCTGAAATCAGCAATTT 1380
 OY 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGCAATTTGCTGCTACAAAGAA 1440
 DB 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGCAATTTGCTGCTACAAAGAA 1440
 OY 1441 AAGCAGATGCCAAATATCTTCTGAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
 DB 1441 AAGCAGATGCCAAATATCTTCTGAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
 OY 1501 TCAGAGAGAGTCCAAAGGCTTGAAGGCGATGAAATGGCCAGCAGAGCTAGAAAT 1560
 DB 1501 TCAGAGAGAGTCCAAAGGCTTGAAGGCGATGAAATGGCCAGCAGAGCTAGAAAT 1560
 OY 1561 TTTATGCTTTCGAAAGAAATGAAGAGACGGAAGTACTATGTCGATTTCCAGAAAC 1620
 DB 1561 TTTATGCTTTCGAAAGAAATGAAGAGACGGAAGTACTATGTCGATTTCCAGAAAC 1620
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 DB 1621 CTGACATTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTCAAGAAAGAGC 1680
 OY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACAGTGAAGAGTATCAGAGTGAAGAA 1740
 DB 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACAGTGAAGAGTATCAGAGTGAAGAA 1740
 OY 1741 CAAATGATATCTCAGAAAGCAATTTTGAAGAAACAGAACTGGAATATACAGAGAG 1800
 DB 1741 CAAATGATATCTCAGAAAGCAATTTTGAAGAAACAGAACTGGAATATACAGAGAG 1800
 OY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAGAGTGTGAAGAAATGAATTTGAGCTTCT 1860
 DB 1801 ATTCTGATTCATGAAGAAAGCAGATAGAGAGTGTGAAGAAATGAATTTGAGCTTCT 1860
 OY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATATGTAAGTGGCGGAGAAATTT 1920

Db 1861 CTTAGTGTAGAGAAAAGACATCTTCATGAAATAGTACGTCGGGAGAAATT 1920
QY 1921 GCCATGCTAGAGCTGAGCTAGACCAATGAAATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAGAGCTGAGCTAGACCAATGAAATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
AAC81013
ID AAC81013 standard; cDNA; 2040 BP.
AC AAC81013;
XX 13-FEB-2001 (first entry)
DE Human B1Agl antigen splice isoform B1IC-9-16 cDNA.
XX Human; breast tumour-specific antigen; cytostatic; vaccine;
KM breast cancer; B18Agl; B1Agl; B15Agl; ss.
XX Homo sapiens.
XX WO200061753-A2.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-US09312.
XX 09-APR-1999; 99US-0289198.
PR 28-OCT-1999; 99US-0429755.
PR 23-MAR-2000; 2000US-0534825.
XX (CORI-) CORIXA CORP.
XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX WPI: 2000-628403/60.
DR P-PSDB; AAB28630.
XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX Claim 4; Page 178; 187pp; English.

XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit the development of
CC cancer.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
SQ

Query Match 77.5%; Score 1551; DB 21; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGTTGATTCATCCGGCTGCTTCTGTGAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGTTGATTCATCCGGCTGCTTCTGTGAGAGCAATTTGGTCTC 60

QY 61 AGAGCAAGATGGCGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGAGCAAGATGGCGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGCTGGGCACTTCTGGAGACACAGACAGCTGCTATGAAGACCTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGGAGACACAGACAGCTGCTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGGGCAAGTGGTGGGCGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GCGGCTTGGAGACACAGACAGCTGCTATGAAGACCTCAGAGCAAGTGGGCAAG 300
Db 241 GCGGCTTGGAGACACAGACAGCTGCTATGAAGACCTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGGTGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Db 301 TGGTGGTGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
QY 361 GGAGACTAGATGACAGAGTGGCTTCATGAGGCCAGGTACACGTCCTGGAGAGATCTG 420
Db 361 GGAGACTAGATGACAGAGTGGCTTCATGAGGCCAGGTACACGTCCTGGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGGCACTGACGTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Db 481 CTCAGGGCACTGACGTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGGAATTCAGAGTAGTAAGTCCCTGCTGAGACAGATGTCACATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTAGTAAGTCCCTGCTGAGACAGATGTCACATTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGGAGCAGCTGTGTAAGGCCCTGACAAATGCAAGAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGGAGCAGCTGTGTAAGGCCCTGACAAATGCAAGAGATGAA 660
QY 661 TGTGCGTTAATGTGTGCGAATGCGACATGCGACATGCAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTGTGCGAATGCGACATGCGACATGCAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCGACCTGACCTATATATGAAGATTAATGAGCAAGCAAGCAAGCAAGCAAG 780
Db 721 ACCACTGCGACCTGACCTATATATGAAGATTAATGAGCAAGCAAGCAAGCAAGCAAG 780
QY 781 TATGCTGTATATGCAATCAAAAAACAGCATGGCCACACCACTGTTACTTGGTGTGA 840
Db 781 TATGCTGTATATGCAATCAAAAAACAGCATGGCCACACCACTGTTACTTGGTGTGA 840
QY 841 CATAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAGCAATTAATTAATGCA 900
Db 841 CATAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAGCAATTAATTAATGCA 900
QY 901 CTGATAGATATGAAGAGCTGCTCATACTGCTGATGTTGGATCGACAGATATA 960
Db 901 CTGATAGATATGAAGAGCTGCTCATACTGCTGATGTTGGATCGACAGATATA 960
QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATGCAAGAGC 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATGCAAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATATGATTAATTTGCGATCTTCTGACATAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATATGATTAATTTGCGATCTTCTGACATAC 1080
QY 1081 AAAAAAAAAAGATGCTAAAAATCTCTTGAAGAAAGCAATCAGAAAGCAAGATTAAG 1140
Db 1081 AAAAAAAAAAGATGCTAAAAATCTCTTGAAGAAAGCAATCAGAAAGCAAGATTAAG 1140
QY 1141 CTGACATCAGAGAAAGTCAAAAGGTTCAAGGAGTGAATAATAGCCAGCAGAGAAA 1200

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|||||
Db 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAAGGCGAGTGAATAATGACGACAGAGAAA 1200
Qy 1201 ATGCTCAAGAACCAAAATTAATAAGATGATGATAGAGAGCTTCAACAAAGAAAGAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATAAGATGATGATAGAGAGCTTCAACAAAGAAAGAAG 1260
Qy 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Qy 1321 AATGCTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1380
Db 1321 AATGCTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 CCTGACAAAGAAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1441 AAGCATGATGCAAAATGATCTTCTGTAAGAACAGCAACCAAGCAAGCAAGCAAGCAAGCA 1500
Db 1441 AAGCATGATGCAAAATGATCTTCTGTAAGAACAGCAACCAAGCAAGCAAGCAAGCAAGCA 1500
Qy 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGCGAGTGAAGAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGCGAGTGAAGAAATGGCCAGCCAGAG 1551

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RESULT 11

AA167213
ID AA167213 standard; cDNA; 2040 BP.

AC AA167213;

DI 11-FEB-2002 (first entry)

DE B305D isoform C splice variant 3 encoding cDNA.

KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
cancer; B305D; ss.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 1..2016

FT /tag= a /product= "B305D isoform C splice variant"

PN WO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR 20-JUL-2000; 2000US-219862P.

PR 27-JUL-2000; 2000US-221300P.

PR 18-DEC-2000; 2000US-256592P.

XX (CORI-) CORIXA CORP.

PI Houghton RL, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH;

DR WPI; 2001-626449/72.

DR P-PSDB; AAG65978.

PT Identifying tissue (tumour)-specific polynucleotides overexpressed in

PS tissue of interest, compared to control tissue, for detecting cancer

XX polymerase chain reaction -

CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SP1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SP1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 77.5%; Score 1551; DB 22; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGCTGTTGAGTGTATTCATGCCGCTCCTCTTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTTGAGTGTATTCATGCCGCTCCTCTTGTGAAGAACCATTTGGTCTC 60
Qy 61 AAGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AAGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
Qy 181 ATGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Qy 241 GGGGCTTGGGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
Db 241 GGGGCTTGGGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
Qy 301 TGGTGGTGGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGGCGCTTG 360
Db 301 TGGTGGTGGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGGCGCTTG 360
Qy 361 GGAGCTACGATGACAGTGGCTTCATGAGACCCAGGTACCAAGTCCGCTGGAGAAATCTG 420
Db 361 GGAGCTACGATGACAGTGGCTTCATGAGACCCAGGTACCAAGTCCGCTGGAGAAATCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCCATCGTCATG 480
Db 421 GACAACTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCCATCGTCATG 480
Qy 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTGAAGTAAATCTCTGAGAGAGAGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTGAAGTAAATCTCTGAGAGAGAGTCAACTTAAT 600
Qy 601 GTCCCTGACAAACAAAGAGGACAGCTGATTAAGGCGTAAATGCAAGCAAGCAAGTGA 660
Db 601 GTCCCTGACAAACAAAGAGGACAGCTGATTAAGGCGTAAATGCAAGCAAGCAAGTGA 660
Qy 661 TGTGCTTAATGCTTGTGGAACATGAGCAAGTCAAAATATTCAGATGATGAAGT 720
Db 661 TGTGCTTAATGCTTGTGGAACATGAGCAAGTCAAAATATTCAGATGATGAAGT 720
Qy 721 ACCACTGCACTACGCTATCTATTAATGAAGATAAATTAATGGCAAGCAAGTCTTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGAAGATAAATTAATGGCAAGCAAGTCTTTA 780

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QY 781 TATGTCGTATATCATCAAAAAACAGCATGGCTCAGACACTGTCTTACTTGTTGA 840
Db 781 TATGTCGTATATCATCAAAAAACAGCATGGCTCAGACACTGTCTTACTTGTTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
QY 901 CTGATGATATGAGAGAGCTGCTCATCTACTGCTGATATGTTGGATTCAGAGTATA 960
Db 901 CTGATGATATGAGAGAGCTGCTCATCTACTGCTGATATGTTGGATTCAGAGTATA 960
QY 961 GTCAAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAAGCATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
Db 1081 AAAAGAAAAAGCATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAGGCAAGTGAATAATAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAGGCAAGTGAATAATAGCCAGCAGAGAAA 1200
QY 1201 ATGCTCTCAAGAACCAAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATGAG 1260
Db 1201 ATGCTCTCAAGAACCAAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAATTAATATGTTGGATTACTAGAAAACCTGACTAATGTTGCTACTGCTGC 1320
Db 1261 AAGCATGAAATTAATATGTTGGATTACTAGAAAACCTGACTAATGTTGCTACTGCTGC 1320
QY 1321 AATGCTGTAATGATTAATTCCTCAAGAGAGCAGAACACCTGAAATTCAGCAATTT 1380
Db 1321 AATGCTGTAATGATTAATTCCTCAAGAGAGCAGAACACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAACGAAATGAAAGATATCAGAGATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAACGAAATGAAAGATATCAGAGATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAGAGAGTCAAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAGAGAGTCAAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

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RESULT 12
AAS63809 standard; cDNA; 2040 BP.

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AC AAS63809;
XX
XX 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #10.
XX
KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN M02001.73032-A2.
XX
PD 04-OCT-2001.
PF 27-MAR-2001; 2001MO-US09919.
XX

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PR 27-MAR-2000; 2000US-05316857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0583793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvyck NS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
DR WPI: 2001-639232/73.
DR P-PSDB: AAU69779.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 350; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polypeptides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SO Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

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Query Match 77.5%; Score 1551; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTGCTGAGTGGATTCATCCGCTGCTCTTCTGAGAAAGCCATTGGCTC 60
Db 1 ATGCTGCTGAGTGGATTCATCCGCTGCTCTTCTGAGAAAGCCATTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTGCTCCCTGCTCAGAGAGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTGCTCCCTGCTCAGAGAGCGCGCAAG 120
QY 121 AGCAACGTGGGCACTTGTGAGACACGACACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTGTGAGACACGACACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCTTCTGAGAGACAGAGACTGCTGATGAAGACACTCAGAGCAAGATGGCAAG 300
Db 241 GGGCTTCTGAGAGACAGAGACTGCTGATGAAGACACTCAGAGCAAGATGGCAAG 300
QY 301 TGTGCTGCCACTCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCCACTCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTATGAGAGCGCCAGGTAACACGTCCTGGAGAAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGGCTTATGAGAGCGCCAGGTAACACGTCCTGGAGAAAGATCTG 420

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QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTAAG 480
    |||||||
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTAAG 480
QY 481 CTCAGGAGACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
    |||||||
DB 481 CTCAGGAGACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TGTGCAATGGGAATTCAGAAATAGTAAACCTCGCTGGACAGAGATGCAACTTAAT 600
    |||||||
DB 541 TGTGCAATGGGAATTCAGAAATAGTAAACCTCGCTGGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTGTATAAAGCCGTCAATGCGCAGAGATGAA 660
    |||||||
DB 601 GTCTTGAACAACAAAAGAGACAGCTGTATAAAGCCGTCAATGCGCAGAGATGAA 660
QY 661 TGTGGCTTAATGTGTGCTGGAACATGGCAGCTGATCCAAATATTCCAGATGATGGAAT 720
    |||||||
DB 661 TGTGGCTTAATGTGTGCTGGAACATGGCAGCTGATCCAAATATTCCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGCGCTATCTATATGAAGATTAATGCGCAAGCAAGCTGCTTA 780
    |||||||
DB 721 ACCACTCTGCACTAGCGCTATCTATATGAAGATTAATGCGCAAGCAAGCTGCTTA 780
QY 781 TATGGTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGA 840
    |||||||
DB 781 TATGGTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTGTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGA 900
    |||||||
DB 841 CATGAGCAAAAACAGCAAGCTGTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGA 900
QY 901 CTGGATATGATGGAAGAGCTGCTCATACTGCTGTATGTTGGATGGAGACAGATATA 960
    |||||||
DB 901 CTGGATATGATGGAAGAGCTGCTCATACTGCTGTATGTTGGATGGAGACAGATATA 960
QY 961 GTCAAGCTTCTACTTGAGCAAAAATATGATGTATCTTCTCAAGATCTATCTGGACAGAG 1020
    |||||||
DB 961 GTCAAGCTTCTACTTGAGCAAAAATATGATGTATCTTCTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGCACTAC 1080
    |||||||
DB 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGCACTAC 1080
QY 1081 AAGAAGAAACATATGTTAAATCTCTGTAACAGAACAGAACAGAACAACTTAAG 1140
    |||||||
DB 1081 AAGAAGAAACATATGTTAAATCTCTGTAACAGAACAGAACAGAACAACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
    |||||||
DB 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAGATGAAG 1260
    |||||||
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAGATGAAG 1260
QY 1261 AAGCAATGAAGTAATTAATGAGTACTAGAGAAAACCTCAATTAAGTGTCACTGTGGC 1320
    |||||||
DB 1261 AAGCAATGAAGTAATTAATGAGTACTAGAGAAAACCTCAATTAAGTGTCACTGTGGC 1320
QY 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAACACCTGAATAATAGCAATTT 1380
    |||||||
DB 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAACACCTGAATAATAGCAATTT 1380
QY 1381 CCTGACAACGAAGTGAAGATATCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA 1440
    |||||||
DB 1381 CCTGACAACGAAGTGAAGATATCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA 1440
QY 1441 AAACGATAGCCAAATTAATCTTCTGAAAACAGCAACCCGAAACAGACTTAAGAGTGAA 1500
    |||||||
DB 1441 AAACGATAGCCAAATTAATCTTCTGAAAACAGCAACCCGAAACAGACTTAAGAGTGAA 1500
QY 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCAGAG 1551

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DB 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCAGAG 1551
    |||||||
RESULT 13
ID AAH93716 standard; cDNA; 2040 BP.
XX
XX AAH93716;
AC
XX 04-OCT-2001 (first entry)
DT
XX
XX Human prostate-specific cDNA sequence B305D splice variant #10.
DE
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytostatic; gene therapy; metastasis; ss.
OS
XX Homo sapiens.
PN
XX WO200151633-A2.
PD
XX 19-JUL-2001.
PF
XX 16-JAN-2001; 2001WO-US01574.
PR
XX 14-JAN-2000; 2000US-0483672.
PA
XX (CORI-) CORIXA CORP.
PI
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;
PI Wang A, Meagher MJ;
XX
XX WPI: 2001-425873/45.
DR
XX
XX
XX New polynucleotide encoding a prostate-specific protein, for
XX diagnosing, monitoring and treating prostate cancer in a patient and
XX for use in vaccines -
XX
XX Claim 1: Page 348; 543pp; English.
XX
XX
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated
XX T cells prepared using (I) or (II) are used treat cancer in a patient.
XX (I) and the antibodies are also used in the detection of cancer in a
XX patient. The cancer that is diagnosed or treated is particularly
XX prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX (I) and (II) can be used for monitoring the progression of cancer in a patient.
XX (I) and (II) can also be used to improve diagnostic and therapeutic
XX methods for prostate cancer. They can indicate the level of metastasis
XX as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
XX AAH01318 represent polynucleotide and amino acid sequences used in the
XX exemplification of the present invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
Query Match 77.5%; Score 1551; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGCTGAGTGTATTCATGCGGCTGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
    |||||||
DB 1 ATGCTGCTGAGTGTATTCATGCGGCTGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTTGCCTTCCCTGCGAGGAGAGCGGCAAG 120
    |||||||
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTTGCCTTCCCTGCGAGGAGAGCGGCAAG 120
QY 121 ACCAAGCTGGGCACTTCTGAGACCAAGCAAGCACTGTATGAAGCACTAGAGCAAG 180
    |||||||
DB 121 ACCAAGCTGGGCACTTCTGAGACCAAGCAAGCACTGTATGAAGCACTAGAGCAAG 180

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QY 181 ATGGGCAAGTGTGCGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGACGACGTG 240
    |||||||
Db 181 ATGGGCAAGTGTGCGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGACGACGTG 240
QY 241 GGGGCTTCTGGAGACGACGACGCTGCTATGAAAGACACTCAGGAACAAGATGGGCAAG 300
    |||||||
Db 241 GGGGCTTCTGGAGACGACGACGCTGCTATGAAAGACACTCAGGAACAAGATGGGCAAG 300
QY 301 TGGTGTGCTGACCTGCTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGGTGGGCTTGG 360
    |||||||
Db 301 TGGTGTGCTGACCTGCTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTCATGAGAGCCGACGATCAGCTGCTGAGAAAGATCTG 420
    |||||||
Db 361 GGAGACTACGATGACAGTGGCTTCATGAGAGCCGACGATCAGCTGCTGAGAAAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
    |||||||
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAGAGCTGCTTACATCTGGCC 540
    |||||||
Db 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCGCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGCTCACTTAA 600
    |||||||
Db 541 TCTGCGCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGCTCACTTAA 600
QY 601 GTCTCTGACAAACAAAAGAGACAGCTCTGTATTAAGGCCGCTACAGTCCAGGAAGATGA 660
    |||||||
Db 601 GTCTCTGACAAACAAAAGAGACAGCTCTGTATTAAGGCCGCTACAGTCCAGGAAGATGA 660
QY 661 TGTGCTTAATGTTGTGCGAAGCATGGCATGATCCAATATTCAGATGATGATGAAT 720
    |||||||
Db 661 TGTGCTTAATGTTGTGCGAAGCATGGCATGATCCAATATTCAGATGATGATGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATATTAAGATTAATTAATGAGCAAGCAAGCTGCTTA 780
    |||||||
Db 721 ACCACTCTGCACTACGCTATCTATATTAAGATTAATTAATGAGCAAGCAAGCTGCTTA 780
QY 781 TATGCTCTGATATGCAATCAAAAACAGCATGGCTCACACCACTGTTACTTGATGTA 840
    |||||||
Db 781 TATGCTCTGATATGCAATCAAAAACAGCATGGCTCACACCACTGTTACTTGATGTA 840
QY 841 CATGAGCAAAAACGCAAGTCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
    |||||||
Db 841 CATGAGCAAAAACGCAAGTCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATATGATATGAGAGACTGCTCTCATACTGCTGATGTTGATGATCAGCAAGTATA 960
    |||||||
Db 901 CTGATATGATATGAGAGACTGCTCTCATACTGCTGATGTTGATGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTTGAGCAAAATATGATGTTCTCAAGATCTATCTGACAGACG 1020
    |||||||
Db 961 GTCAGCCTTCTACTTGAGCAAAATATGATGTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATGCTGCTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACATC 1080
    |||||||
Db 1021 GCCAGAGATGCTGCTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACATC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGMAAACAGCAATCCAGAACAGACTTAAAG 1140
    |||||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGMAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCCAAAGGTTCAAGGCAAGTGAATAATGACCAAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAGAGTCCAAAGGTTCAAGGCAAGTGAATAATGACCAAGAGAAA 1200
QY 1201 ATGTCTCAAGAGACGAAATTAATTAAGATGCTATAGAGAGGTTGAAGAAATGAAG 1260
    |||||||
Db 1201 ATGTCTCAAGAGACGAAATTAATTAAGATGCTATAGAGAGGTTGAAGAAATGAAG 1260
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QY 1261 AACCATGAAAGTAAATAATGATGATTACTAGAAAACCTGACTAATGCTGCTGCTG 1320
    |||||||
Db 1261 AACCATGAAAGTAAATAATGATGATTACTAGAAAACCTGACTAATGCTGCTGCTGCTG 1320
QY 1321 AATGCTATTAATGATTAATTTCTCTCAAGAGAAAGCAAGCACTGAAATTCAGCAATT 1380
    |||||||
Db 1321 AATGCTATTAATGATTAATTTCTCTCAAGAGAAAGCAAGCACTGAAATTCAGCAATT 1380
QY 1381 CTTGACAAAGCAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CTTGACAAAGCAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTCTGAAAACGACACCAACCAAGCACTTAAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCCAAATATCTTCTGAAAACGACACCAACCAAGCACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCACAAAGGCTTGGAGGCAAGTGAATAATGGCCAGCCAGAG 1551
    |||||||
Db 1501 TCAGAGGAAGAGTCACAAAGGCTTGGAGGCAAGTGAATAATGGCCAGCCAGAG 1551
```

RESULT 14

AAH85030 standard; cDNA; 2040 BP.

AAH85030;

25-SEP-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #10.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

chromosome 22q11.2; prostate-specific protein; chromosome 1;

prostate specific antigen; PSA; ss.

Homo sapiens.

WO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000MO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

Kalos MD, Retler MW, Stolk JA, Day CH, Skeiky YW, Wang A;

WPI; 2001-308785/32.

Claim 31; Page 248; 325pp; English.

The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production.

The polypeptide, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer.

Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on

chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification

of the present invention.

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 77.5%; Score 1551; Db 22; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTGGTTGAGGTGATTCCATGCCGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
Db 1 ATGTGGTTGAGGTGATTCCATGCCGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGTCAGAGGAGCCGCAAG 120
Db 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGTCAGAGGAGCCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTTGAGACCAAGCACTGCTATGAAGCACTCGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTTGAGACCAAGCACTGCTATGAAGCACTCGAGCAAG 180
QY 181 ATGGGCAAGTGTGGCCGCACTGCTTCCCTGTCAGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGGCCGCACTGCTTCCCTGTCAGAGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGTTCTGGAGACCAAGCACTGCTATGAAGCACTCGAGCAAGCAAGTGGCAAG 300
Db 241 GGGCGTTCTGGAGACCAAGCACTGCTATGAAGCACTCGAGCAAGCAAGTGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGTCAGAGGAGGAGGCAAGCAAGTGGGCGCTTG 360
Db 301 TGGTCTGCACTGCTTCCCTGTCAGAGGAGGAGGCAAGCAAGTGGGCGCTTG 360
QY 361 GGAGACTAGATGACAGTGTCTTCTGAGAGCCAGTACAGTCCGTGGAGAGATCTG 420
Db 361 GGAGACTAGATGACAGTGTCTTCTGAGAGCCAGTACAGTCCGTGGAGAGATCTG 420
QY 421 GACAAAGTCTCAGAGAGTGTCTGAGAGTCCAGAGAGAGATCTCATCTGATG 480
Db 421 GACAAAGTCTCAGAGAGTGTCTGAGAGTCCAGAGAGAGATCTCATCTGATG 480
QY 481 CTCAGGAGACACTGAGTGAACAAGAGCAAGCAAGAGAGTCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGAGTGAACAAGAGCAAGCAAGAGAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGAGAGATGCACTTAAT 600
QY 601 GTCCCTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCCCTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGGCTTAATGTGCTGGAACATGGCACTGATCCAAATATCCAGATGATGAAT 720
Db 661 TGTGGCTTAATGTGCTGGAACATGGCACTGATCCAAATATCCAGATGATGAAT 720
QY 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATGAGCAAGCACTGCTCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATGAGCAAGCACTGCTCTTA 780
QY 781 TATGTGTGATATGATCAAAAAACAAGCATGAGTGCACACCACTGTTACTGGTGA 840
Db 781 TATGTGTGATATGATCAAAAAACAAGCATGAGTGCACACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGA 900
QY 901 CTGATATGATATGAAGAGAGTGTCTACTTGTATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAGAGAGTGTCTACTTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTTACTGAGCAAAAAATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTGAGCTTCTTACTGAGCAAAAAATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020

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QY 1021 GCCAGAGATATGCTGTTCTATCATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTATCATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATTCAGAACAGCTTAAAG 1140
Db 1081 AAAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATTCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAAGTAATGCCAGCAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAAGTAATGCCAGCAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGTAATTAATAGATGGATGATAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGTAATTAATAGATGGATGATAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGAGTATCTAGAAAACCTGACTAATGTTGCTCACTGCTGCG 1320
Db 1261 AAGCATGAAGATTAATGAGTATCTAGAAAACCTGACTAATGTTGCTCACTGCTGCG 1320
QY 1321 AATGTGATATGATTAATTCCTCAAGAGAGAGCAGAACCTGAAAATATGCAATTT 1380
Db 1321 AATGTGATATGATTAATTCCTCAAGAGAGAGCAGAACCTGAAAATATGCAATTT 1380
QY 1381 CCTGACAAAGAGTGAAGATATGACAGATTTGGATTTGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAGTGAAGATATGACAGATTTGGATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGTCAACAAAGGCTTGAGGAGCTGAAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGTCAACAAAGGCTTGAGGAGCTGAAAATGGCCAGCCAGAG 1551

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RESULT 15
 AAH02781
 ID AAH02781 standard; cDNA, 2040 BP.
 AC AAH02781;
 XX
 AC
 DT 14-JUN-2001 (first entry)
 XX
 DE prostate tumour antigen determined cDNA splice variant of B305D #10.
 XX
 KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 XX prostate cancer; immunogenic; cytosolic; vaccine; ss.
 OS Homo sapiens.
 XX
 OS
 PN WO200125272-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US27464.
 XX
 PR 04-OCT-1999; 99US-0157455.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Skeiky YAM, Reed SG, Cheever MA;
 DR WPI: 2001-245062/25.
 DR P-PSDB; AAB74817.
 XX
 PT Prostate specific protein and its encoding polynucleotide, useful for
 PS the treatment and diagnosis of prostate cancer -
 XX
 PS Claim 50; Page 233; 276pp; English.
 CC The present invention describes an isolated polypeptide (I) comprising

CC at least an immunogenic portion of a prostate tumour antigen protein or
 CC its variant. (i) have cytostatic activity and can be used in vaccine
 CC production. (ii) prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (i), and a
 CC pharmaceutical composition containing (i) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridize to a
 CC polynucleotide that encodes a prostate specific protein are useful
 CC for detecting the presence or absence of a cancer or monitoring the
 CC progression the progression of a cancer, especially prostate cancer.
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
 CC used in the exemplification of the present invention.

XX
 SO Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 77.5%; Score 1551; DB 22; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1551: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTGAAGTGAATCCATCCGGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
DB 1 ATGGTGGTGAAGTGAATCCATCCGGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGGAGACACAGACACTGCTATGAAGACACTGAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTGTGGAGACACAGACACTGCTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 ATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 GGGCTTGTGAGACACAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GGGCTTGTGAGACACAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TGGTGGTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 TGGTGGTGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGTACCACTGCTGCTGCTGCTGCTGCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGTACCACTGCTGCTGCTGCTGCTGCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTGAGGGACACTGACGTGAACAAAGAGCAAGAAAGAGAGTGCCTCATCTGAGCC 540
DB 481 CTGAGGGACACTGACGTGAACAAAGAGCAAGAAAGAGAGTGCCTCATCTGAGCC 540
QY 541 TCTGCAATGGGAATGAGAAAGTAAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TCTGCAATGGGAATGAGAAAGTAAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTCTTGAACAACAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 GTCTTGAACAACAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGATGGAAT 720
DB 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGATGGAAT 720
QY 721 ACCACTGCTACGCTATCTATATGAAGATAAATTAATGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 ACCACTGCTACGCTATCTATATGAAGATAAATTAATGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TATGCTGCTGATATGATCAAAAAAAGAGATGGCTCACACCACTGTTACTTGGTGA 840
DB 781 TATGCTGCTGATATGATCAAAAAAAGAGATGGCTCACACCACTGTTACTTGGTGA 840

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DB 781 TATGCTGCTGATATGATCAAAAAAAGAGATGGCTCACACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACGCAAGTGTGAATTTTATATCAAGAAAAAGCAATTTAATATGA 900
DB 841 CATGAGCAAAAAACGCAAGTGTGAATTTTATATCAAGAAAAAGCAATTTAATATGA 900
QY 901 CTGATGATATGAGAAAGAGTGTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 CTGATGATATGAGAAAGAGTGTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 GTCAGCTTCTACTTGGACAAATATGATGATCTTCTCAAGATCTATCTGCAAGAC 1020
DB 961 GTCAGCTTCTACTTGGACAAATATGATGATCTTCTCAAGATCTATCTGCAAGAC 1020
QY 1021 GCCAGAGATGATGCTGCTTCTGATCATCATCATATGATTTGCCAGTACTTTCGACTAC 1080
DB 1021 GCCAGAGATGATGCTGCTTCTGATCATCATCATATGATTTGCCAGTACTTTCGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAACACGAAATCCGAAACAGACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAACACGAAATCCGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAAAGTGTCAAAAGTTCAAGGCAAGTAAATAGCCAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGTGTCAAAAGTTCAAGGCAAGTAAATAGCCAGCCAGAGAAA 1200
QY 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGCTATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1380
DB 1321 AATGCTATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1380
QY 1381 CCTGACAAAGCAAGTGAAGATATCACAGATTTGCCAATTAATTAATTAATTAATTAATTA 1440
DB 1381 CCTGACAAAGCAAGTGAAGATATCACAGATTTGCCAATTAATTAATTAATTAATTAATTA 1440
QY 1441 AAACAGATGCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
DB 1441 AAACAGATGCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
QY 1501 TCAGAGAAAGTGTCAAAAGGCTTGAAGGCGAGTGAATAATGGCCAGCCAGAG 1551
DB 1501 TCAGAGAAAGTGTCAAAAGGCTTGAAGGCGAGTGAATAATGGCCAGCCAGAG 1551

RESULT 16
ABL95180
ID ABL95180 standard; cDNA; 2040 BP.
XX
AC ABL95180;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human B305D splice variant cDNA sequence SEQ ID NO 375.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.

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QY 1261 AAGCATGAAAGTAAATGTTGGATTACTAGAAAACTGACTAAATGGTGCATGCTGGC 1320
DB 1261 AAGCATGAAAGTAAATGTTGGATTACTAGAAAACTGACTAAATGGTGCATGCTGGC 1320
QY 1321 AATGGTATATATGATTAATTTCCCAAGAGAGCAGACACCTGAAATACACATTT 1380
DB 1321 AATGGTATATATGATTAATTTCCCAAGAGAGCAGACACCTGAAATACACATTT 1380
QY 1381 CCTGACACAGCAAGTGAAGATATACAGAAATTTGCGAATTTGTTGACTACAAAGAA 1440
DB 1381 CCTGACACAGCAAGTGAAGATATACAGAAATTTGCGAATTTGTTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAAAAATGGCCAGCAGAG 1551
DB 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAAAAATGGCCAGCAGAG 1551

RESULT 17
AAS9859 standard; cDNA; 2040 BP.
AAS9859;
12-MAR-2002 (first entry)
Breast tumour-specific DNA B1la1 splice variant B11C-9.16.
Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
tumour; vaccine; immunogenic.
Homo sapiens.
MO200190152-A2.
29-NOV-2001.
22-MAY-2001; 2001MO-US16776.
24-MAY-2000; 2000US-0577505.
08-JUN-2000; 2000US-0590583.
26-OCT-2000; 2000US-069295.
16-MAR-2001; 2001US-0810936.
(CORI-) CORIXA CORP.
Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
Wang A, Skeiky YAW, Harlocker SL, Day CH;
WPI: 2002-089919/12.
P-PSDB; AAU74379.
New breast tumour proteins and polynucleotides encoding them, useful for
treating and/or preventing cancer, particularly breast cancer, and for
eliciting humoral and/or cellular immune response -
Claim 1; Page 224-225; 245pp; English.
The invention relates to novel breast tumour polynucleotides and
polypeptides. The polypeptides and polynucleotides are useful in
pharmaceutical compositions for treating and/or preventing cancer,
particularly breast cancer, and for eliciting an immune response,
particularly humoral and/or cellular immune response. The polynucleotides
may be used as probes or primers for nucleic acid hybridisation, in the
design and preparation of ribozyme molecules for inhibiting expression of
cancer polypeptides and proteins, and in recombinant DNA molecules to
direct expression of a polypeptide in host cells. AAS9570-AAS9988
represent novel human breast cancer protein coding sequences and
PCR primers of the invention.

XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
Query Match 77.5%; Score 1551; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGGTGTGAGTGGTATTCATCCATGCGGCTGCTCTCTGTGAAGAAAGCATTTGGTCTC 60
DB 1 AATGGTGTGAGTGGTATTCATCCATGCGGCTGCTCTCTGTGAAGAAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAACGTGGGCACTTTGTGAGACACAGACACTCTGCTATGAAGACACTAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTTGTGAGACACAGACACTCTGCTATGAAGACACTAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTCCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGACACAGACACTCTGCTATGAAGACACTAGAGCAAGATGGCAAG 300
DB 241 GGGCTTCTGAGACACAGACACTCTGCTATGAAGACACTAGAGCAAGATGGCAAG 300
QY 301 TGGTGTGGCCACCTGCTCCCTGCTGCAAGGGGAGGCGGCAAGCAAGATGGGCTTGG 360
DB 301 TGGTGTGGCCACCTGCTCCCTGCTGCAAGGGGAGGCGGCAAGCAAGATGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGTACCAAGCTCCGTGGAAGATCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGTACCAAGCTCCGTGGAAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGCTGGGCTAAATGCCAGAAAGATCTCATGCTATG 480
DB 421 GACAGCTCCACAGAGCTGCTGCTGGGCTAAATGCCAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGAGCAAGAAAGAGACTGCTACATCTGGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAAGAGAGCAAGAAAGAGACTGCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGCATGCTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGCATGCTCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATAAGGCCGTACAAATGCCAGGAAGATGAA 660
DB 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATAAGGCCGTACAAATGCCAGGAAGATGAA 660
QY 661 TGTGCTTAATGTGTGTAAGCATGCGCATGATCAATATTCAGATGATGATGAAT 720
DB 661 TGTGCTTAATGTGTGTAAGCATGCGCATGATCAATATTCAGATGATGATGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCATGCTCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCATGCTCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAGATGGCTCACACACTGTTACTTGGTGTGA 840
DB 781 TATGCTGCTGATATGCAATCAAAAACAGATGGCTCACACACTGTTACTTGGTGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTAATTTTATATCAAGAAAAAGGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTCGTAATTTTATATCAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATGATATGATGAAGAGACTGCTCTATCTTCTATGTTGTGATCAGCAAGATATA 960
DB 901 CTGATGATATGATGAAGAGACTGCTCTATCTTCTATGTTGTGATCAGCAAGATATA 960
QY 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020

Db 961 GTCAACCTTCTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGGACAGCG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCACTTCTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCACTTCTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCTACAAAGTTCAAAGCAGTGAATAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCTACAAAGTTCAAAGCAGTGAATAATAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCGAAATTAATAGATGGTGTATAGAGAGCTGAGAAAGAAATGAG 1260
Db 1201 ATGTCTCAAGAACCGAAATTAATAGATGGTGTATAGAGAGCTGAGAAAGAAATGAG 1260
Oy 1261 AAGCATGAAGATATATATGCTGGATTTACTAGAAAACTGACTAATGCTCTGCTGCG 1320
Db 1261 AAGCATGAAGATATATATGCTGGATTTACTAGAAAACTGACTAATGCTCTGCTGCG 1320
Oy 1321 AATGCTGATATGATGATTAATCTCTCAAGAGAGACAGAACCTGAAATATGCAATTT 1380
Db 1321 AATGCTGATATGATGATTAATCTCTCAAGAGAGACAGAACCTGAAATATGCAATTT 1380
Oy 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
Db 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
Oy 1441 AAACGATGCGCAAAATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCGCAAAATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAG 1551

RESULT 18
AA06600
ID AA06600 standard; cDNA: 2040 BP.
XX
AC AAA06600;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuguu J, Xu J, Mitcham JL,
XX
DR WPI; 2000-171268/15.

XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 50; Page 223-224; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06641 to AA06651 and
CC AA06651 to AA06661 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 2040 BP; 716 A; 393 C; 500 G; 431 T; 0 other:
Query Match 75.0%; Score 1500; DB 21; Length 2040;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 AATGCTGATATGATGATTAATCTCTCAAGAGAGACAGAACCTGAAATATGCAATTT 60
Db 1 AATGCTGATATGATGATTAATCTCTCAAGAGAGACAGAACCTGAAATATGCAATTT 60
Oy 61 AAGAGCAAGATGAGGAGAGTGTGCTGCTTCCCTGCTGAGAGAGAGCGGCAAG 120
Db 61 AAGAGCAAGATGAGGAGAGTGTGCTGCTTCCCTGCTGAGAGAGAGCGGCAAG 120
Oy 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACTCAGAGCAAG 180
Oy 181 AATGGCAAGTGTGGCGGCGACGCTTCCCTGCTGAGAGAGAGTGGCAAGCAAGCG 240
Db 181 AATGGCAAGTGTGGCGGCGACGCTTCCCTGCTGAGAGAGAGTGGCAAGCAAGCG 240
Oy 241 GAGGCTTCTGAGACACAGACGACTGCTATGAAGACTCAGAGCAAGTGGGCAAG 300
Db 241 GAGGCTTCTGAGACACAGACGACTGCTATGAAGACTCAGAGCAAGTGGGCAAG 300
Oy 301 TGGTCTGCTGCTGCTTCCCTGCTGAGAGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCTGCTGCTTCCCTGCTGAGAGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACACAGTCCGTGGAAGAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACACAGTCCGTGGAAGAATCTG 420
Oy 421 GACAAAGCTCAGAGAGCTGCTGAGAGAGTAAAGTCCAGAAAGAGATTCATGCTGATG 480
Db 421 GACAAAGCTCAGAGAGCTGCTGAGAGAGTAAAGTCCAGAAAGAGATTCATGCTGATG 480
Oy 481 CTCAGGAGACCTGAGCTGAACAAGAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACCTGAGCTGAACAAGAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
Oy 541 TCTGCAATGGGAATTCAGAAATGTAATAATCTGCTGAGAGAGAGTCAATCTATAT 600
Db 541 TCTGCAATGGGAATTCAGAAATGTAATAATCTGCTGAGAGAGAGTCAATCTATAT 600
Oy 601 GTCTTGAACAACAAAAGAGAGAGTGTGATGAAGAGCGCTCAATGCCAGAGAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGAGAGTGTGATGAAGAGCGCTCAATGCCAGAGAGATGAA 660
Oy 661 TGTGGTTAATGTTGTGTAACATGGCACTGATTCCAAAATATTCAGATGATGTAAT 720
Db 661 TGTGGTTAATGTTGTGTAACATGGCACTGATTCCAAAATATTCAGATGATGTAAT 720

QY 721 ACCACTCTGCATACGCTATCTATATGAAGATTAATTAATGAGCAAGCAGCTGCTTA 780
 DB 721 ACCACTCTGCATACGCTATCTATATGAAGATTAATTAATGAGCAAGCAGCTGCTTA 780
 QY 781 TATGCTCTGATATCGAATCAAAAACAGCAGTGGCTCACACCACTGTTACTTGTTGA 840
 DB 781 TATGCTCTGATATCGAATCAAAAACAGCAGTGGCTCACACCACTGTTACTTGTTGA 840
 QY 841 CATGAGCAAAAACAGCAGTGGCTGAAATTTTAAATCAAGAAAAAGGAAATTTAAATGA 900
 DB 841 CATGAGCAAAAACAGCAGTGGCTGAAATTTTAAATCAAGAAAAAGGAAATTTAAATGA 900
 QY 901 CTGATATGATATGAAAGAGCTGCTCATATCTGCTATGCTGATGCTGATGAGCAAGTATA 960
 DB 901 CTGATATGATATGAAAGAGCTGCTCATATCTGCTATGCTGATGCTGATGAGCAAGTATA 960
 QY 961 GTACAGCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 DB 961 GTACAGCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
 DB 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAAAGATTAAAG 1140
 DB 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAAAGATTAAAG 1140
 QY 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAAAGGCTGAAAGGCTTGAAGAAATGAAG 1200
 DB 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAAAGGCTGAAAGGCTTGAAGAAATGAAG 1200
 QY 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
 DB 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATTAATGAGATTACTAGAAAAACCTGACTAATGCTGCTACTGTCGC 1320
 DB 1261 AAGCATGAAAGTAAATTAATGAGATTACTAGAAAAACCTGACTAATGCTGCTACTGTCGC 1320
 QY 1321 AATGCTATTAATGATTAATCTCTCAAAAGAGAGCAAGAACCTGTAATTAATGAGCAATTT 1380
 DB 1321 AATGCTATTAATGATTAATCTCTCAAAAGAGAGCAAGAACCTGTAATTAATGAGCAATTT 1380
 QY 1381 CTTGACAAAGAGTGAAGATATCAAGAAATTTGCAATTAATTTGCTGACTACAAAGAA 1440
 DB 1381 CTTGACAAAGAGTGAAGATATCAAGAAATTTGCAATTAATTTGCTGACTACAAAGAA 1440
 QY 1441 AAACAGATGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
 DB 1441 AAACAGATGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
 QY 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCAATGAAATTTGCTGAGCCAGCCAGAG 1551
 DB 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCAATGAAATTTGCTGAGCCAGCCAGAG 1551

PN W0200061753-A2.
 XX 19-OCT-2000.
 PD 07-APR-2000; 2000MO-US09312.
 PF 09-APR-1999; 9905-0289198.
 PR 28-OCT-1999; 9905-0429755.
 PR 23-MAR-2000; 2000US-0534825.
 XX (CORI-) CORIXA CORP.
 XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
 PI WPI: 2000-628403/60.
 DR P-PADB; AAB28628.
 PT An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -
 XX
 PS Claim 4; Page 177; 187pp; English.
 CC The present sequence is given in a specification relating to compositions
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
 CC sequences that are preferentially expressed in breast tumour tissue, and
 CC the polypeptides encoded by such nucleotide sequences, are used in
 CC compositions and vaccines to inhibit the development of cancer.
 CC especially breast cancer. The progression of a cancer may be monitored by
 CC carrying out detection of tumour-specific antigens at subsequent time
 CC points and comparing the results from the different time points.
 CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
 CC with tumour-specific polypeptides, polynucleotides encoding the
 CC polypeptides or antigen presenting cells expressing the polypeptides. The
 CC cells are then administered to the patient to inhibit development of
 CC cancer.
 XX
 SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
 Query Match 56.4%; Score 1128; DB 21; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
 Matches 1128; Conservative 0; Indels 0;
 QY 1 ATGCTGTTAGAGTGAATCCAGCCGCTGCTCTTCTGGAAGAACCATTTGGTCTC 60
 DB 1 ATGCTGTTAGAGTGAATCCAGCCGCTGCTCTTCTGGAAGAACCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGCGGCAAG 120
 DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGCGGCAAG 120
 QY 121 AGCAAGTGGGCACTTGTGAGACCAAGAGACTGCTGTGAAGACATCAGAGAGCA 180
 DB 121 AGCAAGTGGGCACTTGTGAGACCAAGAGACTGCTGTGAAGACATCAGAGAGCA 180
 QY 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
 DB 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
 QY 241 GGGGCTTGTGAGACCAAGAGACTGCTGTATGAACACTCAGGAACAAGATGGGCAAG 300
 DB 241 GGGGCTTGTGAGACCAAGAGACTGCTGTATGAACACTCAGGAACAAGATGGGCAAG 300
 QY 301 TGGGCTGCTGAGTGGTCCCTGCTGAGGAGGAGGAGGCAAGAGCAAGTGGGCGCTTG 360
 DB 301 TGGGCTGCTGAGTGGTCCCTGCTGAGGAGGAGGAGGCAAGAGCAAGTGGGCGCTTG 360
 QY 361 GGAGACTACGATGACATGCTTCAATGAGCCAGATACAGCTCCGTGAGAGAAATCTG 420
 DB 361 GGAGACTACGATGACATGCTTCAATGAGCCAGATACAGCTCCGTGAGAGAAATCTG 420
 QY 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
 DB 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480

RESULT 19
 AAC81011
 ID AAC81011 standard; cDNA; 1155 BP.
 XX
 AC AAC81011;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 XX Human B1lag1 antigen splice isoform B11C-15 cDNA.
 XX
 KM Human; breast tumour-specific antigen; cytosolic; vaccine;
 XX breast cancer; B1BAG1; B1lag1; B15AG1; ss.
 OS Homo sapiens.
 XX

Db 421 GACAACTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
 QY 481 CTCAGGAGACCTGACGTGAACAAGAGGACCAAGCAAGAGAGCTGCTACATCTGGCC 540
 Db 481 CTCAGGAGACCTGACGTGAACAAGAGGACCAAGCAAGAGAGCTGCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCAATTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCAATTAAT 600
 QY 601 GTCTTGAACAACAAAAGAGAGAGAGCTGTGATTAAGGCCCTACAAATGCCAGAGATGAA 660
 Db 601 GTCTTGAACAACAAAAGAGAGAGAGCTGTGATTAAGGCCCTACAAATGCCAGAGATGAA 660
 QY 661 TGTGCTTATATGTTGGTGGAAATGGACATGGACATGCCAAATTTCCAGATGGATGGAAT 720
 Db 661 TGTGCTTATATGTTGGTGGAAATGGACATGGACATGCCAAATTTCCAGATGGATGGAAT 720
 QY 721 ACCACTCTGACATGACCTATCTATTAATGAAGATAAATTAATGGCCAAAGCAGCTGCTTTA 780
 Db 721 ACCACTCTGACATGACCTATCTATTAATGAAGATAAATTAATGGCCAAAGCAGCTGCTTTA 780
 QY 781 TATGGTGTGATATTCGATCAATCAAAAACAGAGATGGCCCTCACACACTGTTACTTGGTGA 840
 Db 781 TATGGTGTGATATTCGATCAATCAAAAACAGAGATGGCCCTCACACACTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAGGAATTAATTAATGCA 900
 Db 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAGGAATTAATTAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
 Db 901 CTGGATAGATATGGAAGAGAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
 QY 961 GTGAGCTTCTACTTGAACAAAATATTGATGTAATCTTCTCAAGATCTATCTGACAGACG 1020
 Db 961 GTGAGCTTCTACTTGAACAAAATATTGATGTAATCTTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGATATGCTGTTTACTGATCATCATGATATTTGCCAGATCTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTTACTGATCATCATGATATTTGCCAGATCTTCTGACTAC 1080
 QY 1081 AAGAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
 Db 1081 AAGAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
 RESULT 20
 ID AAA06598 standard; cdna; 1155 BP.
 AC AAA06598:
 XX
 DE 13-JUN-2000 (first entry)
 XX
 DE Human immunogenic prostate tumour protein cdna sequence SEQ ID NO:373.
 KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW Immunogenic; cytostatic; vaccine; ss.
 OS Homo sapiens.
 OS
 PN MO200004149-A2.
 PD 27-JAN-2000.
 PD
 PF 14-JUL-1999; 99MO-US15838.
 PF
 PR 14-JUL-1998; 98US-0115453.
 PR 14-JUL-1998; 98US-0116134.
 PR 23-SEP-1998; 98US-0159612.
 PR 23-SEP-1998; 98US-0159622.
 PR 15-JAN-1999; 99US-0232149.

PR 15-JAN-1999; 99US-0232880.
 PR 09-APR-1999; 99US-0288946.
 XX
 PA (COR-) CORIXA CORP.
 PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
 DR WPI; 2000-171268/15.
 XX
 PT New polypeptide useful for treating and diagnosing prostate cancer
 PT comprises an immunogenic portion of prostate tumor protein -
 PS
 XX
 XX Claim 50; Page 22; 263pp; English.
 CC The present invention describes isolated polypeptides, comprising an
 CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express
 CC the polypeptides, antibodies against the polypeptides and vaccines
 CC comprising them can be used for inhibiting the development of prostate
 CC cancer in a patient. The polypeptides can be used to generate antibodies
 CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
 CC the polynucleotides encoding the polypeptides can be used as a probe or
 CC to modulate the expression of the polypeptides. AAA06241 to AAA06591 and
 CC AAY82000 to AAY82020 represent sequences used in the exemplification of
 CC the present invention.
 CC
 XX
 SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
 Query Match 56.4%; Score 1128; DB 21; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGTTAGATGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCATTTGCTC 60
 Db 1 ATGTGTTAGATGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCATTTGCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGACAGAGAGCGGCAAG 120
 Db 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGACAGAGAGCGGCAAG 120
 QY 121 AGCAACGTGGGCACTTCTGAGACACAGAGACTCTCTATGAAGACTCAGAGCAAG 180
 Db 121 AGCAACGTGGGCACTTCTGAGACACAGAGACTCTCTATGAAGACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGACAGGGGAGTGCAGAGCACTG 240
 Db 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGACAGGGGAGTGCAGAGCACTG 240
 QY 241 GCGGCTTCTGAGAGCCAGAGAGCTGCTATGAAGACTCAGAGCAAGATGGGCAAG 300
 Db 241 GCGGCTTCTGAGAGCCAGAGAGCTGCTATGAAGACTCAGAGCAAGATGGGCAAG 300
 QY 301 TGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
 Db 301 TGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
 QY 361 GGAGACTACAGTACAGTGCCTTTCATGAGAGCCAGTACACGCTCCGTGGAGAGATCTG 420
 Db 361 GGAGACTACAGTACAGTGCCTTTCATGAGAGCCAGTACACGCTCCGTGGAGAGATCTG 420
 QY 421 GACAAGCTCCACAGAGTGGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTCATG 480
 Db 421 GACAAGCTCCACAGAGTGGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTCATG 480
 QY 481 CTCAGGAGACCTGACGTGAACAAGAGGACCAAGCAAGAGAGCTGCTACATCTGGCC 540
 Db 481 CTCAGGAGACCTGACGTGAACAAGAGGACCAAGCAAGAGAGCTGCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCAATTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCAATTAAT 600

QY 601 GTCTTGACAAACAAAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGGAAGATGAA 660
 DB 601 GTCTTGACAAACAAAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGGAAGATGAA 660
 QY 661 TGTGCGTTAAGTGTGCGTGAACATGCGACCTATCCAAATATCCAGATGATGAAAT 720
 DB 661 TGTGCGTTAAGTGTGCGTGAACATGCGACCTATCCAAATATCCAGATGATGAAAT 720
 QY 721 ACCACTGTGACCTACCTATCTATATGAAGATTAATATGCGCAAGACCTGCTCTTA 780
 DB 721 ACCACTGTGACCTACCTATCTATATGAAGATTAATATGCGCAAGACCTGCTCTTA 780
 QY 781 TATGCTGCTGATATGCAATCAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 781 TATGCTGCTGATATGCAATCAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 841 CATGAGCAAAACAGCAAGCTGTAATTTTATCAAGAAAGCAATTTAAATGCA 900
 DB 841 CATGAGCAAAACAGCAAGCTGTAATTTTATCAAGAAAGCAATTTAAATGCA 900
 QY 901 CTGATGATATGAG 960
 DB 901 CTGATGATATGAG 960
 QY 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGACAGAG 1020
 DB 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGACAGAG 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTATCTTCTGACATC 1080
 DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTATCTTCTGACATC 1080
 QY 1081 AAAGAAAAACAGATGCTAAATATCTCTTCTGAAACAGCAATCCAGAA 1128
 DB 1081 AAAGAAAAACAGATGCTAAATATCTCTTCTGAAACAGCAATCCAGAA 1128

RESULT 21
 ID AA167211 standard; cDNA; 1155 BP.
 XX AA167211;

XX 11-FEB-2002 (first entry)
 DT 11-FEB-2002 (first entry)
 XX B305D isoform C splice variant 1 encoding cDNA.

XX Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
 KW cancer; B305D; ss.

XX Homo sapiens.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT CDS 1..1155
 FT /*tag- a
 FT /product= "B305D isoform C splice variant"

PN MO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR 20-JUL-2000; 2000US-219862P.

PR 27-JUL-2000; 2000US-221300P.

PR 18-DEC-2000; 2000US-256592P.

PA (CORI-) CORIXA CORP.
 XX Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
 XX

DR WPI: 2001-626449/72.
 DR P-PSDB: AAG65976.
 XX
 PT Identifying tissue (tumour)-specific polynucleotides overexpressed in
 PT tissue of interest as compared to control tissue, for detecting cancer
 PT cells in patient, comprises DNA microarray analysis or quantitative
 PT polymerase chain reaction -
 XX
 PS Claim 4; Page 93-94; 127pp; English.
 CC The invention relates to identifying tissue-specific polynucleotides (P)
 CC from tissue of interest (TI), performing DNA microarray analysis to
 CC identify first subset of polynucleotides (SPI) at least 2-fold over
 CC expressed in TI, and performing quantitative polymerase chain reaction
 CC (PCR) analysis on SPI to identify second subset of (P). The method is
 CC useful for determining the presence or absence of a cancer cell in a
 CC patient, monitoring the progression of cancer in a patient using a
 CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
 CC urine or a tumour biopsy sample. The methods are useful for determining
 CC the presence or absence of or monitoring progression of prostate, breast,
 CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
 CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
 CC sequence represents a cDNA encoding a B305D isoform C splice variant.
 XX
 SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCGCGCTGCTCTCTGTGAAGAACCATTTGGTCTC 60
 DB 1 ATGGTGGTTGAGTTGATTCATGCGCGCTGCTCTCTGTGAAGAACCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 DB 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 QY 121 AGCAAGCTGGGCACTTCTGAGACACAGACAGCTCTGATGAGACACTGAGAGCAAG 180
 DB 121 AGCAAGCTGGGCACTTCTGAGACACAGACAGCTCTGATGAGACACTGAGAGCAAG 180
 QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
 DB 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
 QY 241 GGGCTTCTGAGACACAGACAGCTCTGATGAGACACTGAGAGCAAGATGGGCAAG 300
 DB 241 GGGCTTCTGAGACACAGACAGCTCTGATGAGACACTGAGAGCAAGATGGGCAAG 300
 QY 301 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
 DB 301 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
 QY 361 GGAGACTAGATGACAGTGGCTTTCATGAGAGCCAGTACCAAGTCCGTGAGAAATCTG 420
 DB 361 GGAGACTAGATGACAGTGGCTTTCATGAGAGCCAGTACCAAGTCCGTGAGAAATCTG 420
 QY 421 GACAACTCCACAGAGCTGCTGTTGGGTAAATCTCCCAAGAAAGATCTCATGTCATG 480
 DB 421 GACAACTCCACAGAGCTGCTGTTGGGTAAATCTCCCAAGAAAGATCTCATGTCATG 480
 QY 481 CTGAGGGACCTGAGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 481 CTGAGGGACCTGAGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 TCTGCAATGGAATTCAGAGTAAATCTCTGCTGAGACAGAGATGCAACTTAAT 600
 DB 541 TCTGCAATGGAATTCAGAGTAAATCTCTGCTGAGACAGAGATGCAACTTAAT 600
 QY 601 GTCTTGACAAACAAAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGGAAGATGAA 660
 DB 601 GTCTTGACAAACAAAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGGAAGATGAA 660

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DB 601 GTCCTTGACACAAAAGAGACAGCTGTGATAAAGCCGTACAAATGCCAGGAAGATGAA 660
QY 661 TGTGGTTAAATGTTGCTGGAACATGGCACTGATCCAAATATCCAGATGATGAAAT 720
DB 661 TGTGGTTAAATGTTGCTGGAACATGGCACTGATCCAAATATCCAGATGATGAAAT 720
QY 721 ACCACTGTGCACTAGCTGTCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTGTGCACTAGCTGTCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTGCTGATATGCAATCAAAAACAAGCATGGCCCTCACACCCTGTTACTTGCTGA 840
DB 781 TATGTGCTGATATGCAATCAAAAACAAGCATGGCCCTCACACCCTGTTACTTGCTGA 840
QY 841 CATGAGCAAAAACAGCAATCGTGAATTTTAAATCAAAAACCAATTAATTAATGA 900
DB 841 CATGAGCAAAAACAGCAATCGTGAATTTTAAATCAAAAACCAATTAATTAATGA 900
QY 901 CTGATATGATATGAAGAGCTGCTCATATCTTGTGATGTTGTTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAGAGCTGCTCATATCTTGTGATGTTGTTGATCAGCAAGTATA 960
QY 961 GTACGCTTCTACTGTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTACGCTTCTACTGTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAAGAGATATGCTTTCTAGTCAATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAAGAGATATGCTTTCTAGTCAATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAGAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAA 1128
DB 1081 AAGAGAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAA 1128

RESULT 22
AAS63807
ID AAS63807 standard; cDNA; 1155 BP.
XX
AC AAS63807;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #8.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Ronger GR, Reiter MW, Stolk JA, Day CH, Vedicick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
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DR P-PSDB; AAU69777.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 349; 579pp; English.
XX
PS The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other:
XX
Query Match 56.4%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGTGTGATTCATGCCGCTGCTCTTGTGTAAGAACCATTTGGTCTC 60
DB 1 ATGTGTTGAGTGTGATTCATGCCGCTGCTCTTGTGTAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAATATGGCAAGTGTGCTCCGTTTCCCTGCTGAGGGAGAGAGCCGCAAG 120
DB 61 AGGAGCAATATGGCAAGTGTGCTCCGTTTCCCTGCTGAGGGAGAGAGCCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGAGGGAGAGAGCAAGCAAGTGTG 240
DB 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGAGGGAGAGAGCAAGCAAGTGTG 240
QY 241 GGGGCTTGGAGACCAAGCAAGCTGTATGAAGCAAGTGTGAGAGTGGGCAAG 300
DB 241 GGGGCTTGGAGACCAAGCAAGCTGTATGAAGCAAGTGTGAGAGTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGAGAGAGCAAGTGTGAGAGTGTG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGAGAGAGCAAGTGTGAGAGTGTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGTCCGTGAGAGTGTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGTCCGTGAGAGTGTG 420
QY 421 GACAAGCTCCACAGACCTCGTGGGGTAAAGTCCCAAGAAAGATGCAATCGTCAG 480
DB 421 GACAAGCTCCACAGACCTCGTGGGGTAAAGTCCCAAGAAAGATGCAATCGTCAG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGCTCTTACTATCGGCG 540
DB 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGCTCTTACTATCGGCG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGAGAGAGAGATGCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGAGAGAGAGATGCAACTTAAT 600
QY 601 GTCCCTGACAAAAGAGAGAGCTGTGATTAAGGCGGTCAAAAGCCAGGAAGATGAA 660
DB 601 GTCCCTGACAAAAGAGAGAGCTGTGATTAAGGCGGTCAAAAGCCAGGAAGATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
```

Db 661 TGTGCGTTAATGTTGCTGGAAACATGGCATGTCACCAATATATTCAGATGAGTATGGAAT 720
QY ACCACTGTGACACTACGCTATCTATATGAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGTGACACTACGCTATCTATATGAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAAACAGCATGGCCTCACACACACTGTTACTTGATGTA 840
Db 781 TATGTCCTGATATGCAATCAAAAAACAGCATGGCCTCACACACACTGTTACTTGATGTA 840
QY 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATGATGATGAGAGACACTGCTCATACTTCTGTATGTGTGATCGACAGATATA 960
Db 901 CTGATGATGATGAGAGACACTGCTCATACTTCTGTATGTGTGATCGACAGATATA 960
QY 961 GTCAGCCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTCAGCCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATAGTGTCTTCTAGTCATCANCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATAGTGTCTTCTAGTCATCANCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGTGAAAAACAGCAATCCAGAA 1128

RESULT 23
AAH93714
ID AAH93714 standard; cDNA; 1155 BP.
XX

XX AAH93714;

XX 04-OCT-2001 (first entry)

DE Human prostate-specific cDNA sequence B305D splice variant #8.

KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;

KW cytoskeletal; gene therapy; metastasis; ss.

OS Homo sapiens.

PN M0200151633-A2.

PD 19-JUL-2001.

PF 16-JAN-2001; 2001MO-US01574.

PR 14-JAN-2000; 2000US-0483672.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kelos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelky YAW;
PI Wang A, Mesgher MJ;

DR WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -

XX Claim 1; Page 347; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytoskeletal activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.

CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) and (II) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH0115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGTTGATTCATCCGCGTCTCTTCTGTGAAGAACCTTTGGTCTC 60
Db 1 ATGCTGTTGAGTTGATTCATCCGCGTCTCTTCTGTGAAGAACCTTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGAGAGGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGAGAGGCGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACCAAGCACTCTCTATGAAGACCTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACCAAGCACTCTCTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCCACTGCTTCCCTGCTGAGAGGAGATGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGGTGGCGCCCACTGCTTCCCTGCTGAGAGGAGATGGCAAGCAAGT 240
QY 241 GGCGCTTCTGGAGACCAAGCACTCTGCTATGAAGACCTCAGAGCAAGATGGCAAG 300
Db 241 GGCGCTTCTGGAGACCAAGCACTCTGCTATGAAGACCTCAGAGCAAGATGGCAAG 300
QY 301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCTGGCGCTTG 360
Db 301 TGTGTGTCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCTGGCGCTTG 360
QY 361 GGAGACTACGATGACATGCTTATGAGCGCCAGGATACACAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACATGCTTATGAGCGCCAGGATACACAGTCCGTGGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGTGGCTGGTGGGATTAATCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAAGCTCCACAGAGTGGCTGGTGGGATTAATCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACGTGAACCAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGAACCAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGGACAGACATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGGACAGACATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGGACAGCTGTGATAAGGCCGTAACATCCAGGAAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGGACAGCTGTGATAAGGCCGTAACATCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTATATGAAAGATTAATTAATGGCCAAAGCACTGCTT 780
Db 721 ACCACTGTGACACTACGCTATCTATATGAAAGATTAATTAATGGCCAAAGCACTGCTT 780
QY 781 TATGTCCTGATATGCAATCAAAAAACAGCATGGCCTCACACACACTGTTACTTGATGTA 840
Db 781 TATGTCCTGATATGCAATCAAAAAACAGCATGGCCTCACACACACTGTTACTTGATGTA 840
QY 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900

Db 1021 GCGAGAGATGCTGTTCTAGTCATCATCTAATTTGCGAGTCTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
RESULT 25
AAH02779
ID AAH02779 standard; cDNA; 1155 BP.
XX AAH02779;
AC AAH02779;
XX
DT 14-JUN-2001 (first entry)
DE Prostate tumour antigen determined cDNA splice variant of B305D #8.
XX
KW Human: prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW Prostate cancer; immunogenic; cytosolic; vaccine; ss.
XX Homo sapiens.
OS
XX W0200125272-A2.
PN 12-APR-2001.
XX
PD 04-OCT-2000; 2000MO-US27464.
XX
PF 04-OCT-1999; 99US-0157455.
XX
PR (CORI-) CORIXA CORP.
XX
PA Xu J, Skelky YAM, Reed SG, Cheever MA;
PI WPI: 2001-245062/25.
XX P-PSDB; AAB74815.
DR
XX
XX Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 50; Page 231-232; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes or absence of a cancer or monitoring the
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Query Match 56.4%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 AGCAAGTGGGCACTTTCGAGACACAGACGACTCTGTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTCCGCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCCTTCTGGAGACACAGAGACTGTGATGAAGACACTCAGGAACCAAGATGGCAAG 300
Db 241 GGGCCTTCTGGAGACACAGAGACTGTGATGAAGACACTCAGGAACCAAGATGGCAAG 300
QY 301 TGGTGTGCCACCTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGTTGG 360
Db 301 TGGTGTGCCACCTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGACAGTCCAGTCCGTGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGACAGTCCAGTCCGTGAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGTGATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGTGATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGACAGCAAGAAAGAGACTGCTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAAGAGAGACAGCAAGAAAGAGACTGCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGAGCTGTGATAAGGCCGTACAATGCGAGGAAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGAGAGCTGTGATAAGGCCGTACAATGCGAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCGGAACATGCGACATGATCCAAATATTCAGATGGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCGGAACATGCGACATGATCCAAATATTCAGATGGATGAAAT 720
QY 721 ACCACTGTGACACTGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTGA 780
Db 721 ACCACTGTGACACTGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTGA 780
QY 781 TATGTGCTGATATCGAATCAAAAAACAGATGCGCTCACACCACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATCGAATCAAAAAACAGATGCGCTCACACCACTGTTACTTGGTGA 840
QY 841 CATAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Db 841 CATAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCTCATACTTCTGTATGTTGGATGCAAGATATA 960
Db 901 CTGATAGATATGGAAGAGACTGCTCTCATACTTCTGTATGTTGGATGCAAGATATA 960
QY 961 GTCAAGCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACACAG 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACACAG 1020
QY 1021 GCGAGAGATGATGCTGTTTCTAGTCATCATCATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCGAGAGATGATGCTGTTTCTAGTCATCATCATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
RESULT 26
ABL95178
ID ABL95178 standard; cDNA; 1155 BP.
XX ABL95178;
XX

DT 19-JUL-2002 (first entry)
XX Human B305D splice variant cDNA sequence SEQ ID NO 373.
DE Human; cancer: prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
KW Homo sapiens.
XX US2002022248-A1.
PN
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK J S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKET/) SKELKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick JS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
DR WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
XX Claim 1: SEQ ID NO 373; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
SQ
Query Match 56.4%; Score 1128; DB 24; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTTGAGTGTGATTCATGCGCGCTGCTTCTGTGAAGAACGATTTGGTCTC 60
DB 1 ATGGTGGTTGAGTGTGATTCATGCGCGCTGCTTCTGTGAAGAACGATTTGGTCTC 60
QY 61 AGAGCAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGAGCAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGGTGGGCACTTCTGAGACCCAGACGACTCTGCTATGAACACTCAGAGCAAG 180
DB 121 AGCAAGGTGGGCACTTCTGAGACCCAGACGACTCTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCTGCTTCCCTGCTGAGGAGAGTGGCAAGCAACTG 240
DB 181 ATGGGCAAGTGGTGGCCGCTGCTTCCCTGCTGAGGAGAGTGGCAAGCAACTG 240
QY 241 GGGGCTTCTGAGACCCAGACGACTCTGCTATGAACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGACCCAGACGACTCTGCTATGAAGCAACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GGAGCTTACGATGACAGTCTTCATGAGCCAGGTACAGTCCGCTGGAGAAATCTG 420
DB 361 GGAGCTTACGATGACAGTCTTCATGAGCCAGGTACAGTCCGCTGGAGAAATCTG 420
QY 421 GACAACTCCACAGAGCTCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAACTCCACAGAGCTCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACTGAAACAAAGAGCAAGCAAGAGCAAGTCTTACATCTGGGC 540
DB 481 CTCAGGACACTGACTGAAACAAAGAGCAAGCAAGAGCAAGTCTTACATCTGGGC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGAGAGAGATGTCACCTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGAGAGAGATGTCACCTTAAT 600
QY 601 GTCCCTTGACAAACAAAGAGACGCTGTATGAAGGCGGTACATGCCAGAAATGAA 660
DB 601 GTCCCTTGACAAACAAAGAGAGACGCTGTATGAAGGCGGTACATGCCAGAAATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATTTCCCAATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATTTCCCAATGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATGAAGATTAATGAGCCAAACACTGCTTTA 780
DB 721 ACCACTGCACTACGCTATCTATGAAGATTAATGAGCCAAACACTGCTTTA 780
QY 781 TATGCTGTGATATGATCAATCAAAAAAAGCATGAGCTCACACCTGTACTTGGTGA 840
DB 781 TATGCTGTGATATGATCAATCAAAAAAAGCATGAGCTCACACCTGTACTTGGTGA 840
QY 841 CATGACCAAAACAGCAAGTCTGAAATTTTAAATGAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGACCAAAACAGCAAGTCTGAAATTTTAAATGAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGAGAGAGCTGCTCATATCTGCTATGTTGGATCAGCAATATA 960
DB 901 CTGATAGATATGAGAGAGCTGCTCATATCTGCTATGTTGGATCAGCAATATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020

QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTGACTAC 1080
|||||
Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
|||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
RESULT 27
AAS99857 standard; cDNA: 1155 BP.
AC AAS99857;
XX 12-MAR-2002 (first entry)
DE Breast tumour-specific DNA B11a1 splice variant B11C-15.
XX
KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN WO200190152-A2.
XX
PD 29-NOV-2001.
XX
PE 22-MAY-2001; 2001KO-US16776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-069295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAW, Harlocker SL, Day CH;
XX
DR WPI: 2002-089919/12.
DR P-PSDB; AA074377.
XX
XX New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response -
PS Claim 1; Page 223; 245pp; English.
XX
XX The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Query Match 56.4%; Score 1128; DB 24; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 AGAGCAAGATGGCAAGTGTGCTGCGTTGCTTCCCTGCTCAGAGGAGGCGCAAG 120
|||||
QY 121 AGCAACGTGGGACACTTCTGGAGACCAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
|||||
Db 121 AGCAACGTGGGACACTTCTGGAGACCAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCGGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG 240
|||||
Db 181 ATGGGCAAGTGTGCTGCGGCACTGCTCCCTGCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG 240
QY 241 GCGGCTTCTGAGACCAAGACGAGCTGCTATGAAAGCACTCAGAGCAAGAGTGGCAAG 300
|||||
Db 241 GCGGCTTCTGAGACCAAGACGAGCTGCTATGAAAGCACTCAGAGCAAGAGTGGCAAG 300
QY 301 TGGTGTGCGGCACTGCTCCCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTTG 360
|||||
Db 301 TGGTGTGCGGCACTGCTCCCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCAAGTCCGTGGAGAGATCTG 420
|||||
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCAAGTCCGTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGGGTTAAAGTCCCCAGAAAGATCTCATCTCATG 480
|||||
Db 421 GACAAGCTCCACAGAGCTGCTGCTGGGTTAAAGTCCCCAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGACAAAGAAAGAGTGCCTCATCTGCTG 540
|||||
Db 481 CTCAGGGACACTGACGTGAACAAGAGACAAAGAAAGAGTGCCTCATCTGCTG 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTCGCTGAGACAGCATGCAACTTAAT 600
|||||
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTCGCTGAGACAGCATGCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGCAGCTGTGTAAGGCCGTACATGCCAGGAAGATGAA 660
|||||
Db 601 GTCTTGACAAACAAAAGAGAGCAGCTGTGTAAGGCCGTACATGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAAACATGCAATGCAATTAATTCAGATGATGAAAT 720
|||||
Db 661 TGTGCGTTAATGTTGCTGGAAACATGCAATGCAATTAATTCAGATGATGAAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGATGAATTAATGAGCAAGCAAGCACTGCTT 780
|||||
Db 721 ACCACTGCACTACGCTATCTATATGATGAATTAATGAGCAAGCAAGCACTGCTT 780
QY 781 TATGCTGTGATATGATGATCAAAAACAGCATGCGCTCACACCATGTTACTTGGTGA 840
|||||
Db 781 TATGCTGTGATATGATGATCAAAAACAGCATGCGCTCACACCATGTTACTTGGTGA 840
QY 841 CATAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATATGA 900
|||||
Db 841 CATAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATATGA 900
QY 901 CTGATGATATGAGAGAGCTCTCATACTCTGCTATGTTTGGATCAGCAAGTATA 960
|||||
Db 901 CTGATGATATGAGAGAGCTCTCATACTCTGCTATGTTTGGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGTCTATCTGAGCAAGC 1020
|||||
Db 961 GTGAGCCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGTCTATCTGAGCAAGC 1020
QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTGACTAC 1080
|||||
Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
|||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
RESULT 28

AA59869
ID AA59869 standard: DNA; 1590 BP.
XX
AC AA59869;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific gene B305D fusion construct.
XX
KM Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN W020190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAW, Harlocker SL, Day CH;
XX
DR WPI; 2002-089919/12.
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
PS Example 8; Page 235; 245bp; English.
XX
CC The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AA59570-AA59888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
SQ Sequence 1590 BP; 424 A; 403 C; 433 G; 329 T; 1 other:
Query Match 52.2%; Score 1044; DB 24; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 709 AAGACACTCAGGAAACAGATGGGCAAGTGGTCTGCGACATGGCTCCCTGCGAGGGG 768
|||
QY 334 ACCGGCAGAGCAGAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCAATGAGCC 393
|||
DB 769 ACCGGCAGAGCAGAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCAATGAGCC 828
|||
QY 394 AGGTACACATGCTCGTGGAGAGATCTGACAGCTCCACAGAGCTGCTGATGGGATA 453
|||
DB 829 AGCTACACCTGCTGAGAGAGATCTGACAGCTCCACAGAGCTGCTGATGGGATA 888
|||
QY 454 GTCCCGAGAAAGATCTCATGCTCATGCTCAGGAGACTAGCTGAACAAGAGCAAG 513
|||
DB 889 GTCCCGAGAAAGATCTCATGCTCATGCTCAGGAGACTAGCTGAACAAGAGCAAG 948
|||
QY 514 CAAAAGAGAGCTGCTTACATCTGGCTTGGCAATGGGAATTCAGACTAGTAAACTC 573
|||
DB 949 CAAAAGAGAGCTGCTTACATCTGGCTTGGCAATGGGAATTCAGACTAGTAAACTC 1008
|||
QY 574 CTGCTGACAGAGATGTCACCTTAATGCTTGAACAAAAGAGAGAGAGCTGAT 633
|||
DB 1009 CTGCTGACAGAGATGTCACCTTAATGCTTGAACAAAAGAGAGAGAGCTGAT 1068
|||
QY 634 AAGCGCTCAATGCGCAGAGAGATGATGCTTAACTGCTGAGACATGACACTGAT 693
|||
DB 1069 AAGCGCTCAATGCGCAGAGAGATGATGCTTAACTGCTGAGACATGACACTGAT 1128
|||
QY 694 CCAATATTCAGAGATGATGGAATACCACTGCTGACATGCTTCAATATGAGAT 753
|||
DB 1129 CCAATATTCAGAGATGATGGAATACCACTGCTGACATGCTTCAATATGAGAT 1188
|||
QY 754 AATTAATGGCCAAAGCACTGCTTATATGGCTGATGGAATCAAAAACAAGAT 813
|||
DB 1189 AATTAATGGCCAAAGCACTGCTTATATGGCTGATGGAATCAAAAACAAGAT 1248
|||
QY 814 GGCCTTCACACACTGCTTACTGCTGATGAGCAAAAACAGCAAGCTGGAATTTTA 873
|||
DB 1249 GGCCTTCACACACTGCTTACTGCTGATGAGCAAAAACAGCAAGCTGGAATTTTA 1308
|||
QY 874 ATCAGAAAAAAGCCATTTAATGCACTGATAGATGAGAGACTGCTCATACTT 933
|||
DB 1309 ATCAGAAAAAAGCCATTTAATGCACTGATAGATGAGAGACTGCTCATACTT 1368
|||
QY 934 GCTGTATGTTGGATGACCAAGTATGACGCTTCTGAGCAAAATATGATGA 993
|||
DB 1369 GCTGTATGTTGGATGACCAAGTATGACGCTTCTGAGCAAAATATGATGA 1428
|||
QY 994 TCTTCAAGATCTATCTGACAGAGCGCCAGAGATAGCTGTTCTAGTCATCAT 1053
|||
DB 1429 TCTTCAAGATCTATCTGACAGAGCGCCAGAGATAGCTGTTCTAGTCATCAT 1488
|||
QY 1054 GTAATTTGCCAGTACTTCTGACTACAAAGAAAAACAGATGCTAATCTCTGAA 1113
|||
DB 1489 GTAATTTGCCAGTACTTCTGACTACAAAGAAAAACAGATGCTAATCTCTGAA 1548
|||
QY 1114 AACAGCAATCCAGAA 1128
|||
DB 1549 AACAGCAATCCAGAA 1563
|||
RESULT 29
AA59872
ID AA59872 standard: DNA; 1155 BP.
XX
AC AA59872;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific gene B305D homologue #2.
XX
KM Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX

OS Homo sapiens.
XX
PN WO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
XX WPI; 2002-089919/12.
DR P-SDB; AAU74390.
XX
XX New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
XX Claim 1: Page 239; 245pp; English.
XX
XX The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
XX Sequence 1155 BP; 346 A; 253 C; 296 G; 260 T; 0 other;
SQ
Query Match 48.8%; Score 975; DB 24; Length 1155;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTGGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTGGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTCTGCTATGAAGACATCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGTGT 240
DB 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGTGT 240
QY 241 GGGCTTCTGGAGACAGAGAGACTCTGCTATGAAGACACTCAGAGCAAGANTGGCAAG 300
DB 241 GGGCTTCTGGAGACAGAGAGACTCTGCTATGAAGACACTCAGAGCAAGANTGGCAAG 300
QY 301 TGGTGGTCCAGCTCTTCCCTGCTGAGGAGGAGCGGCAAGAGCAAGTGGGCTTGG 360
DB 301 TGGTGGTCCAGCTCTTCCCTGCTGAGGAGGAGCGGCAAGAGCAAGTGGGCTTGG 360
QY 361 GGAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 420
DB 361 GGAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 420

QY 421 GACAAGCTCCAGAGAGCTGCTGCTGGGTAAGTCCCAAGAAAGATCTCANTGCATG 480
DB 421 GACAAGCTCCAGAGAGCTGCTGCTGGGTAAGTCCCAAGAAAGATCTCANTGCATG 480
QY 481 CTCAGGAGACATGACGTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGGAGACATGACGTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTCCCAATGGGAATTCAGAAAGTAACTCCCTGCTGAGACAGCATGCAACTTAAT 600
DB 541 TCTCCCAATGGGAATTCAGAAAGTAACTCCCTGCTGAGACAGCATGCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 GTCTTGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCTTAATGTTGCTGAGAAACATGAGCAAGTCAATATTCAGATGATGAAAT 720
DB 661 TGTGCTTAATGTTGCTGAGAAACATGAGCAAGTCAATATTCAGATGATGAAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAAGATTAATTAAGGCAAGCACTGCTCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATGAAGATTAATTAAGGCAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGCTGCTGATATGCAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAGAGAGAGAGAGAGAG 900
DB 841 CATAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAGAGAGAGAGAGAGAG 900
QY 901 CTGATGATATGAG 960
DB 901 CTGATGATATGAG 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAG 1020
QY 1021 GCCAGAGAGTATGCTGTTTATGATCATCATCATCATCATCATCATCATCATCAT 1080
DB 1021 GCCAGAGAGTATGCTGTTTATGATCATCATCATCATCATCATCATCATCATCAT 1080
QY 1081 AAAGAAAAACAGATGCTAAATATCTTCTGAAAACAGCAATCCAGAA 1128
DB 1081 AAAGAAAAACAGATGCTAAATATCTTCTGAAAACAGCAATCCAGAA 1128
RESULT 30
AAV68995
ID AAV68995 standard; DNA; 1512 BP.
XX
AC AAV68995;
XX
DT 22-JAN-1999 (first entry)
XX
DE DNA molecule encoding a breast tumour specific polypeptide #187.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW vaccine; epitope; endogenous; retroviral element; ss.
OS Homo sapiens.
XX
XX WO9845328-A2.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98MO-US06939.
XX
XX 11-DEC-1997; 97US-0991789.
XX
XX 09-APR-1997; 97US-0838762.
XX

PA (CORI-) CORIXA CORP.
 XX Frudakis TN, Reed SG, Smith JM;
 XX WPI: 1998-557473/47.
 DR
 XX New DNA sequences isolated from endogenous human retroviral element
 PT - and related vectors, transformed cells, proteins and antibodies,
 PT useful for diagnosis, treatment and prevention of breast cancer
 XX
 XX Claim 1: Page 137-138; 173pp; English.
 PS
 XX AA688800 to AA68998 represent nucleotide sequences which encode human
 CC breast tumour specific polypeptides. Detection or measurement of
 CC human breast tumour specific polypeptides and nucleotide sequences,
 CC or the corresponding RNA in a sample, is used for diagnosis and
 CC monitoring of breast cancer. Human breast tumour specific polypeptides
 CC and nucleotide sequences, and the vectors containing the DNAs, are also
 CC useful in vaccines for inhibiting development (for prevention or
 CC therapy) of breast cancer. The polypeptides may also be used to
 CC raise monoclonal antibodies, used as immunosassay reagents.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 19; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 4.4e-177;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTGTGAAGAAGCATTGTTGTCAGAGCAGATGGGCAAGTGTGCGCTTGC 93
 DB 256 TTTTCTGTGAAGAAGCATTGTTGTCAGAGCAGATGGGCAAGTGTGCGCTTGC 315
 OY 94 TTCCCTGCTGCAGGAGAGCGGCAAGCAACGTGGCACTTGTGAGACCAAGCAGC 153
 DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGCAACGTGGCACTTGTGAGACCAAGCAGC 375
 OY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGCAAGTGTGCGCCACTGCTTCCCTGC 213
 DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGCAAGTGTGCGCCACTGCTTCCCTGC 435
 OY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTGTGAGACCAAGCACTGTGTAG 273
 DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTGTGAGACCAAGCACTGTGTAG 495
 OY 274 AAGCACTCAGGACAGAGTGGGCAAGTGTGCTGCACTGCTTCCCTGTCAGAGGG 333
 DB 496 AAGCACTCAGGACAGAGTGGGCAAGTGTGCTGCACTGCTTCCCTGTCAGAGGG 555
 OY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGAGCC 393
 DB 556 AGCAGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGAGCC 615
 OY 394 AGTACACAGTCCGTGGAGAAAGATGTGACAGCTCCACAGAGTCCGTGGGGTAA 453
 DB 616 AGTACACAGTCCGTGGAGAAAGATGTGACAGCTCCACAGAGTCCGTGGGGTAA 675
 OY 454 GTCCCAAGAAAGATCTCATCTGTCATGTCACAGGACACTGACGTGAACAAGAGCAAG 513
 DB 676 GTCCCAAGAAAGATCTCATCTGTCATGTCACAGGACACTGACGTGAACAAGAGCAAG 735
 OY 514 CAAAAGAGAGCTGCTTACATCTGGCCTTGGCAATGGGAATTCAGAGTAAACTTC 573
 DB 736 CAAAAGAGAGCTGCTTACATCTGGCCTTGGCAATGGGAATTCAGAGTAAACTTC 795
 OY 574 CTGTGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAGAGGACACTGTGATA 633
 DB 796 STGCTGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAGAGGACACTGTGATA 855
 OY 634 AAGGCGGTACAAATGCGCAGGAAGATGAATGCGTTAATGTTCTGTGGAACATGGCACTGAT 693
 DB 856 AAGGCGGTACAAATGCGCAGGAAGATGAATGCGTTAATGTTCTGTGGAACATGGCACTGAT 915
 OY 694 CCAAAATATTCAGATGAGTATGGAATATACACTCT 728

DB 916 CCAAAATATTCAGATGAGTATGGAATATACACTCT 950

|||||
 RESULT 31
 ID AAC81006 standard; cDNA; 1512 BP.
 AC AAC81006;
 XX 13-FEB-2001 (first entry)
 DT
 DE Human B1Ag1 antigen protein coding exon cDNA SEQ ID NO: 294.
 XX
 XX Human; breast tumour-specific antigen; cytostatic; vaccine;
 KW breast cancer; B18Ag1; B1Ag1; B15Ag1; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO20061753-A2.
 PN
 PD 19-OCT-2000.
 XX
 XX 07-APR-2000; 2000WO-US09312.
 PF
 XX 09-APR-1999; 99US-0289198.
 PR 28-OCT-1999; 99US-0429755.
 PR 23-MAR-2000; 2000US-0534825.
 XX

PA (CORI-) CORIXA CORP.

PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
 XX WPI: 2000-628403/60.
 DR

PT An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -
 XX
 PS Claim 4: Page 172; 187pp; English.

CC The present sequence is given in a specification relating to compositions
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
 CC sequences that are preferentially expressed in breast tumour tissue, and
 CC the polypeptides encoded by such nucleotide sequences, are used in
 CC compositions and vaccines to inhibit the development of cancer,
 CC especially breast cancer. The progression of a cancer may be monitored by
 CC carrying out detection of tumour-specific antigens at subsequent time
 CC points and comparing the results from the different time points.
 CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
 CC with tumour-specific polypeptides, polynucleotides encoding the
 CC polypeptides or antigen presenting cells expressing the polypeptides. The
 CC cells are then administered to the patient to inhibit development of
 CC cancer.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 21; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 4.4e-177;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTGTGAAGAAGCATTGTTGTCAGAGCAGATGGGCAAGTGTGCGCTTGC 93
 DB 256 TCTTGTGAAGAAGCATTGTTGTCAGAGCAGATGGGCAAGTGTGCGCTTGC 315
 OY 94 TTCCCTGCTGCAGGAGAGCGGCAAGCAACGTGGCACTTGTGAGACCAAGCAGC 153
 DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGCAACGTGGCACTTGTGAGACCAAGCAGC 375
 OY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGCCACTGCTTCCCTGC 213
 DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGCCACTGCTTCCCTGC 435

QY 214 TGCAGGGGAGTGGCAAGACGACGTCGGCGCTTCTGAGAGCACGACGACTGCTATG 273
|||||
Db 436 TGCAGGGGAGTGGCAAGACGACGTCGGCGCTTCTGAGAGCACGACGACTGCTATG 495
QY 274 AAGCACTCAGGAACAAGATGGGCAAGTGGTGTCTGCGCACTGCTTCCCTGCTGACGGGG 333
|||||
Db 496 AAGCACTCAGGAACAAGATGGGCAAGTGGTGTCTGCGCACTGCTTCCCTGCTGACGGGG 555
QY 334 AGCGCAAGAGCAAGTGGGGGCTTGGGGAGACTACGATGACATGGCTTCATGGAGGCC 393
|||||
Db 556 AGCGCAAGAGCAAGTGGGGGCTTGGGGAGACTACGATGACATGGCTTCATGGAGGCC 615
QY 394 AGTACCAAGCTCCGTGGAGAAAGATCTGAGCAAGCTCCACAGAGCTGCTGGTGGGTTAAA 453
|||||
Db 616 AGTACCAAGCTCCGTGGAGAAAGATCTGAGCAAGCTCCACAGAGCTGCTGGTGGGTTAAA 675
QY 454 GTCCCAAGAAAGATCTCATCTGTATGCTCAGGAGACACTGACGTGGAACAGAGAGACAAG 513
|||||
Db 676 GTCCCAAGAAAGATCTCATCTGTATGCTCAGGAGACACTGACGTGGAACAGAGAGACAAG 735
QY 514 CAAAGAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAAAGCTC 573
|||||
Db 736 CAAAGAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAAAGCTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTCTGATA 633
|||||
Db 796 STGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGACAGCTCTGATA 855
QY 634 AAGGCCCTTACCAATGCCAGGAAGATGATGTGCGTTAATGTTGCTGGAACATGGCAGTGTAT 693
|||||
Db 856 AAGGCCCTTACCAATGCCAGGAAGATGATGTGCGTTAATGTTGCTGGAACATGGCAGTGTAT 915
QY 694 CCAATATTCAGATGATGATGATAATACCACTCT 728
|||||
Db 916 CCAATATTCAGATGATGATGATAATACCACTCT 950
RESULT 32
AAA06593
ID AAA06593 standard; cDNA; 1512 BP.
XX
AC AAA06593;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:368.
XX
KW Human: prostate cancer; diagnosis; tumour; gene therapy; detection;
KW Immunogenic; cytosolic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99MO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 50; Page 219; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA08200 to AA08200 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;
XX
Query Match 24.6%; Score 491; DB 21; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4,4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAACCATTTGCTCTCAGAGACAGATGGGCAAGTGGTGGCTGCTTGC 93
|||||
Db 256 TCTTCTGTAAGAACCATTTGCTCTCAGAGACAGATGGGCAAGTGGTGGCTGCTTGC 315
QY 94 TTCCCTGCTGCAAGGAGAGCGGCAAGACAGCTGGGCACTTGTGAGACACAGACAGC 153
|||||
Db 316 TTCCCTGCTGCAAGGAGAGCGGCAAGACAGCTGGGCACTTGTGAGACACAGACAGC 375
QY 154 TCTGCTATGAAAGACACACAGAGAGCAAGTGGGCAAGTGGTGGCGCCGCTTCCCTGC 213
|||||
Db 376 TCTGCTATGAAAGACACACAGAGAGCAAGTGGGCAAGTGGTGGCGCCGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGACGACGTCGGCGCTTCTGAGAGCACGACGACTGCTATG 273
|||||
Db 436 TGCAGGGGAGTGGCAAGACGACGTCGGCGCTTCTGAGAGCACGACGACTGCTATG 495
QY 274 AAGCACTCAGGAACAAGATGGGCAAGTGGTGTCTGCGCACTGCTTCCCTGCTGACGGGG 333
|||||
Db 496 AAGCACTCAGGAACAAGATGGGCAAGTGGTGTCTGCGCACTGCTTCCCTGCTGACGGGG 555
QY 334 AGCGCAAGAGCAAGTGGGGGCTTGGGGAGACTACGATGACATGGCTTCATGGAGGCC 393
|||||
Db 556 AGCGCAAGAGCAAGTGGGGGCTTGGGGAGACTACGATGACATGGCTTCATGGAGGCC 615
QY 394 AGTACCAAGCTCCGTGGAGAAAGATCTGAGCAAGCTCCACAGAGCTGCTGGTGGGTTAAA 453
|||||
Db 616 AGTACCAAGCTCCGTGGAGAAAGATCTGAGCAAGCTCCACAGAGCTGCTGGTGGGTTAAA 675
QY 454 GTCCCAAGAAAGATCTCATCTGTATGCTCAGGAGACACTGACGTGGAACAGAGAGACAAG 513
|||||
Db 676 GTCCCAAGAAAGATCTCATCTGTATGCTCAGGAGACACTGACGTGGAACAGAGAGACAAG 735
QY 514 CAAAGAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAAAGCTC 573
|||||
Db 736 CAAAGAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAAAGCTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTCTGATA 633
|||||
Db 796 STGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTCTGATA 855
QY 634 AAGGCCCTTACCAATGCCAGGAAGATGATGTGCGTTAATGTTGCTGGAACATGGCAGTGTAT 693
|||||
Db 856 AAGGCCCTTACCAATGCCAGGAAGATGATGTGCGTTAATGTTGCTGGAACATGGCAGTGTAT 915
QY 694 CCAATATTCAGATGATGATGATAATACCACTCT 728
|||||
Db 916 CCAATATTCAGATGATGATGATAATACCACTCT 950

XX	AA63802	standard; cDNA: 1512 BP.
XX	AA63802;	
XX	29-JAN-2002	(first entry)
XX	Human prostate cDNA clone B305D	splice variant #3.
XX	Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.	
XX	Homo sapiens.	
XX	MO200173032-A2.	
XX	04-OCT-2001.	
XX	27-MAR-2001; 2001WO-US09919.	
XX	27-MAR-2000; 2000US-0536857.	
XX	09-MAY-2000; 2000US-0568100.	
XX	12-MAY-2000; 2000US-0570737.	
XX	13-JUN-2000; 2000US-0593793.	
XX	27-JUN-2000; 2000US-0605783.	
XX	10-AUG-2000; 2000US-0636215.	
XX	29-AUG-2000; 2000US-0651236.	
XX	06-SEP-2000; 2000US-0657279.	
XX	02-OCT-2000; 2000US-0679426.	
XX	10-OCT-2000; 2000US-0685166.	
XX	(CORI-) CORIXA CORP.	
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kaios MD;	
XX	Fanger GR, Retter MW, Stolk JA, Day CH, Vedicvik TS, Carter D;	
XX	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;	
XX	WPI; 2001-639232/73.	
XX	New human prostate-specific polypeptides and polynucleotides useful for	
XX	the diagnosis and treatment of cancer, especially prostate cancer -	
XX	Claim 1; Page 345-346; 579pp; English.	
XX	The invention relates to isolated prostate-specific	
XX	polynucleotides, polypeptides, fusion proteins of the polypeptides,	
XX	antibodies raised against the polypeptides (or antigenic epitopes	
XX	derived from them) and antigen-presenting cells expressing the	
XX	polypeptides. The antibodies are useful for detecting the presence of	
XX	cancer, especially prostate cancer. The polypeptides, polynucleotides and	
XX	the antigen-presenting cells are useful for stimulating and/or expanding	
XX	T cells specific for a tumour protein, and for inhibiting the development	
XX	of cancer especially prostate cancer. Compositions comprising the	
XX	polynucleotide and/or polypeptide are useful for stimulating an immune	
XX	response, and for treating cancer. The oligonucleotide is useful for	
XX	detecting cancer. The present sequence is a prostate specific	
XX	polynucleotide of the invention.	
XX	Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;	
XX	Query Match 24.6%, Score 491; DB 22; Length 1512;	
XX	Best Local Similarity 99.4%; Pred. No. 4.4e-177;	
XX	Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
XX	34 TCTTCTGGAAGAACCATTTGGTCTCAGAGCAAGATGGCAAGTGGTGGCCGTGC 93	
XX	DB 256 TCTTCTGGAAGAACCCATTGGTCTCAGAGCAAGATGGCAAGTGGTGGCCGTGC 315	
XX	94 TTCCCTGCTCAGAGGAGGAGCGGCAAGACAACGTGGCACTTTCGAGACGACGACGAC 153	
XX	DB 316 TTCCCTGCTCAGAGGAGGAGCGGCAAGACAACGTGGCACTTTCGAGACGACGACGAC 375	
XX	154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTTCCCTGTC 213	

Db	376	TTCTGTTATGAAGACCTTCAGAGCAAAATATGGGCAATGTGTGCCGCACTCTTCCCTG	435
Oy	214	TGCAAGGGGAGTGTGGCAAGACACGTGGGCGCTTCTGGAGACACACAGCACTGTGTATG	273
Db	436	TGCAAGGGGAGTGTGGCAAGACACGTGGGCGCTTCTGGAGACACACAGCAATGTGTATG	435
Oy	274	AAGACACTCAGGAACACAGATGGGCAAGTGTGTCTGCCACTGTTCCTCCCTCTGCAGGGG	333
Db	496	AAGACACTCAGGAACCAAGATGGGCAAGTGTGTCTGCCACTGTTCCTCCCTCTGCAGGGG	555
Oy	334	AGCGCAGAGACCAAGTGGGGCGCTTGGGGAGACTACATGACAGTGGCTTCATGGAGCCC	393
Db	556	AGCAGCAAGACCAAGTGGGGCGCTTGGGGAGACTACATGACAGTGGCTTCATGGAGCCC	615
Oy	394	AGGTACACACGTCCGTGGAGAACTGTGGACAAAGCTCCACAGAGCTGCTGTGGGGTAA	453
Db	616	AGGTACACACGTCCGTGGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGTGGGGTAA	675
Oy	454	GTCCCCAGAAAGATCTTCATCTGTCATGCTCAGGGACACTGACGTGAACAAAGAGACAG	513
Db	676	GTCCCCAGAAAGATCTTCATCTGTCATGCTCAGGGACACTGACGTGAACAAAGAGACAG	735
Oy	514	CAAAAAGAGACTGCTCTTACATCTGGCCTCTGGCCAAATGGGAATTGAGAAATGTAACCTC	573
Db	736	CAAAAAGAGACTGCTCTTACATCTGGCCTCTGGCCAAATGGGAATTCAGAAATGTAACCTC	795
Oy	574	CTGGTGACACAGCATGTGCACACTTAATGTCTTGACAAACAAAAGAGACAGCTGTGATA	633
Db	796	STGCTGGACACAGCATGTGCACACTTAATGTCTTGACAAACAAAAGAGACAGCTGTGATA	855
Oy	634	AAGCCCTGACAAATGCCAGGAAGATATGTGCGTTAAATGTTGCTGGAACATGGCACTGAT	693
Db	856	AAGCCCTGACAAATGCCAGGAAGATATGTAATGTGCGTTAAATGTTGCTGGAACATGGCACTGAT	915
Oy	694	CCAAATATTCCAGATGAGTATGGAATTAACCACTCT	728
Db	916	CCAAATATTCCAGATGAGTATGGAATTAACCACTCT	950
RESULT 34			
AAH93709			
ID	AAH93709	standard; cDNA; 1512 BP.	
AC	AAH93709;		
XX			
XX	04-OCT-2001	(first entry)	
DT			
DE	Human prostate-specific cDNA sequence B305D splice variant #3.		
XX			
KW	Human; prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cytostatic; gene therapy; metastasis; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200151633-A2.		
XX			
PD	19-JUL-2001.		
XX			
PF	16-JAN-2001; 2001WO-US01574.		
XX			
PR	14-JAN-2000; 2000US-0483672.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,		
PI	Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW,		
PI	Wang A, Meagher MJ;		
XX			
DR	WPI: 2001-425873/45.		
XX			
PT	New polynucleotide encoding a prostate-specific protein, for		
PT	diagnosing, monitoring and treating prostate cancer in a patient and		

PT for use in vaccines -
 XX
 .PS
 XX Claim 1; Page 343-344; 543pp; English.

CC The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated
 CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
 CC (I) and the antibodies are also used in the detection of cancer in a
 CC patient. The cancer that is diagnosed or treated is particularly
 CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
 CC (I) can be used for monitoring the progression of cancer in a patient.
 CC (I) and (II) can also be used to improve diagnostic and therapeutic
 CC methods for prostate cancer. They can indicate the level of metastasis
 CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
 CC AAH01318 represent polynucleotide and amino acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 4.4e-177; Indels 0; Gaps 0;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 93
 DB 256 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 315
 QY 94 TTCCCTGCTGCAAGGAGGAGCGGCAAGCAACCTGGGCACTTGTGAGACACGACGAC 153
 DB 316 TTCCCTGCTGCAAGGAGGAGCGGCAAGCAACCTGGGCACTTGTGAGACACGACGAC 375
 QY 154 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCAAGTGGCTGCGCTTGC 213
 DB 376 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCAAGTGGCTGCGCTTGC 435
 QY 214 TGCAGGGGAGTGCCAAAGACACAGTGGGCGCTTCTGAGACACGACGACGATGATG 273
 DB 436 TGCAGGGGAGTGCCAAAGACACAGTGGGCGCTTCTGAGACACGACGATGATG 495
 QY 274 AAGCACTCAGGAACAAGATGGGCAAGTGGCTGCTGCACTGCTTCCCTGCTGAGGGG 333
 DB 496 AAGCACTCAGGAACAAGATGGGCAAGTGGCTGCTGCACTGCTTCCCTGCTGAGGGG 555
 QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACATGCTTCATGGAGCC 393
 DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACATGCTTCATGGAGCC 615
 QY 394 AGTACCACGCTCGTGAGAGATCTGAGACAGCTCCACAGAGCTGCTGGGGTAAA 453
 DB 616 AGTACCACGCTCGTGAGAGATCTGAGACAGCTCCACAGAGCTGCTGGGGTAAA 675
 QY 454 GTCCCCGAAGAAGATCTCATCTGTCATGCTCAGGAGACACTGACGTAACAAGAGCAAG 513
 DB 676 GTCCCCGAAGAAGATCTCATCTGTCATGCTCAGGAGACACTGACGTAACAAGAGCAAG 735
 QY 514 CAAAAGAGAGCTGCTACATCTGAGCTTGCCTGCAATGGAGATTGAGAGTAAATCTC 573
 DB 736 CAAAAGAGAGCTGCTACATCTGAGCTTGCCTGCAATGGAGATTGAGAGTAAATCTC 795
 QY 574 CTGTGACAGAGAGATGCACTTAATGCTTGACAAACAAAAGAGAGACGCTCTGATA 633
 DB 796 STGTGACAGAGAGATGCACTTAATGCTTGACAAACAAAAGAGAGACGCTCTGATA 855
 QY 634 AAGGCGCTACAAATGCCAGGAAGATGAATGTCGTTAATGTTCTGCGAATGACATGAT 693
 DB 856 AAGGCGCTACAAATGCCAGGAAGATGAATGTCGTTAATGTTCTGCGAATGACATGAT 915
 QY 694 CCAAAATATTCAGATGATGATGAATACACACT 728
 DB 916 CCAAAATATTCAGATGATGATGAATACACACT 950

RESULT 35
 AAH85023
 ID AAH85023 standard; cDNA; 1512 BP.

XX AAH85023;

AC 25-SEP-2001 (first entry)

DE Human prostate-specific cDNA sequence B305D splice variant #3.

KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

KW chromosome 22q11.2; prostate-specific protein; chromosome 1;

KW prostate specific antigen; PSA; ss.

OS Homo sapiens.

PN W0200134802-A2.

PD 17-MAY-2001.

PE 09-NOV-2000; 2000MO-US30904.

PR 12-NOV-1999; 99US-0439313.

PR 18-NOV-1999; 99US-0443686.

PA (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Rietter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;

PI WPI; 2001-308785/32.

PT Isolated polypeptide comprising at least an immunogenic portion of a

PT prostate-specific protein, useful in the diagnosis and therapy of a

PT prostate cancer -

XX Claim 31; Page 243-244; 325pp; English.

XX The present invention describes an isolated polypeptide (P1) comprising

XX at least an immunogenic portion of a prostate-specific protein, or its

XX variant. Also described are polynucleotides (N1) encoding (P1). (P1) and

XX (N1) have cytosolic activity and can be used in vaccine production.

XX The polypeptides, nucleic acids and antibodies from the present

XX invention are useful in the diagnosis and therapy of prostate cancer.

XX Prostate specific genes P704P, P712P, P774P, P775P and B305D are located

XX in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome

XX region. Prostate specific antigen (PSA) P501S was located on

XX chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent

XX CC polynucleotide and polypeptide sequences used in the exemplification

XX of the present invention.

XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 4.4e-177; Indels 0; Gaps 0;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 93
 DB 256 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 315
 QY 94 TTCCCTGCTGCAAGGAGGAGCGGCAAGCAACCTGGGCACTTGTGAGACACGACGAC 153
 DB 316 TTCCCTGCTGCAAGGAGGAGCGGCAAGCAACCTGGGCACTTGTGAGACACGACGAC 375
 QY 154 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCGGCACTGCTTCCCTGC 213
 DB 376 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCGGCACTGCTTCCCTGC 435
 QY 214 TGCAGGGGAGTGCCAAAGACACAGTGGGCGCTTCTGAGACACGACGACGATGATG 273
 DB 436 TGCAGGGGAGTGCCAAAGACACAGTGGGCGCTTCTGAGACACGACGACGATGATG 495

QY	274	AAACACTCAGGAAACAAGATGAGGCAATGGTGCACACTGCTTCCCTCCTCGAGGGGG	3333
Db	496	AAGACATCTAGGAACAAGATGGGCAAGTGGTGCTCCACATGCTTCCCTCCTCGAGGGGG	5555
QY	334	AGCGCAGAGAGACAAGTGGGGGCGCTTGGGGAGACTACATGATACAGTGGCTTCATGAGCCC	3939
Db	556	AGCHGCAAGAGACAAGTGGGGGCGTTGGGGAGACTAGATGACAGTGGCTTCATGAGAGCCC	6151
QY	394	AGGTACACACTGCTCGTAGAAGATCTGGACANAGTCCAACAGAGCTGCTTGGTGGGTTAA	4535
Db	616	AGGTACACAGCTCGCTGGAGAAAGATCTGGACANAGTCCAACAGAGCTGCTTGGTGGGTTAA	6797
QY	454	GTCCCCAGAAAGATGATCTCATGCTATGCTCGAGGACACTGACGTGCAACAAGAAAGACAAG	5131
Db	676	GTCCCCAGAAAGATGATCTCATGCTATGCTCGAGGACACTGACGTGCAACAAGAAAGACAAG	7355
QY	514	CAAAAGAGAGACTGCTCTACATCTGGCCCTGCGCAATGGGAATTCAGAAAGTATGTAATTAATC	5737
Db	736	CAAAAGAGAGACTGCTCTACATCTGGCCCTGCGCAATGGGAATTCAGAAAGTATGTAATTAATC	7959
QY	574	CTGCTGACACAGACATATGTCAACTTAAATGTCTTTACACAACAAAAAGAGACAGCTCTATATA	6333
Db	796	STGTGTGACACACATATGTCAACTTAAATGTCTTTACACAACAAAAAGAGACAGCTCTATATA	8555
QY	634	AAGCCCGTACAAATGCCAGGAAGATATGTCGTTAATGTTCGCGAACAATGGCAGCAT	6939
Db	856	AAGCCCGTACAAATGCCAGGAAGATATGTCGTTAATGTTCGCGAACAATGGCAGCAT	9151
QY	694	CCAAATATTCAGATGAGTATGAAATACACACTCT	728
Db	916	CCAAATATTCAGATGAGTATGAAATACACACTCT	950

CC	AAH02774	standard; cDNA: 1512 BP.
CC	AAH02774	
CC	AAH02774	
CC	14-JUN-2001	(first entry)
CC	Prostate tumour antigen determined	cDNA splice variant of B305D #3.
CC	Human; prostate tumour antigen;	prostate tumour; therapy; diagnosis;
CC	prostate cancer; immunogenic;	cytostatic; vaccine; ss.
CC	Homo sapiens.	
CC	MO200125272-A2.	
CC	12-APR-2001.	
CC	04-OCT-2000; 2000WO-US27464.	
CC	04-OCT-1999; 99US-0157455.	
CC	(CORI-) CORIXA CORP.	
CC	Xu J, Skeiky YAW, Reed SG, Cheever MA;	
CC	WPI; 2001-245062/25.	
CC	Prostate specific protein and its encoding polynucleotide,	useful for
CC	the treatment and diagnosis of prostate cancer -	
CC	Claim 50; Page 229; 276pp; English.	
CC	The present invention describes an isolated polypeptide (I) comprising	
CC	at least an immunogenic portion of a prostate tumour antigen protein or	
CC	its variant. (I) have cytostatic activity and can be used in vaccine	
CC	production. (I), prostate tumour antigen polynucleotides, an antigen	
CC	presenting cell (APC e.g. a dendritic cell) that expresses (I), and a	

CC pharmaceutical composition containing (1) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH28172, AAB744798 to AAB744821 and AAB744830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 22; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match	24.68;	Score 491;	DB 22;	Length 1512;
Best Local Similarity	99.48;	Pred. No. 4.4e-177;		
Matches 691;	Conservative	0;	Mismatches 4;	Indels 0;
Gaps				
OY	34	TCTTCTGGAAGAGCCATTGTGCTCAGAGACAAAGTATGGGCAAGTGGTCTGCTCCGTTGC	93	
Db	256	TCTTCTGGAAGAGCCATTGTGCTCAGAGACAAAGTATGGGCAAGTGGTCTGCTCCGTTGC	315	
OY	94	TTCCCTGCTGTCAGAGGAGAGCGGCAAGACCAACGTGGGCACTTCTTGAGACACAGACAG	153	
Db	316	TTCCCTGCTGTCAGAGGAGAGCGGCAAGACCAACGTGGGCACTTCTTGAGACACAGACAG	375	
OY	154	TCTGCTATGAAGAACATCTCAGAGACGAATATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC	213	
Db	376	TCTGCTATGAAGAACATCTCAGAGACGAATATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC	435	
OY	214	TGCAGGGGAGATGGCCAGAGCAAGTGGGCGCTTCTGAGACCAAGCACTGCTGATG	273	
Db	436	TGCAGGGGAGATGGCCAGAGCAAGTGGGCGCTTCTGAGACCAAGCAATCTGCTATG	495	
OY	274	AAGACACTCAGAGAACAAAGATGGGCAAGTGGTGTGTCGCCACTGTTCCCTGCTCAGGGGG	333	
Db	496	AAGACACTCAGAGAACAAAGATGGGCAAGTGGTGTGTCGCCACTGTTCCCTGCTCAGGGGG	555	
OY	334	AGCGGCAAGAGACCAAGTGGGGCGCTTGGGGAGACTACGATACAAATGGCTTCATAGAACCC	393	
Db	556	AGCRRCAAGAGACCAAGTGGGGCGCTTGGGGAGACTACGATACCACTGCTTCATAGAACCC	615	
OY	394	AGGTACCAAGCTCGTGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGTGGGTAA	453	
Db	616	AGGTACCAAGCTCGTGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGTGGGTAA	675	
OY	454	GTCCCCAGAAAGATCTTCATGTCATGCTCAGGGACACTGACGTGAACAAGAGACAAAG	513	
Db	676	GTCCCCAGAAAGATCTTCATGTCATGCTCAGGGACACTGACGTGAACAAGAGACAAAG	735	
OY	514	CAAAAAGAGACTGCTCTTACATCTGTGGCCTCTCCCAATGGGAATTCAGAAAGTATGAAAATC	573	
Db	736	CAAAAAGAGACTGCTCTTACATCTGTGGCCTCTCCCAATGGGAATTCAGAAAGTATGAAAATC	795	
OY	574	GTGCTGGACAGACGATGTCATCTTAATGTCTTGTACAACAAAAAGAGACAGCTGTATA	633	
Db	796	GTGCTGGACAGACGATGTCATCTTAATGTCTTGTACAACAAAAAGAGACAGCTGTATA	855	
OY	634	AAGGCCGTAACAATGCCAGGAAGATGAATGTGCGTTAAATGTTGCTGGAACATGGCAGTAT	693	
Db	856	AAGGCCGTAACAATGCCAGGAAGATGAATGTGCGTTAAATGTTGCTGGAACATGGCAGTAT	915	
OY	694	CCAAATATTCAGATGAGTATGAAATTCACCTCT	728	
Db	916	CCAAATATTCAGATGAGTATGAAATTCACCTCT	950	

RESULT	37
ABL95173	
ID	ABL95173 standard; CDNA; 1512 BP.
XX	
AC	ABL95173;
XX	
DT	19-JUL-2002 (first entry)
DE	Human B305D splice variant cDNA sequence SEQ ID NO 368

XX Human: cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
XX US2002022248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001. 2001US-0759143.
XX 25-FEB-1997. 97US-0806099.
XX 01-AUG-1997. 97US-0904804.
XX 09-FEB-1998. 98US-0020956.
XX 25-FEB-1998. 98US-0030607.
XX 14-JUL-1998. 98US-0115453.
XX 23-SEP-1998. 98US-0159812.
XX 15-JAN-1999. 99US-0232149.
XX 09-APR-1999. 99US-0288946.
XX 13-JUL-1999. 99US-0352616.
XX 12-NOV-1999. 99US-0439313.
XX 18-NOV-1999. 99US-0443686.
XX 14-JAN-2000. 2000US-0483672.
XX 27-MAR-2000. 2000US-0536857.
XX 09-MAY-2000. 2000US-0568100.
XX 12-MAY-2000. 2000US-0570737.
XX 13-JUN-2000. 2000US-0593793.
XX 27-JUN-2000. 2000US-0605783.
XX 10-AUG-2000. 2000US-0636215.
XX 29-AUG-2000. 2000US-0651236.
XX 06-SEP-2000. 2000US-0657279.
XX 10-OCT-2000. 2000US-0679426.
XX 10-OCT-2000. 2000US-0685166.
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI: 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer
XX
XX Claim 1: SEQ ID NO 368; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a cDNA
XX described in the invention.
XX
XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
XX
XX Query Match 24.6%; Score 491; DB 24; Length 1512;

Best Local Similarity 99.4%; Pred. No. 4,4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGTCCTGTC 93
XX |
XX 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGTCCTGTC 315
XX |
XX 94 TTCCCTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 153
XX |
XX 316 TTCCCTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375
XX |
XX 154 TCTGCTATGAAGACACTCAGAGGCAAGATGGGCAAGTGTGTCCTGTCCTGTC 213
XX |
XX 376 TCTGCTATGAAGACACTCAGAGGCAAGATGGGCAAGTGTGTCCTGTCCTGTC 435
XX |
XX 214 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCTTCTGGAACCAAGCACTGCTATG 273
XX |
XX 436 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCTTCTGGAACCAAGCACTGCTATG 495
XX |
XX 274 AAGACACTCAGAGCAAGATGGGCAAGTGGGCTTCTGGAACCAAGCACTGCTATG 333
XX |
XX 496 AAGACACTCAGAGCAAGATGGGCAAGTGGGCTTCTGGAACCAAGCACTGCTATG 555
XX |
XX 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCATGAGCC 393
XX |
XX 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCATGAGCC 615
XX |
XX 394 AGTACCACGTCCTGAGAGAGATCTGAGACAGTCCACAGAGTGGCTGGGCTAA 453
XX |
XX 616 AGTACCACGTCCTGAGAGAGATCTGAGACAGTCCACAGAGTGGCTGGGCTAA 675
XX |
XX 454 GTCCCCAGAAAGATCTCATCTGTCATCTCAGGACACTACGAGCAAGAGAGCAAG 513
XX |
XX 676 GTCCCCAGAAAGATCTCATCTGTCATCTCAGGACACTACGAGCAAGAGAGCAAG 755
XX |
XX 514 CAAAAGAGACTGCTTACATCTGGCCCTTGCCAATGGGAATTCAGAGTAAACTC 573
XX |
XX 736 CAAAAGAGACTGCTTACATCTGGCCCTTGCCAATGGGAATTCAGAGTAAACTC 795
XX |
XX 574 CTGCTGACAGAGAGATGCACTTAATGTCCTTGACAAACAAAAGAGAGAGCTGATA 633
XX |
XX 796 STGCTGACAGAGAGATGCACTTAATGTCCTTGACAAACAAAAGAGAGAGCTGATA 855
XX |
XX 634 AAGGCCGTACAAATGCCAGAAATGAATGTCCTTAATGTTGGAAACATGGCAGTAT 693
XX |
XX 856 AAGGCCGTACAAATGCCAGAAATGAATGTCCTTAATGTTGGAAACATGGCAGTAT 915
XX |
XX 694 CCAAAATATTCAGATGAGTATGGAATATCCACTCT 728
XX |
XX 916 CCAAAATATTCAGATGAGTATGGAATATCCACTCT 950
XX |
XX
XX RESULT 38
XX ABR46896
XX ID ABR46896 standard; DNA; 1512 BP.
XX
XX ABR46896;
XX
XX 05-JUN-2002 (first entry)
XX
XX Human breast tumour-specific DNA B11ag1, protein coding exon #3.
XX
XX Human: breast tumour-specific protein; vaccine; breast cancer;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX US6344550-B1.
XX
XX 05-FEB-2002.
XX
XX 17-APR-1998. 98US-0062451.
XX

.PR 01-JAN-1996; 96US-0585392.
.PR 20-AUG-1996; 96US-0700014.
.PR 10-JAN-1997; 97WO-US00485.
.PR 09-APR-1997; 97US-0838762.
.PR 11-DEC-1997; 97US-0991789.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG;
XX
XX WPI: 2002-215084/27.
XX
XX Polynucleotide encoding breast-specific tumour polypeptides useful as
XX vaccine for preventing and treating breast cancer in a subject -
XX
XX
XX Claim 1: Column 211-213; 128pp; English.
XX
XX The invention relates to an isolated DNA molecule (I) encoding breast-
XX tumour-specific polypeptides. (I) is useful as a vaccine for preventing
XX and treating breast cancer in a subject. The polypeptide encoded by (I)
XX is used for production of compounds such as antibodies useful in
XX diagnosing and monitoring the progression of breast cancer. ABK4614-
XX ABK4689 represent human breast tumour-specific coding sequences and
XX related PCR primers of the invention.
XX
XX
XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 24; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTGTGTAAGAACCATTTGCTCAGAGCAGATGGGCAAGTGGTGGCCGTTGC 93
DB 256 TCTTGTGTAAGAACCATTTGCTCAGAGCAGATGGGCAAGTGGTGGCCGTTGC 315
OY 94 TTCCCTGCTGCGAGGAGAGCGGCAAGACAGTGGGCACTTGTGAGACGACGAC 153
DB 316 TTCCCTGCTGCGAGGAGAGCGGCAAGACAGTGGGCACTTGTGAGACGACGAC 375
OY 154 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGGCACTTGTGAGACGAC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGGCACTTGTGAGACGAC 435
OY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTGTGAGACGACGACACTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTGTGAGACGACGACACTGCTATG 495
OY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGTGGCACTGCTTCCCTGCTGACGAGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGTGGCACTGCTTCCCTGCTGACGAGG 555
OY 334 AGCGGCAAGAGCAGAGTGGGCGCTTGGGAGCACTACGATGACAGTGGCTTCATGAGCCC 393
DB 556 AGCRCACAGAGCAGAGTGGGCGCTTGGGAGCACTACGATGACAGTGGCTTCATGAGCCC 615
OY 394 AGGTACACAGTCCGCGGAGAAATCTGGACAGCTCCACAGAGTGGCGTGGGGGTAA 453
DB 616 AGGTACACAGTCCGCGGAGAAATCTGGACAGCTCCACAGAGTGGCGTGGGGGTAA 675
OY 454 GTCCCCAGAAAGATCTCATCTGTCATGTCAGAGGACACTGACGTAAACAAGAGCAAG 513
DB 676 GTCCCCAGAAAGATCTCATCTGTCATGTCAGAGGACACTGACGTAAACAAGAGCAAG 735
OY 514 CAAAAGAGAGCTGCTTCATCATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAACTC 573
DB 736 CAAAAGAGAGCTGCTTCATCATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAACTC 795
OY 574 CTGCTGAGAGAGAGTGCATCTTATGCTTGAACAACAAAGAGGAGCAGCTCGATA 633
DB 796 STGCTGAGAGAGAGTGCATCTTATGCTTGAACAACAAAGAGGAGCAGCTCGATA 855
OY 634 AAGGCCGTACATGCAGAGAGATGAATGTGCTTAATGTTCTGGAACATGGCAGTAT 693
DB 855 AAGGCCGTACATGCAGAGAGATGAATGTGCTTAATGTTCTGGAACATGGCAGTAT 693

DB 856 AAGCCGTACATGCAGAGAGATGAATGTGCTTAATGTTCTGGAACATGGCAGTAT 915
OY 694 CCAATATATCCAGATGAGATGGAATATACACTCT 728
DB 916 CCAATATATCCAGATGAGATGGAATATACACTCT 950

RESULT 39

AAS99852
ID AAS99852 standard; cDNA; 1512 BP.

AC AAS99852;

XX 12-MAR-2002 (first entry)

DE Breast tumour-specific DNA #225.

XX Human: breast cancer; PCR primer; ss; cytosolic; immunostimulant;

XX tumour; vaccine; immunogenic.

OS Homo sapiens.

PN WO200190152-A2.

XX 29-NOV-2001.

PF 22-MAY-2001; 2001WO-US16776.

XX 24-MAY-2000; 2000US-0577505.

PR 08-JUN-2000; 2000US-0590583.

PR 26-OCT-2000; 2000US-0699295.

PR 16-MAR-2001; 2001US-0810936.

XX (CORI-) CORIXA CORP.

XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;

XX Wang A, Skelky YAW, Harlocker SL, Day CH;

XX WPI: 2002-089919/12.

XX Claim 1: Page 219; 245pp; English.

XX The invention relates to novel breast tumour polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response,
XX particularly humoral and/or cellular immune response. The polynucleotides
XX may be used as probes or primers for nucleic acid hybridisation. In the
XX design and preparation of ribozyme molecules for inhibiting expression of
XX tumour polypeptides and proteins, and in recombinant DNA molecules to
XX direct expression of a polypeptide in host cells. AAS99570-AAS99888
XX represent novel human breast cancer protein coding sequences and
XX PCR primers of the invention.

XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 24; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTGTGTAAGAACCATTTGCTCAGAGCAGATGGGCAAGTGGTGGCCGTTGC 93
DB 256 TCTTGTGTAAGAACCATTTGCTCAGAGCAGATGGGCAAGTGGTGGCCGTTGC 315
OY 94 TTCCCTGCTGCGAGGAGAGCGGCAAGACAGTGGGCACTTGTGAGACGACGAC 153
DB 316 TTCCCTGCTGCGAGGAGAGCGGCAAGACAGTGGGCACTTGTGAGACGACGAC 375
OY 154 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTGC 213

```

Db 376 TCTGCTATGAAAGACACACAGAGAGAGATGGCAAGTGGCCGACCTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAGAGCAAGCTGGGCGCTTCTGGAGCCAGCAGCTGCTATG 273
Db 436 TGCAGGGGAGTGGCAGAGCAAGCTGGGCGCTTCTGGAGCCAGCAGCTGCTATG 495
QY 274 AAGACTCTCAGGAACAAGATGGGCAAGTGGTCTGCTGCACTGCTTCCCTGCGAGGGG 333
Db 496 AAGACTCTCAGGAACAAGATGGGCAAGTGGTCTGCTGCACTGCTTCCCTGCGAGGGG 555
QY 334 AGGGGCAAGCAAGTGGGCGCTTGGGAGACTACAGTACAGTGGCTTCTATGGAGCC 393
Db 556 AGCGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGTACAGTGGCTTCTATGGAGCC 615
QY 394 AGGTACCACTCGTGGAGAAATCTGAGCAAGCTCCAGAGCTGGCTGGGGTAAA 453
Db 616 AGGTACCACTCGTGGAGAAATCTGAGCAAGCTCCAGAGCTGGCTGGGGTAAA 675
QY 454 GTCCCAAGAAAGATCTCATCTCATCTCATGAGGACACTGACGTGAACAAGAGCAAG 513
Db 676 GTCCCAAGAAAGATCTCATCTCATCTCATGAGGACACTGACGTGAACAAGAGCAAG 735
QY 514 CAAAGAGGAGTCTCATCTCATCTCATGAGGACACTGACGTGAACAAGAGCAAG 573
Db 736 CAAAGAGGAGTCTCATCTCATCTCATGAGGACACTGACGTGAACAAGAGCAAG 795
QY 574 CTGTGGACAGAGCTGACCTTACCTTGGCCATGGGAATTCAGAGTAAGTAAGTCT 633
Db 796 STGTGGACAGAGCTGACCTTACCTTGGCCATGGGAATTCAGAGTAAGTAAGTCT 855
QY 634 AAGCCCTACAAATGCCAGAAATGAATGTCCTTGGACAAAAGAGAGAGCTGTATA 693
Db 856 AAGCCCTACAAATGCCAGAAATGAATGTCCTTGGACAAAAGAGAGAGCTGTATA 915
QY 694 CCAATATTCAGATGATGGAATACCACTCT 728
Db 916 CCAATATTCAGATGATGGAATACCACTCT 950

RESULT 40
AAV68996
ID AAV68996 standard; DNA: 1853 BP.
XX
AC AAV68996;
XX
DT 22-JAN-1999 (first entry)
XX
DE DNA molecule encoding a breast tumour specific polypeptide #188.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
XX vaccine; epitope; endogenous; retroviral element; ss.
XX
OS Homo sapiens.
XX
PN WO9845328-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98MO-US06939.
XX
PR 11-DEC-1997; 97US-0991789.
XX
PR 09-APR-1997; 97US-0838762.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM;
XX
DR WPI; 1998-557473/47.
XX
PT New DNA sequences isolated from endogenous human retroviral element
PT - and related vectors, transformed cells, proteins and antibodies,
PT useful for diagnosis, treatment and prevention of breast cancer

```

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XX
PS Claim 1; Page 138-139; 173pp; English.
XX
AAV68800 to AAV68998 represent nucleotide sequences which encode human
CC breast tumour specific polypeptides. Detection or measurement of
CC human breast tumour specific polypeptides and nucleotide sequences,
CC or the corresponding RNA in a sample, is used for diagnosis and
CC monitoring of breast cancer. Human breast tumour specific polypeptides
CC and nucleotide sequences, and the vectors containing the DNAs, are also
CC useful in vaccines for inhibiting development (for prevention or
CC therapy) of breast cancer. The polypeptides may also be used to
CC raise monoclonal antibodies, used as immunoassay reagents.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
XX
Query Match 12.6%; Score 252; DB 19; Length 1853;
Best Local Similarity 99.7%; Pred. No. 2,4e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTGAAGAACCCATTGCTCTGAGAGCAAGATGGGCAAGTGGTCTGCTGC 93
Db 256 TCTTCTGTGAAGAACCCATTGCTCTGAGAGCAAGATGGGCAAGTGGTCTGCTGC 315
QY 94 TTCCCTGCTGCAGGAGAGACCGCAAGCAACGTGGGCACTTCTGAGACACAGAGAC 153
Db 316 TTCCCTGCTGCAGGAGAGACCGCAAGCAACGTGGGCACTTCTGAGACACAGAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCACTGCTTCCCTGC 213
Db 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCACTGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAACGTGGGCGCTTCTGGAGCAACGAGACTGCTATG 273
Db 436 TGCAGGGGAGTGGCAAGCAACGTGGGCGCTTCTGGAGCAACGAGACTGCTATG 495
QY 274 AAGACTCTCAGGAACAAGATGGGCAAGTGGTGGTCTGCTGCACTGCTTCCCTGCGAGGGG 333
Db 496 AAGACTCTCAGGAACAAGATGGGCAAGTGGTGGTCTGCTGCACTGCTTCCCTGCGAGGGG 555
QY 334 AGC 336
Db 556 AGC 558

RESULT 41
AAC81007
ID AAC81007 standard; cDNA; 1853 BP.
XX
AC AAC81007;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B14g1 antigen protein coding exon cDNA SEQ ID NO: 295.
XX
KW Human; breast tumour-specific antigen; cytosolic; vaccine;
XX breast cancer; B14g1; B14g1; ss.
XX
OS Homo sapiens.
XX
PN WO200061753-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000MO-US09312.
XX
PR 09-APR-1999; 99US-0289198.
XX
PR 28-OCT-1999; 99US-0429755.
XX
PR 23-MAR-2000; 2000US-0534825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX

```


DE	Human prostate cDNA clone B305D splice variant #4.
XX	Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
KM	
OS	Homo sapiens.
XX	
PN	WO200173032-A2.
XX	
PD	04-OCT-2001.
XX	
PF	27-MAR-2001; 2001WO-US09919.
XX	
PR	27-MAR-2000; 2000US-0536857.
PR	09-MAY-2000; 2000US-0568100.
PR	12-MAY-2000; 2000US-0570737.
PR	13-JUN-2000; 2000US-0593793.
PR	27-JUN-2000; 2000US-0605783.
PR	10-AUG-2000; 2000US-0636215.
PR	29-AUG-2000; 2000US-0651236.
PR	06-SEP-2000; 2000US-0657279.
PR	02-OCT-2000; 2000US-0679426.
PR	10-OCT-2000; 2000US-0685166.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Ratter NW, Stolk JA, Day CH, Vedick TS, Carter D;
PI	Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX	
DR	WPI: 2001-639232/73.
XX	
PT	New human prostate-specific polypeptides and polynucleotides useful for
PT	the diagnosis and treatment of cancer, especially prostate cancer -
XX	
PS	Claim 1; Page 346-347; 579pp; English.
XX	
CC	The invention relates to isolated prostate-specific
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC	antibodies raised against the polypeptides (or antigenic epitopes
CC	derived from them) and antigen-presenting cells expressing the
CC	polypeptides. The antibodies are useful for detecting the presence of
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC	the antigen-presenting cells are useful for stimulating and/or expanding
CC	T cells specific for a tumour protein, and for inhibiting the development
CC	of cancer especially prostate cancer. Compositions comprising the
CC	polynucleotide and/or polypeptide are useful for stimulating an immune
CC	response, and for treating cancer. The oligonucleotide is useful for
CC	detecting cancer. The present sequence is a prostate specific
CC	polynucleotide of the invention.
XX	
SO	Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
XX	
Query Match	12.6%; Score 252; DB 22; Length 1853;
Best Local Similarity	99.7%; Pred. No. 2,4e-86;
Matches 302; Conservative	0; Mismatches 1; Indels 0; Gaps 0
34	TTTTCTGTGAAGAAGCCATTGTGCTCAGAGCAAGATGGGCAAGTGGTCCGCTGC 93
DB	TTTTCTGTGTGAAGAAGCCATTGTGCTCAGAGCAAGATGGGCAAGTGGTCCGCTGC 315
94	TTTCCCTGCTGCAGGAGAGAGCGGCAAGACCAACGTGGGCACTTCTTGAGACCAAGACGAGAC 153
DB	TTTCCCTGCTGCAGGAGAGAGCGGCAAGACCAACGTGGGCACTTCTTGAGACCAAGACGAGAC 375
154	TTCTGCTATGAACACTCAGAGCAAGATGGGCAAGTGGTGCACATGCTTCCCTGC 213
DB	TTCTGCTATGAACACTCAGAGCAAGATGGGCAAGTGGTGCACATGCTTCCCTGC 435
214	TTCAGGGGAGTGGCAAGAGCAACGCGGGCGCTTCTTGAGACCAAGACGACACTGTATG 273
DB	TTCAGGGGAGTGGCAAGAGCAACGCGGGCGCTTCTTGAGACCAAGACGACACTGTATG 495
274	AAGACACTGAGAACAAAGATGGGCAAGTGGTGTGCTGCACATGCTTCCCTGCTCAGAGGGG 333

DB	496	AAAGACCTGAGGAACAAGATGGGCAAGTGTGCTGCACTGCTCCCTGCTGACAGGGG	555
QY	334	ACC 336	
DB	556	AGC 558	
RESULT 44			
AAH93710	ID		
AAH93710	standard; cDNA; 1853 BP.		
AAH93710;	04-OCT-2001 (first entry)		
Human prostate-specific cDNA sequence B305D splice variant #4.			
Human; prostate cancer; prostate-specific; diagnosis; vaccine;			
cytostatic; gene therapy; metastasis; ss.			
Homo sapiens.			
MO20015163-A2.			
19-JUL-2001.			
16-JAN-2001; 2001WO-US01574.			
14-JAN-2000; 2000US-0483672.			
(CORI-) CORIXA CORP.			
Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;			
Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;			
Wang A, Neagher MJ;			
WPI; 2001-425873/45.			
New polynucleotide encoding a prostate-specific protein, for			
diagnosing, monitoring and treating prostate cancer in a patient and			
for use in vaccines -			
Claim 1; Page 344-345; 543pp; English.			
The present invention describes polynucleotide sequences (I) which encode			
prostate-specific proteins (II). (I) and (II) have cytosolic activity,			
and can be used in vaccine production and gene therapy. (I), (II),			
antibodies to (II), fusion proteins comprising (II), and isolated			
T cells prepared using (I) or (II) are used treat cancer in a patient.			
(I) and the antibodies are also used in the detection of cancer in a			
patient. The cancer that is diagnosed or treated is particularly			
prostate cancer. (I) and (II) can be used in vaccines. The antibodies or			
(I) can be used for monitoring the progression of cancer in a patient.			
(I) and (II) can also be used to improve diagnostic and therapeutic			
methods for prostate cancer. They can indicate the level of metastasis			
as well as the prostate volume. AAH93357 to AAH93944 and AAH0115 to			
AAH01318 represent polynucleotide and amino acid sequences used in the			
exemplification of the present invention.			
Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;			
Query Match	12.6%	Score 252;	DB 22;
Best Local Similarity	99.7%	Pred. No. 2,4e-86;	Length 1853;
Matches 302; Conservative	0;	Mismatches 1;	Indels 0;
		Gaps	0;
34 TCTTGTGTGAAGAACCATTTGGTCTCAGAGACAAGATGGGCAAGTGTGCTGCCGTTGC	93		
256 TCTTGTGTGAAGAACCATTTGGTCTCAGAGACAAGATGGGCAAGTGTGCTGCCGTTGC	315		
94 TTCCCTGCTGAGGAGAGCGGCAAGACAAGTGGGCACTTCTTGAGACCAAGACGAC	153		
316 TTCCCTGCTGAGGAGAGCGGCAAGACAAGTGGGCACTTCTTGAGACCAAGACGAC	375		

QY 154 TCTGCTATGACAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTTC 213
DB 376 TCTGCTATGACAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTTC 435
QY 214 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGACACTGCTGTATG 273
DB 436 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGACAGATGCTGTATG 495
QY 274 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGACACTGCTGTATG 333
DB 496 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGACAGATGCTGTATG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 45
AAH85024
ID AAH85024 standard: cDNA; 1853 BP.
AC AAH85024;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #4.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
XX
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Reltter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
XX prostate cancer -
XX
PS Claim 31; Page 244; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.6%; Score 252; DB 22; Length 1853;
Best Local Similarity 99.7%; Pred. No. 2.4e-86;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAAGCATTTTGGTCTCAGAGACAGATGGGCAAGTGGTGGCGCTTC 93
DB 256 TCTTCTGTAAGAAGCATTTTGGTCTCAGAGACAGATGGGCAAGTGGTGGCGCTTC 315
QY 94 TTCCCTGCTGAGGAGAGCGGCAAGAGCAAGTGGGCAAGTGGTGGCGCTTC 153
DB 316 TTCCCTGCTGAGGAGAGCGGCAAGAGCAAGTGGGCAAGTGGTGGCGCTTC 375
QY 154 TCTGCTATGACAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTTC 213
DB 376 TCTGCTATGACAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTTC 435
QY 214 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGACACTGCTGTATG 273
DB 436 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGACAGATGCTGTATG 495
QY 274 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGACACTGCTGTATG 333
DB 496 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGACAGATGCTGTATG 555
QY 334 AGC 336
DB 556 AGC 558

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Job time : 393.277 secs

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(Without alignments)
12879.875 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgttgaggttgatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1430706

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	9.0	521	17	AQ204617 HS_3229_B
2	141	6.9	865	12	BF676987 602084215
3	140	6.9	451	9	AI804733 tu42b03.x
4	137	6.7	289	9	AA533501 nJ96a04.s
5	129	6.3	531	17	AQ615477 HS_5144_B
6	117	5.7	621	14	BM763942 K-EST0045

7	117	5.7	633	14	BM763453 K-EST0044
8	117	5.7	817	17	BQ441373 AGENCOURT
9	89	4.4	400	14	AO124119 HS_3122_A
10	87	4.3	399	17	AQ030111 RPT111-39
11	87	4.3	544	9	AL703938 DKF2686E
12	79	3.9	279	13	BI461255 603206584
13	73	3.6	385	17	AQ063365 CITR1-E1-
14	59	2.9	707	17	AG045796 Pan trogl
15	57	2.8	607	17	B48260 RPT111-6K4
16	52	2.5	380	12	BF328652 RCG-BN027
17	50	2.5	592	17	AQ372700 RPT111-14
18	49	2.4	495	17	AQ469831 CITR1-E1-
19	49	2.4	557	17	AQ469663 CITR1-E1-
20	49	2.4	667	17	AG156382 Pan trogl
21	49	2.4	697	17	AQ030113 RPT111-39
22	47	2.3	187	10	BE069869 CMT-BT039
23	47	2.3	476	17	AQ392059 CITR1-E1-
24	46	2.3	400	17	AQ057106 CITR1-E1-
25	45	2.2	894	12	BF675049 602136643
26	44	2.2	460	17	AQ360298 HS_5035_A
27	41	2.0	710	17	AG165908 Pan trogl
28	40	2.0	503	17	B55862 CITR1-HSP-200
29	39	1.9	1011	17	AQ0900910 HS_-2055_B
30	38	1.9	458	17	AQ247090 HS_-2055_B
31	37	1.8	424	17	AQ763344 HS_3162_A
32	37	1.8	694	12	BG720647 602692528
33	36	1.8	652	17	AG054405 Pan trogl
34	35	1.7	156	9	AI349163 ta73C06.x
35	35	1.7	157	9	AI251211 qv38H06.x
36	35	1.7	160	9	AI305627 qw72F03.x
37	35	1.7	164	9	AI343314 tb93912.x
38	35	1.7	186	10	AW302924 xrb6907.x
39	35	1.7	199	10	AW302925 xrb6908.x
40	35	1.7	224	9	AI344928 tb01a04.x
41	35	1.7	232	9	AI336592 ta94d12.x
42	35	1.7	239	9	AI344933 tb01a11.x
43	35	1.7	239	9	AI344936 tb01b03.x
44	35	1.7	250	9	AI335449 tb79F03.x
45	35	1.7	360	9	AI494279 qy98c11.x

ALIGNMENTS

RESULT 1
LOCUS AQ204617 521 bp DNA linear GSS 17-SEP-1998
DEFINITION HS_3229_B1_G12_T7 CITR Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3229 COL=23 Row=N, DNA sequence.
ACCESSION AQ204617
VERSION AQ204617.1 GI:3615187
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 row: N column: 23

Class: BAC ends
High quality sequence stop: 521.
Location/Qualifiers
1. 521

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="CIR Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBLOBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 161 a 94 c 99 g 161 t 6 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGCTAGAAATTTTATGCTATCGAAGAAATGAAGAGCAGGAGTACTGATGCGAT 1654
|||||
DB 231 AGCTAGAAATTTTATGCTATCGAAGAAATGAAGAGCAGGAGTACTGATGCGAT 290
|||||
QY 1655 TCCCAAAAAACCTGACTAATGTCGACATGCTGATGATGATTAATTCCTC 1714
|||||
DB 291 TCCCAAAAAACCTGACTAATGTCGACATGCTGATGATGATTAATTCCTC 350
|||||
QY 1715 CAAGAGAAGACAGACACCTGAAAGCCAGCAATTCCTGACACTGAGAAATGAAGATATC 1774
|||||
DB 351 CAAGAGAAGACAGACACCTGAAAGCCAGCAATTCCTGACACTGAGAAATGAAGATATC 410
|||||
QY 1775 ACAG 1778
|||||
DB 411 ACAG 414

RESULT 2
B676987 865 bp mRNA linear EST 21-DEC-2000
LOCUS 602084215F1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4248746 5',
DEFINITION mRNA sequence.
ACCESSION B676987
VERSION B676987.1 GI:11950882
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers

FEATURES
source
1. 865
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="NIH_MGC_83"
/clone_11b="NIH_MGC_83"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccgcgcgc); Site_2: SfiI (ggcattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGGCCGCGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 297 a 140 c 211 g 217 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 ACTGCTCTCATCTACTGCTGATGTTGGATCAGCAAGTATGACCTTCTACTTGTAG 978
|||||
DB 353 ACTGCTCTCATCTACTGCTGATGTTGGATCAGCAAGTATGACCTTCTACTTGTAG 412
|||||
QY 979 CAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGTT 1038
|||||
DB 413 CAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGTT 472
|||||
QY 1039 TCTAGTCATCATCATGTAATT 1059
|||||
DB 473 TCTAGTCATCATCATGTAATT 493
|||||

RESULT 3
A1804733 451 bp mRNA linear EST 07-MAR-2000
LOCUS tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens CDNA clone IMAGE:2253677 3',
DEFINITION mRNA sequence.
ACCESSION A1804733
VERSION A1804733.1 GI:5370205
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 451)
AUTHORS NCI-CGAP http://www.nci.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 543 Std Error: 0.00
Seq primer: -400P from gibco.
Location/Qualifiers

FEATURES
source
1. 451
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="NCI_CGAP_Pr28"
/clone_11b="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 110192-1101959, and 1217928-1220615)."
Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 128 a 79 c 91 g 153 t
ORIGIN
Query Match 6.9%: Score 140; DB 9; Length 451;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 916 AGAGCTCTCTCATCTGCTGTATGTTGTGATCAGCAGCAATATAGTCAGCTTCTACTT 975
DB 47 AGAGCTCTCTCATCTGCTGTATGTTGTGATCAGCAGCAATATAGTCAGCTTCTACTT 106
QY 976 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGCGCCAGAGATATGCT 1035
DB 107 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGCGCCAGAGATATGCT 166
QY 1036 GTTCTAGTCTCATCATGCT 1055
DB 167 GTTCTAGTCTCATCATGCT 186
RESULT 4
LOCUS AA533501
DEFINITION AA533501 289 bp mRNA linear EST 21-AUG-1997
mRNA sequence.
ACCESSION AA533501
VERSION AA533501.1 GI:2277597
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 289)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chunqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLM at:
www-bio.linn.gov/bdrip/image/image.html
Insert Length: 217 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham.
FEATURES
source
Location/Qualifiers
1..289
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1000302"
/clone_1lb="NCI-CGAP_Prl1"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells. cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Kitzman, NIH."
BASE COUNT 121 a 36 c 66 g 66 t
ORIGIN
Query Match 6.7%: Score 137; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 4.9e-24;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1788 AAATGATACCTGAGAGCAATTTTGTGAAGACAGAACTGGAATATTACAGATGAGAT 1847
DB 9 AAATGATACCTGAGAGCAATTTTGTGAAGACAGAACTGGAATATTACAGATGAGAT 68

QY 1848 TCTGATTCATGAAGAAAGAGATGAGTGTGAAAAAATGAATTCGACCTTCTCT 1907
DB 69 TCTGATTCATGAAGAAAGAGATGAGTGTGAAAAAATGAATTCGACCTTCTCT 128
QY 1908 TAGTGTGAAGAAAGAA 1924
DB 129 TAGTGTGAAGAAAGAA 145
RESULT 5
LOCUS A0615477
DEFINITION HS.5144.B1.G01.T7A.RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=720 Col=1 Row=N, DNA sequence.
ACCESSION A0615477
VERSION A0615477.1 GI:5076753
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 531)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Library are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web server:
<http://www.htsc.washington.edu>
Plate: 720 row: N column: 1
Seq primer: T7
Class: BAC ends
High quality sequence stop: 531.
FEATURES
source
Location/Qualifiers
1..531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=720 Col=1 Row=N"
/clone_1lb="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site: 1: EcoRI; Site: 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 167 a 92 c 92 g 169 t
ORIGIN
Query Match 6.3%: Score 129; DB 17; Length 531;
Best Local Similarity 100.0%; Pred. No. 2.3e-22;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 682 CATGCACATGATCCAAATATTCAGATGATGGAATATACACTCTGACATACGCTATTC 741
DB 117 CATGCACATGATCCAAATATTCAGATGATGGAATATACACTCTGACATACGCTATTC 176
QY 742 TATAATGAAGATTAATTAATGAGCCAAAGACACTGCTTATATATGATGCTGATATGCAATCA 801
DB 177 TATAATGAAGATTAATTAATGAGCCAAAGACACTGCTTATATATGATGCTGATATGCAATCA 236

OY 802 AAAAACAAG 810
 |||||
 Db 237 AAAACAAG 245

RESULT 6
 BM763942 621 bp mRNA linear EST 04-MAR-2002
 LOCUS K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-A11 5',
 DEFINITION mRNA sequence.

ACCESSION BM763942
 VERSION BM763942.1 GI:19093557
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 621)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 25 row: A column: 11
 High quality sequence stop: 621.

FEATURES
 source Location/Qualifiers

1..621
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S13KMS5-25-A11"
 /clone_11b="S13KMS5"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10F"
 /note="Vector: PCNS; Site.1: EcoRI; Site.2: NotI. The poly
 (A)+ RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10F by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

BASE COUNT 216 a 123 c 127 g 155 t
 ORIGIN

Query Match 5.7%; Score 117; DB 14; Length 621;
 Best Local Similarity 99.1%; Pred. No. 1.7e-19;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 510 CAAGCAAAAGAGAGAGCTGTACATCTGGCCTTGCCTGCAATGGGAATTCAGAGTAGTAA 569
 |||||
 Db 1 CAAGCAAAAGAGAGAGCTGTACATCTGGCCTTGCCTGCAATGGGAATTCAGAGTAGTAA 60
 OY 570 ACTCCTGCTGGACAGAGATGTCACTTAATGTCCTTGACAAACAAAAGAGACAGCTCT 629
 |||||
 Db 61 ACTCCTGCTGGACAGAGATGTCACTTAATGTCCTTGACAAACAAAAGAGACAGCTCT 120

OY 630 GATTAAGCCCGCTACATGCGAGGAAGATGATGCTGCTGGAACATGGCAC 689
 |||||
 Db 121 GACAAAGCCCGCTACATGCGAGGAAGATGATGCTGCTGGAACATGGCAC 180
 OY 690 TGATCCAAATATTCAGATGATGGAATACCACTCT 728
 |||||
 Db 181 TGATCCAAATATTCAGATGATGGAATACCACTCT 219

RESULT 7
 BM763453 633 bp mRNA linear EST 04-MAR-2002
 LOCUS K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
 DEFINITION mRNA sequence.

ACCESSION BM763453
 VERSION BM763453.1 GI:19093068
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 633)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 16 row: A column: 11
 High quality sequence stop: 633.

FEATURES
 source Location/Qualifiers

1..633
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S13KMS5-16-A11"
 /clone_11b="S13KMS5"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10F"
 /note="Vector: PCNS; Site.1: EcoRI; Site.2: NotI. The poly
 (A)+ RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10F by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

BASE COUNT 221 a 125 c 129 g 157 t 1 others
 ORIGIN

Query Match 5.7%; Score 117; DB 14; Length 633;
 Best Local Similarity 99.1%; Pred. No. 1.7e-19;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 510 CAAGCAAAAGAGAGAGCTGTACATCTGGCCTTGCCTGCAATGGGAATTCAGAGTAGTAA 569
 |||||
 Db 1 CAAGCAAAAGAGAGAGCTGTACATCTGGCCTTGCCTGCAATGGGAATTCAGAGTAGTAA 60
 OY 570 ACTCCTGCTGGACAGAGATGTCACTTAATGTCCTTGACAAACAAAAGAGACAGCTCT 629

|||||
Db 61 ACTCGTGTGGACACAGCGTGTCACTTAATCTCTTGACACAAAGAGACAGCTCT 120
Oy 630 GATAAGGCGCCGTAACATGCGAGAGATGAATGCGTAAGTGGCTGAGACATGGCAC 689
Db 121 GACAAAGCGCCGACATGCGAGAGATGAATGCGTAAGTGGCTGAGACATGGCAC 180
Oy 690 TGATCCAAATATTCAGATGATGATGAATATACCACTCT 728
Db 181 TGATCCAAATATTCAGATGATGATGAATATACCACTCT 219
RESULT 8
BQ441373 817 bp mRNA linear EST 24-MAY-2002
LOCUS AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
DEFINITION 5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M2340 row: m column: 08
High quality sequence stop: 516.
Location/Qualifiers
1. 817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6103855"
/clone_lib="NIH_MGC_82"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATATGAGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

BASE COUNT 274 a 183 c 189 g 170 t 1 others
ORIGIN
Query Match 5.7%; Score 117; DB 14; Length 817;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1408 AGAATTTGGAATTTGTTCTACTACAAAGAAAACAGATGCCAAATACTCTTGTGAA 1467
Db 319 AGAATTTGGAATTTGTTCTACTACAAAGAAAACAGATGCCAAATACTCTTGTGAA 378
Oy 1468 AACAGCAACCCGAGACAGACTTAAGCTGACATCGAGAGAGACCAAGGCTT 1524
Db 379 AACAGCAACCCGAGACAGACTTAAGCTGACATCGAGAGAGACCAAGGCTT 435
RESULT 9

AO124119 400 bp DNA linear GSS 22-SEP-1998
LOCUS HS_3122_A1_C07_MR_C17 Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone plate=3122 Col-13 Row=E, DNA sequence.
ACCESSION AO124119
VERSION AO124119.1 GI:3501285
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE
COMMENT Contract: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3122 Row: E Column: 13
Class: BAC ends
High quality sequence stop: 400.
Location/Qualifiers
1. 400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3122 Col=13 Row=E"
/clone_lib="C17 Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 131 a 67 c 88 g 114 t
ORIGIN
Query Match 4.4%; Score 89; DB 17; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 635 AGCGCTACATGCCAGAGATGAATGCGTTAATGTTCTGGAACATGCATGATC 694
Db 237 AGCGCTACATGCCAGAGATGAATGCGTTAATGTTCTGGAACATGCATGATC 296
Oy 695 CAAATATTCAGATGATGATGAATATAC 723
Db 297 CAAATATTCAGATGATGATGAATATAC 325
RESULT 10
AO030111/c 399 bp DNA linear GSS 14-APR-1999
LOCUS RPII11-39K18.TP RPII-11 Homo sapiens genomic clone RPII-11-39K18,
DEFINITION DNA sequence.
ACCESSION AO030111
VERSION AO030111.1 GI:3274075
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 399)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)

COMMENT Other_GSSS: RPOC11-39K18.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org
Clones are derived from the human BAC library RPOC-11. For BAC library availability, please contact Pieter de Jong (pieter@long.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (Inforesgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="GDB:7514849"
/db_xref="taxon:9606"
/clone="RPOC-11-39K18"
/clone_1lb="RPOC-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; RPOC11 Human Male BAC Library"

BASE COUNT 110 a 78 c 73 g 138 t

ORIGIN

Query Match 4.3%; Score 87; DB 17; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.5e-12;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1777 AGTGAAGCAACAAATGATCTACAGACAAATTTGTGTAAGACAGACACGCAATTTA 1836
|||||
Db 102 AGTGAAGCAACAAATGATCTACAGACAAATTTGTGTAAGACAGACACGCAATTTA 43
|||||

QY 1837 CAGCATGAGATTCGATTCATGAAGAA 1863
|||||
Db 42 CAGCATGAGATTCGATTCATGAAGAA 16
|||||

RESULT 11
AL703938 544 bp mRNA linear EST 22-MAR-2002
LOCUS DKFZp686E1728.f1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686E1728.5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 544)
Ottenswaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Well, B. and
Wiemann, S.
EST (Ottenswaelder, B., Obermaier, B., Mewes, H.W., Well, B. and
Wiemann, S.)
Unpublished (2001)
Contact: Ottenswaelder B
MIPS
Am Kioferstr. 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source location/Qualifiers
1..544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp686E1728"
/clone_1lb="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTR1pLx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

BASE COUNT 192 a 94 c 110 g 148 t

ORIGIN

Query Match 4.3%; Score 87; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAACAGCAATCCAGAACAGCTTAAAG 1140
|||||
Db 432 AAGAAAAACAGATGCTAAAAATCTCTTGAAACAGCAATCCAGAACAGCTTAAAG 491
|||||

QY 1141 CTGACATCAGAGGAAGACTCACAAGG 1167
|||||
Db 492 CTGACATCAGAGGAAGACTCACAAGG 518
|||||

RESULT 12
B1461255/c 279 bp mRNA linear EST 21-AUG-2001
LOCUS B1461255
DEFINITION 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
mRNA sequence.
ACCESSION B1461255
VERSION B1461255.1 GI:15251911
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 279)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L14M1687 row: g column: 21
High quality sequence stop: 236.
location/Qualifiers
1..279
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5272364"
/clone_1lb="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVA-3',
size-selected for average insert size 2.2 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 87 a 87 c 60 g 45 t

ORIGIN

Query Match 3.9%; Score 79; DB 13; Length 279;
 Best Local Similarity 100.0%; Pred. No. 5.4e-10;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCTGTTGAGTTGATTCATCCGCGCTCCCTCTGTGAGAACCATTTGCTC 60
 |||||||
 DB 84 ATGCTGTTGAGTTGATTCATCCGCGCTCCCTCTGTGAGAACCATTTGCTC 25
 |||||||

OY 61 AGAGCAAGATGGCAGT 79
 |||||||
 DB 24 AGAGCAAGATGGCAGT 6

RESULT 13
 A0063365
 LOCUS 385 bp DNA linear GSS 31-JUL-1998
 DEFINITION CIT-HSP-2348P17.TR CIT-HSP Homo sapiens genomic clone 2348P17, DNA
 sequence.

ACCESSION A0063365
 VERSION A0063365.1 GI:3361196
 KEYWORDS GSS.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 385)
 Authors: Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
 Golden, K., Berry, K., Granger, D., Sun, E., Wible, C., Shizuya, H.,
 Simon, M., and Venter, J.C.
 Building (1998)
 Use of a random BAC End Sequence Database for Sequence-Ready Map
 Other GSSs: CIT-HSP-2348P17.TF

TITLE JOURNAL
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends

FEATURES
 source Location/Qualifiers
 1..385
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2348P17"
 /clone_1lb="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelBAC11; site_1: HindIII; site_2:
 HindIII"

BASE COUNT 118 a 53 c 79 g 135 t
 ORIGIN

Query Match 3.6%; Score 73; DB 17; Length 385;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1408 AGAATTTGCGAATGATTCGACTACAAAGAAAAAGAGATGCCAAATACTCTTCTAA 1467
 |||||||
 DB 189 AGAATTTGCGAATGATTCGACTACAAAGAAAAAGAGATGCCAAATACTCTTCTAA 248
 |||||||

OY 1468 AACAGCAACCAG 1480
 |||||||
 DB 249 AACAGCAACCAG 261

RESULT 14

AG045796/c 707 bp DNA linear GSS 02-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-024N04.R, genomic survey sequence.
 DEFINITION AG045796
 ACCESSION AG045796.1 GI:16582688
 VERSION GSS.
 KEYWORDS Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male
 BAC library clone: PTB-024N04.R.
 SOURCE Pan troglodytes

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1

REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H., and Sakaki, Y.
 BAC end sequences of library PTB
 Unpublished
 2 (bases 1 to 707)

TITLE JOURNAL
 COMMENT Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suhiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: M13Rev
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..707

FEATURES
 source /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-024N04.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_1lb="PTB Chimpanzee Male BAC library"
 145 c 85 g 237 t 7 others

BASE COUNT 233 a 145 c 85 g 237 t
 ORIGIN

Query Match 2.9%; Score 59; DB 17; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1956 GGAAGAAATTCGACATGCTAGACCTGAGCAATGGAACATCAGAGCCAGCTAA 2014
 |||||||
 DB 226 GGAAGAAATTCGACATGCTAGACCTGAGCAATGGAACATCAGAGCCAGCTAA 168
 |||||||

RESULT 15
 B48260/c 607 bp DNA linear GSS 08-APR-1999
 LOCUS RPICT11-6K4.TV RPICT-11 Homo sapiens genomic clone RPICT-11-6K4, DNA
 DEFINITION sequence.
 ACCESSION B48260
 VERSION B48260.1 GI:2600497
 KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 607)

REFERENCE Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden,
 K., Berry, K., Granger, D., Sun, E., Wible, C., de Jong, P., and Venter,
 J.C.
 Use of BAC End Sequences for Sequence-Ready Map Building
 Unpublished (1997)
 CONTACT: Mark Adams

TITLE JOURNAL
 COMMENT

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org

Clones are derived from the human BAC library RPC11-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://info@resgen.com>). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: 17
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..607
/organism="Homo sapiens"
/db_xref="GDB:7502163"
/db_xref="taxon:9606"
/clone="RPC11-11-6K4"
/clone_lib="RPC11-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC Library"

BASE COUNT
186 a 131 c 109 g 181 t

ORIGIN

Query Match 2.8%; Score 57; DB 17; Length 607;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 TGCTGACACAGCATGCTCACTTAATGCTTCGACAAACAAAAGAGACAGCTCTGA 631
|||||
Db 148 TGCTGACACAGCATGCTCACTTAATGCTTCGACAAACAAAAGAGACAGCTCTGA 92

RESULT 16
BF329652 380 bp mRNA linear EST 22-NOV-2000
LOCUS RC6-BN0276-160600-011-F12 BN0276 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF329652
VERSION BF329652.1 GI:11300400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 380)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and Shogun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC6&t2=RC6-BN0276-160600-011-F12&t3=2000-06-16&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 99

High quality sequence stop: 379.
Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0276"
/dev_stage="Adult"
/note="Organ: breast, normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
80 a 106 c 109 g 85 t

ORIGIN

Query Match 2.5%; Score 52; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GCAAGTGGTGGTGCACCTGCTCCCTGCTGCAGGGGAGGCGACAGACAA 347
|||||
Db 202 GCAAGTGGTGGTGCACCTGCTCCCTGCTGCAGGGGAGGCGACAGACAA 151

RESULT 17
AQ372700 592 bp DNA linear GSS 20-MAY-1999
LOCUS RPC11-14712-TV RPC11-11 Homo sapiens genomic clone RPC11-11-14712,
DEFINITION DNA sequence.
ACCESSION AQ372700
VERSION AQ372700.1 GI:4343723
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 592)
Zhao, S., Adams, M. D., Nierman, W., Malek, J., de Jong, P. and Venter, J. C.
Use of BAC End Sequences from Library RPC11-11 for Sequence-Ready Map Building
Unpublished (1997)
Other GSSs: RPC11-14712-TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPC11-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://info@resgen.com>). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..592
/organism="Homo sapiens"
/db_xref="GDB:7556257"
/db_xref="taxon:9606"
/clone="RPC11-11-14712"
/clone_lib="RPC11-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC Library"

BASE COUNT
199 a 87 c 99 g 207 t

ORIGIN

Query Match 2.5%; Score 50; DB 17; Length 592;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 745 AATGAAGATAAATTAATGCGCAAGACGCTCTTATATGTCGTATAT 794
 |||||||
 DB 153 AATGAAGATAAATTAATGCGCAAGACGCTCTTATATGTCGTATAT 202

RESULT 18
 A0469831 495 bp DNA linear GSS 23-APR-1999
 LOCUS CITBI-EI-2588F5.TF CITBI-EI Homo sapiens genomic clone 2588F5, DNA
 DEFINITION sequence.
 ACCESSION A0469831 GI:4653485
 VERSION A0469831
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 495)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other-GSSs: CITBI-EI-2588F5.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tlgr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source
 1..495
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588F5"
 /clone_11b="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelobAC11; Site_1: ECORI; Site_2: ECORI;
 Caltech Human BAC Library D"

BASE COUNT 179 a 75 c 67 g 174 t

ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAAATGCTCAAGAACCAAGAAATTAATAGATGCTATAGAGAGT 1244
 |||||||
 DB 194 AGAAAATGCTCAAGAACCAAGAAATTAATAGATGCTATAGAGAGT 146

RESULT 19
 A0469663 557 bp DNA linear GSS 23-APR-1999
 LOCUS CITBI-EI-2588M24.TF CITBI-EI Homo sapiens genomic clone 2588M24,
 DEFINITION DNA sequence.
 ACCESSION A0469663
 VERSION A0469663.1 GI:4653317
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 557)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other-GSSs: CITBI-EI-2588M24.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tlgr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source
 1..557
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588M24"
 /clone_11b="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelobAC11; Site_1: ECORI; Site_2: ECORI;
 Caltech Human BAC Library D"

BASE COUNT 201 a 83 c 74 g 199 t

ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAAATGCTCAAGAACCAAGAAATTAATAGATGCTATAGAGAGT 1244
 |||||||
 DB 194 AGAAAATGCTCAAGAACCAAGAAATTAATAGATGCTATAGAGAGT 146

RESULT 20
 AG156382 667 bp DNA linear GSS 09-JAN-2002
 LOCUS AG156382
 DEFINITION Pan troglodytes DNA, clone: RP43-020P19.TJ, genomic survey
 sequence.
 ACCESSION AG156382
 VERSION AG156382.1 GI:16686060
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphocytes DNA, clone_11b:RPCI-43 Chimpanzee
 Male BAC Library clone:RP43-020P19.TJ.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 BAC end sequences of library RPCI-43
 Unpublished
 2 (bases 1 to 667)
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suenho-chou, Tsukuba, Ibaraki, Japan, Kanagawa 230-0045, Japan
 (E-mail:chimpesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
 end was generated during the Red process and may have higher chance
 of clone tracking errors.

PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1.667
/organism="Pan troglodytes"
/db_xref="taxon:9588"
/clone="RP43-020P19.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT 235 a 110 c 98 g 224 t
ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 667;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1196 AGAAATGCTCAAGAACCAATAATAAGTGTGTAGAGAGCT 1244
|||||
Db 212 AGAAATGCTCAAGAACCAATAATAAGTGTGTAGAGAGCT 164

RESULT 21
LOCUS A0030113 697 bp DNA linear GSS 14-APR-1999
DEFINITION RPCI11-39K18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-39K18,
DNA sequence.
ACCESSION A0030113
VERSION A0030113.1 GI:3274077
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 697)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.F., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,T.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSSs: RPCI11-39K18.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieder@jlong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (inforesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1.697
/organism="Homo sapiens"
/db_xref="GDB:751484"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site:1: EcoRI; Site:2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 253 a 120 c 101 g 222 t 1 others
ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1196 AGAAATGCTCAAGAACCAATAATAAGTGTGTAGAGAGCT 1244
|||||
Db 167 AGAAATGCTCAAGAACCAATAATAAGTGTGTAGAGAGCT 119

RESULT 22
LOCUS BE069869 187 bp mRNA EST 09-JUN-2000
DEFINITION CM1-BT0397-201299-073-a11 BT0397 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE069869
VERSION BE069869.1 GI:8414519
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 187)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?Cl=62-CM1-BT0397-201>)
299-073-a11ct3-1999-12-20ct4-1)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 141.
Location/Qualifiers
1.187
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0397"
/dev_stage="adult"
/note="Organ: breast; Vector: puc18; Site:1: SmaI; Site:2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 66 a 45 c 34 g 42 t
ORIGIN

Query Match 2.3%; Score 47; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 790 GATATCGATCAAAAACAGCATGGCTCACCACCTGTTACTTGG 836
|||||
Db 91 GATATCGATCAAAAACAGCATGGCTCACCACCTGTTACTTGG 137

RESULT 23

A0392059/c 476 bp DNA linear GSS 06-MAR-1999
 LOCUS CITBI-EI-2555J3.TR CITBI-EI Homo sapiens genomic clone 2555J3, DNA
 DEFINITION sequence.
 ACCESSION A0392059
 VERSION A0392059.1 GI:4363082
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 476)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE Use of BAC End sequences from Caltech Libraries for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hwe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..476
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2555J3"
 /clone_1lb="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 170 a 75 c 65 g 166 t
 ORIGIN

Query Match 2.3%; Score 47; DB 17; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1550 AGAAGAATCTCAGACAGCAATTAATAGATGATGATAGAGAG 1596
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 209 AGAAGAATCTCAGACAGCAATTAATAGATGATGATAGAGAG 163

RESULT 24
 A0057106 400 bp DNA linear GSS 30-JUL-1998
 LOCUS CIT-HSP-2335J19.TF CIT-HSP Homo sapiens genomic clone 2335J19, DNA
 DEFINITION sequence.
 ACCESSION A0057106
 VERSION A0057106.1 GI:3353632
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M. and Venter,J.C.
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other_GSSs: CIT-HSP-2335J19.TR
 Contact: Mark Adams
 Department of Eukaryotic Genomics

The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: madams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..400
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2335J19"
 /clone_1lb="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 124 a 61 c 83 g 132 t
 ORIGIN

Query Match 2.3%; Score 46; DB 17; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1056 AATTGGCCAGTACTTCTTGACTACAAAGAAAACAGATGCTAATA 1101
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 219 AATTGGCCAGTACTTCTTGACTACAAAGAAAACAGATGCTAATA 264

RESULT 25
 BF675049 894 bp mRNA linear EST 21-DEC-2000
 LOCUS 602136643F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273139 5',
 DEFINITION mRNA sequence.
 ACCESSION BF675049
 VERSION BF675049.1 GI:11948944
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 894)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strussberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LINCMI088 row: e column: 12
 High quality sequence start: 6
 High quality sequence stop: 576.
 Location/Qualifiers
 1..894
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4273139"
 /clone_1lb="NIH_MGC_83"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcgccgcggcc); Site_2: SfiI (ggccatcatggc
); 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGCGGCGCGGCACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average

Insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 239 a 186 c 208 g 261 t

Query Match 2.2%; Score 45; DB 12; Length 894;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GGAAGATGAATGCGTATATGTTGCTGGAACATGGCAGTATCC 695
Db 46 GGAAGATGAATGCGTATATGTTGCTGGAACATGGCAGTATCC 90

RESULT 26
LOCUS AO360298 460 bp DNA linear GSS 06-MAR-1999
DEFINITION HS.5035.A2.C08_SPEE RPC11 Human Male BAC Library Homo sapiens
ACCESSION AO360298
VERSION AO360298.1 GI:4209174
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 460)
Mahliras G.G., Wallace J.C., Smith K., Swartzell S., Holzman T., Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and Hood L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589

JOURNAL Contact: Mahliras GG, Wallace JC, Hood L
MEDLINE High Throughput Sequencing Center
COMMENT University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

FEATURES
source
Location/Qualifiers
1..460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-611 COL-16 Row-E"
/clone_lib="RPC11 Human Male BAC Library"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; RPC11 Human Male BAC Library"
Class: BAC ends
High quality sequence stop: 460.

BASE COUNT 144 a 79 c 95 g 141 t 1 others

Query Match 2.2%; Score 44; DB 17; Length 460;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1717 AGGAAGAGCAGACCTGAAAGCCAGCAATTTCTGACACTGA 1760
Db 335 AGGAAGAGCAGACCTGAAAGCCAGCAATTTCTGACACTGA 378

RESULT 27
LOCUS AG165908 710 bp DNA linear GSS 09-JAN-2002

DEFINITION Pan troglodytes DNA, clone: RP43-033106.TU, genomic survey sequence.

ACCESSION AG165908
VERSION AG165908.1 GI:16695586
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPC1-43 Chimpanzee Male BAC Library clone:RP43-033106.TU.

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Pan.
1
Fujiyama A., Hattori M., Toyoda A., Taylor T.D., Yada T., Totoki Y., Watanabe H. and Sakaki Y.

TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
Unpublished
2 (bases 1 to 710)

REFERENCE Fujiyama A., Hattori M., Toyoda A., Taylor T.D., Yada T., Totoki Y., Watanabe H. and Sakaki Y.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
Unpublished

COMMENT (E-mail:chimpbes@sc.riken.go.jp, URL:http://hnp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPC1-43 This BAC end was generated during the Red process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: TU

LIBRARY Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source
Location/Qualifiers
1..710
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-033106.TU"
/sex="male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-43 Chimpanzee Male BAC Library"

BASE COUNT 218 a 121 c 111 g 258 t 2 others

Query Match 2.0%; Score 41; DB 17; Length 710;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 754 AAATTAATGGCAAGACACTGCTTATATGTCGTGATAT 794
Db 221 AAATTAATGGCAAGACACTGCTTATATGTCGTGATAT 261

RESULT 28
LOCUS B55862 503 bp DNA linear GSS 20-JUN-1998
DEFINITION CIT-HSP-2005F16.TR CIT-HSP Homo sapiens genomic clone 2005F16, DNA sequence.
ACCESSION B55862
VERSION B55862.1 GI:2610196
KEYWORDS GSS.
SOURCE human.

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 503)
Adams M.D., Rounsley S.D., Field C.E., Bass S., Linher K., Golden K., Berry K., Granger D., Suh E., Wible C., Shizuya H., Simon M. and Venter J.C.

TITLE Use of a random BAC End sequence Database for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CIT-HSP-2005F16.TR

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: mdamas@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES

source

1. .503
/organism="Homo sapiens"
/db_xref="GDB:7039242"
/db_xref="taxon:9606"
/clone_id="2005F16"
/clone_id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT 152 a 116 c 87 g 148 t
ORIGIN

Query Match 2.0%; Score 40; DB 17; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1087 AACAGATGCTAAATAATCTCTTGTGAACAGCAATCCAG 1126
|||||
Db 502 AACAGATGCTAAATAATCTCTTGTGAACAGCAATCCAG 463

RESULT 29
AQ900910 1011 bp DNA linear GSS 10-NOV-1999
LOCUS HS.2055_B1.B05.T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-2055 Col=9 Row=D, DNA sequence.
ACCESSION AQ900910
VERSION AQ900910.1 GI:6357012
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1011)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2055 row: D column: 9
Seq primer: T7
Class: BAC ends
High quality sequence stop: 1011.

FEATURES

source

1. .1011
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2055 Col=9 Row=D"

/clone_id="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 216 a 214 c 143 g 438 t
ORIGIN

Query Match 1.9%; Score 39; DB 17; Length 1011;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1054 GTAATTTGCCAGTACTTCTTGACTACAAAGAAAAACAG 1092
|||||
Db 207 GTAATTTGCCAGTACTTCTTGACTACAAAGAAAAACAG 245

RESULT 30
AQ247090 458 bp DNA linear GSS 06-OCT-1998
LOCUS HS.2055_B1.B04.T7 CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-2055 Col=7 Row=D, DNA sequence.
ACCESSION AQ247090
VERSION AQ247090.1 GI:3697272
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 458)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2055 row: D column: 7
Class: BAC ends
High quality sequence stop: 458.

FEATURES

source

1. .458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2055 Col=7 Row=D"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 110 a 122 c 68 g 158 t
ORIGIN

Query Match 1.9%; Score 38; DB 17; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1088 AACAGATGCTAAATAATCTTGTGAACAGCAATCCA 1125
|||||
Db 198 AACAGATGCTAAATAATCTTGTGAACAGCAATCCA 235

RESULT 31
AQ763344 424 bp DNA linear GSS 28-JUL-1999
LOCUS HS.3162_A2.B06.MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3162 Col=12 Row=C, DNA sequence.

```

ACCESSION      AQ763344
VERSION        AQ763344.1
KEYWORDS       GI:5641460
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE      1 (bases 1 to 424)
AUTHORS        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
               Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
               Hood,L.
TITLE          Sequence-tagged connectors: A sequence approach to mapping and
               scanning the human genome
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE        99380589
COMMENT        Contact: Mahairas GG, Wallace JC, Hood L
               High Throughput Sequencing Center
               University of Washington
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
               Tel: (206) 616-3618
               Fax: (206) 616-3887
               Email: jwallace@u.washington.edu
               Clones may be purchased from Research Genetics (info@resgen.com).
               BAC end Web Server: http://www.htsc.washington.edu
               Plate: 3162 row: C column: 12
               Seq primer: M13 Reverse
               Class: BAC ends
               High quality sequence stop: 424.
FEATURES       location/Qualifiers
               1..424
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="Plate=3162 Col=12 Row=C"
               /clone_lib="CIR Approved Human Genomic Sperm Library D"
               /sex="male"
               /note="Organ: sperm; Vector: pBeloblAC11; BAC Clones in
               E-Coli DH10B"
BASE COUNT     147 a 72 c 56 g 146 t 3 others
ORIGIN
Query Match   1.8%; Score 37; DB 17; Length 424;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1208 AAGAACGACGAATTAATAGATGTGTAGACAGGT 1244
|||||
Db 194 AAGAACGACGAATTAATAGATGTGTAGACAGGT 158

RESULT 32
BG720647 602692528F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824630 5',
LOCUS      mRNA sequence.
ACCESSION  BG720647
VERSION    BG720647.1
KEYWORDS   GI:13999834
SOURCE     human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 (bases 1 to 694)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      Mammalian Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-r@mail.nih.gov
           Tissue Procurement: Miklos Palovits, M.D., Ph.D.
           cDNA Library Preparation: Michael J. Brownstein (NHLBI), Shitaki
           Toshinuki and Piero Carninci (RIKEN)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be

```

```

found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM10736 row: h column: 07
High quality sequence stop: 694.
FEATURES       location/Qualifiers
               1..694
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:4824630"
               /clone_lib="NIH_MGC_97"
               /lab_host="DH10B"
               /note="Organ: testis; Vector: pBluescript (modified
               pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
               ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
               size-selected for average insert size 2.2 kb and
               normalized to ROT 5. This is a primary library enriched
               for full-length clones and constructed using the
               Cap-trapper method (Carninci, in preparation). Library
               constructed by M. Brownstein (NHLBI/NHGRI, National
               Institutes of Health). Note: this is a NIH-MGC Library."
BASE COUNT     108 a 173 c 228 g 185 t
ORIGIN
Query Match   1.8%; Score 37; DB 12; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 159 TATGAGACACTCGAGCAAGATGGCAGTGGTGC 195
|||||
Db 645 TATGAGACACTCGAGCAAGATGGCAGTGGTGC 681

RESULT 33
AG054405 652 bp DNA linear GSS 02-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-040B06.F, genomic survey sequence.
ACCESSION  AG054405
VERSION    AG054405.1
KEYWORDS   GI:16591848
SOURCE     GSS.
ORGANISM   Pan troglodytes
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
           Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 652)
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
           Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
           and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
           1-7-22 Suenhiro-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan
           (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
           Tel:81-45-503-9111, Fax:81-45-503-9170)
           Clones are derived from the chimpanzee BAC library PTB This BAC end
           was generated during the R&D process and may have higher chance of
           clone tracking errors.
COMMENT     PRIMERS
           Sequencing: -21M13
           LIBRARY
           Vector : pKS145
           R.Site 1 : SacI
           R.Site 2 : SacI.
           Location/Qualifiers
               1..652
               /organism="Pan troglodytes"
               /db_xref="taxon:9598"
               /clone="PTB-040B06.F"
               /sex="male"
FEATURES       source

```


BASE COUNT 189 a 101 c 152 g 210 t

ORIGIN

Query Match 1.8%; Score 36; DB 17; Length 652;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 ACACCACGTCTGCTGCTACGACGACAAACAG 855
|||||
Db 398 ACACCACGTCTGCTGCTACGACGACAAACAG 433

RESULT 34
LOCUS AI349163 156 bp mRNA linear EST 16-FEB-1999
DEFINITION fa73c06.x2 NCI_CGAP_HSC2 Homo sapiens CDNA clone IMAGE:2049706 3',
mRNA sequence.
ACCESSION AI349163
VERSION AI349163
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert Length: 243 Std Error: 0.00
Seq primer: -40UP from Glibco.

FEATURES
source Location/Qualifiers
1..156
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2049706"
/clone_id="NCI_CGAP_HSC2"
/tissue_type="stem cell 34+/38+"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Bone marrow; Vector: pAMP1; mRNA made from
bone marrow, stem cells 34+/38+, CDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 400 bp. Primary library,
non-amplified."

BASE COUNT 56 a 37 c 36 g 27 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
|||||
Db 111 GCCAGCTAAAAA 145

RESULT 35
LOCUS AI251211 157 bp mRNA linear EST 03-FEB-1999
DEFINITION qv38h06.x1 NCI_CGAP_Ov31 Homo sapiens CDNA clone IMAGE:1983899 3',

RNA sequence.
AI251211
AI251211.1 GI:3847740
EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Unknown library type
Insert Length: 244 Std Error: 0.00
Seq primer: -40UP from Glibco.

FEATURES
source Location/Qualifiers
1..157
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1983899"
/clone_id="NCI_CGAP_Ov31"
/sex="female"
/tissue_type="Papillary serous carcinoma"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian
carcinoma, CDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Non-amplified library."

BASE COUNT 57 a 37 c 36 g 27 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 157;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
|||||
Db 111 GCCAGCTAAAAA 145

RESULT 36
LOCUS AI305627 160 bp mRNA linear EST 09-DEC-1998
DEFINITION qw72f03.x1 NCI_CGAP_Ov33 Homo sapiens CDNA clone IMAGE:1996637 3',
mRNA sequence.
ACCESSION AI305627
VERSION AI305627
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Glibco.

FEATURES
source Location/Qualifiers
1..160
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:1996637"
/clone_1lb="NCI_CGAP_Ov33"
/sex="female"
/tissue_type="borderline ovarian carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: ovary; Vector: PAMPI; mRNA made from
borderline ovarian carcinoma, cDNA made by oligo-dt
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT      59 a      38 c      35 g      26 t      2 others
ORIGIN
Query Match      1.7%; Score 35; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA.2040
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 145

RESULT 37
AI343314      166 bp      mRNA      linear      EST 08-APR-1999
LOCUS      tb93912.x1 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2061958 3',
DEFINITION      mRNA sequence.
ACCESSION      AI343314
VERSION      AI343314.1 GI:4080520
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers
1.166
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2061958"
/clone_1lb="NCI_CGAP_Lu25"
/tissue_type="Bronchioalveolar carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
carcinoma tissue, cDNA made by oligo-dt priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT      57 a      40 c      39 g      30 t
ORIGIN
Query Match      1.7%; Score 35; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
Db 122 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 156

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
```

```
RESULT 38
AM302924      184 bp      mRNA      linear      EST 18-JAN-2000
LOCUS      xr86g07.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767068 3',
DEFINITION      mRNA sequence.
ACCESSION      AM302924
VERSION      AM302924.1 GI:6712604
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco.
High quality sequence stop: 136.
Location/Qualifiers
1.184
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2767068"
/clone_1lb="NCI_CGAP_Lu26"
/tissue_type="Invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dt priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT      92 a      35 c      33 g      24 t
ORIGIN
Query Match      1.7%; Score 35; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 145

RESULT 39
AM302925      199 bp      mRNA      linear      EST 18-JAN-2000
LOCUS      xr86g08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767070 3',
DEFINITION      mRNA sequence.
ACCESSION      AM302925
VERSION      AM302925.1 GI:6712605
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
```

Email: cgabs-r@mail.nih.gov
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Seq primer: -40UP from GIBCO.

FEATURES

Location/Qualifiers

1. 199
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2767070"
/clone_id="NCI_CGAP_Lu26"
/tissue_type="Invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 93 a 38 c 40 g 28 t
ORIGIN

Query Match 1.7%; Score 35; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
Db 111 GCCAGCTAAAAA 145

RESULT 40
LOCUS AI344928 224 bp mRNA linear EST 30-DEC-1998
DEFINITION t01a04.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052270 3',
mRNA sequence.

ACCESSION AI344928
VERSION AI344928.1 GI:4082134
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 224)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Seq primer: -40UP from GIBCO.

FEATURES

Location/Qualifiers

1. 224
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2052270"
/clone_id="NCI_CGAP_Lu26"
/tissue_type="Invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size selected on agarose gel,
average insert size 500 bp. Primary library,

BASE COUNT 119 a 40 c 36 g 29 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
Db 128 GCCAGCTAAAAA 162

RESULT 41
LOCUS AI336592 232 bp mRNA linear EST 16-FEB-1999
DEFINITION ta94d12.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2051735 3',
mRNA sequence.

ACCESSION AI336592
VERSION AI336592.1 GI:4073519
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 232)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Insert length: 302 Std Error: 0.00
Seq primer: -40UP from GIBCO
High quality sequence stop: 225.

FEATURES

Location/Qualifiers

1. 232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2051735"
/clone_id="NCI_CGAP_Lu26"
/tissue_type="Invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 119 a 44 c 40 g 29 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
Db 134 GCCAGCTAAAAA 168

RESULT 42
LOCUS AI344933 239 bp mRNA linear EST 16-FEB-1999
DEFINITION t01a11.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052284 3',
mRNA sequence.

ACCESSION AI344933

VERSION AI344933.1 GI:4082139
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 291 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source
1..239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052284"
/clone_1lb="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue; cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
|||||
Db 146 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 180

RESULT 43
AI344936 239 bp mRNA linear EST 30-DEC-1998
LOCUS tb01b03.x1 NCI_CGAP_Lu26 Homo sapiens CDNA IMAGE:2052269 3',
DEFINITION mRNA sequence.
ACCESSION AI344936
VERSION AI344936.1 GI:4082142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES
source
1..239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052269"
/clone_1lb="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue; cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
|||||
Db 146 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 180

RESULT 44
AI335449 250 bp mRNA linear EST 29-DEC-1998
LOCUS tb79f03.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2060573 3',
DEFINITION mRNA sequence.
ACCESSION AI335449
VERSION AI335449.1 GI:4072376
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 250)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 240.

FEATURES
source
1..250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2060573"
/clone_1lb="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue; cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 136 a 43 c 41 g 30 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
 |||
 Db 134 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 168

RESULT 45

AI494279/c

LOCUS

AI494279 360 bp mRNA linear EST 17-MAR-1999
 qy98c11.x1 NCI-CGAP Brn25 Homo sapiens cDNA clone IMAGE:2020052 3'
 similar to WP:B0432.3 CE07741 ;, mRNA sequence.

ACCESSION

AI494279

VERSION

AI494279.1 GI:4395282

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1

AUTHORS

(bases 1 to 360)

TITLE

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT

National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BrGAP), Tumor Gene Index
 Unpublished (1998)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

JOURNAL

CDNA Library

ORIGIN

Arrayed by: Greg Lennon, Ph.D.

FEATURES

source

location/qualifiers

1..360

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2020052"

/clone_lib="NCI CGAP Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCCGACATAGCTTTTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 69 a 84 c 97 g 110 t
 ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 360;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
 |||
 Db 41 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 7

Search completed: November 8, 2002, 13:33:11
 Job time : 2591.15 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 08:45:54 : Search time 2514.85 Seconds
(without alignments)
12879.875 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000
Sequence: 1 atgtgtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1430567

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estim:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hmv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	9.2	521	17	AQ204617 HS_3229-B
2	141	7.0	865	12	BF676987 602084215
3	140	7.0	451	9	AI804733 t442D03.x
4	137	6.9	289	9	AA533501 n396A04.s
5	129	6.5	531	17	AO615477 HS_5144.B
6	117	5.9	621	14	BM763942 K-EST0045

1413

7	117	5.9	633	14	BM763453
8	117	5.9	817	14	BQ441373
9	87	4.5	400	17	AO124119
10	87	4.3	399	17	AO303011
11	87	4.3	544	9	AL703938
12	79	4.0	279	13	BI461255
13	73	3.6	385	17	AO063365
14	59	2.9	707	17	AG045796
15	57	2.9	607	17	BA8260
16	52	2.6	380	12	BF329652
17	50	2.5	592	17	AQ372700
18	49	2.5	555	17	AQ469831
19	49	2.5	499	17	AQ469663
20	49	2.5	667	17	AG156382
21	49	2.5	697	17	AO030113
22	47	2.4	187	10	BE069869
23	46	2.3	400	17	AO057106
24	45	2.2	894	12	BF675049
25	44	2.2	460	17	AQ360298
26	41	2.1	476	17	AQ392059
27	41	2.1	710	17	AG165908
28	40	2.0	184	10	AM302824
29	40	2.0	199	10	AM302925
30	40	2.0	224	9	AI344928
31	40	2.0	232	9	AI336592
32	40	2.0	239	9	AI344933
33	40	2.0	239	9	AI344936
34	40	2.0	250	9	AI335449
35	40	2.0	360	9	AI194279
36	40	2.0	367	9	AA766864
37	40	2.0	421	14	BQ230307
38	40	2.0	442	14	BO127207
39	40	2.0	503	17	B55862
40	40	2.0	560	12	BF968779
41	40	2.0	616	12	BG491207
42	40	2.0	831	13	BI915244
43	40	2.0	1018	13	BI826922
44	40	2.0	1024	14	BM919526
45	39	1.9	160	9	AI305627

ALIGNMENTS

RESULT 1	AQ204617	521 bp	DNA	linear	GSS 17-SEP-1998
DEFINITION	HS_3229_B1.G12.T7 C1T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3229 COL-23 Row-N, DNA sequence.				
ACCESSION	AQ204617				
VERSION	AQ204617.1	GI:3615187			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)				
MEDLINE	99380589				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3229 Row: N Column: 23				


```

DB 61 ACTCGGCGGAGACAGCATGTCACCTTATGCTGTGACACAAACAAAGAGCAGCTCT 120
QY 630 GATTAAGGCCGCTTACATGCGCAGGAAGATGATGCTTATGCTGTGAAACATGCGAC 689
DB 121 GACAAAGGCCGCTTACATGCGCAGGAAGATGATGCTTATGCTGTGAAACATGCGAC 180
QY 690 TGATCCAAATATTCAGATGATGATGAAATACCTCT 728
DB 181 TGATCCAAATATTCAGATGATGATGAAATACCTCT 219

RESULT 8
LOCUS BQ441373 817 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:5103855
5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (MLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
http://image.llnl.gov
Plate: L1CM2340 row: m column: 08
High quality sequence stop: 516.
Location/Qualifiers
1. 817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5103855"
/clone_1lb="NIH_MGC_82"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
BASE COUNT 274 a 183 c 189 g 170 t 1 others
ORIGIN
Query Match 5.9%; Score 117; DB 14; Length 817;
Best Local Similarity 100.0%; Pred. No. 8,8e-21;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1408 AGAATTGGCAATGATTCTGACTACAAAGAAAACAGATGCCAAATCTCTTGAA 1467
DB 319 AGAATTGGCAATGATTCTGACTACAAAGAAAACAGATGCCAAATCTCTTGAA 378
QY 1468 AACAGCAACCCGAGCAACACTTAAGCTGACATGAGAGAGAGCTCACAAAGGCTT 1524
DB 379 AACAGCAACCCGAGCAACACTTAAGCTGACATGAGAGAGAGCTCACAAAGGCTT 435

RESULT 9

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LOCUS A0124119 400 bp DNA linear GSS 22-SEP-1998
DEFINITION HS_3122_A1_C07_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3122 Col=13 Row=E, DNA sequence.
ACCESSION A0124119
VERSION A0124119.1 GI:3501285
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3122 row: E column: 13
Class: BAC ends
High quality sequence stop: 400.
Location/Qualifiers
1. 400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3122 Col=13 Row=E"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 131 a 67 c 88 g 114 t
ORIGIN
Query Match 4.5%; Score 89; DB 17; Length 400;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 AGGCCGTACAAATGCCAGAAATGATGCGCTTATGCTGTGAAACATGCGACATGATC 694
DB 237 AGGCCGTACAAATGCCAGAAATGATGCGCTTATGCTGTGAAACATGCGACATGATC 296
QY 695 CAAATATTCAGATGAGTATGCAATATCC 723
DB 297 CAAATATTCAGATGAGTATGCAATATCC 325

RESULT 10
LOCUS A0030111 399 bp DNA linear GSS 14-APR-1999
DEFINITION RPC111-39K18.TP RPC1-11 Homo sapiens genomic clone RPC1-11-39K18,
DNA sequence.
ACCESSION A0030111
VERSION A0030111.1 GI:3274075
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 399)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., White,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)

```

COMMENT Other_GSSS: RPCI11-39K18.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.bufileo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from Research Genetics (Inforesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
Source Location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="GDB:7514849"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/clone_1lb="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT 110 a 78 c 73 g 138 t

ORIGIN
Query Match 4.3%; Score 87; DB 17; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.4e-13;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1732 AGTGCACCAACAAATGCTACTCAGAACCAATTTGTGACAGACGACACTGCAATATTA 1791
|||||
Db 102 AGTGCACCAACAAATGCTACTCAGAACCAATTTGTGACAGACGACACTGCAATATTA 43
|||||

QY 1792 CACGATGAGATTCGATTCATGAAGAA 1818
|||||
Db 42 CACGATGAGATTCGATTCATGAAGAA 16
|||||

RESULT 11
AL703938 544 bp mRNA linear EST 22-MAR-2002
LOCUS DKEFZ686E1728_r1.686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKEFZ686E1728 5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 544)
Ottenswaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Well, B. and Wiemann, S.
EST (Ottenswaelder, B., Obermaier, B., Mewes, H.W., Well, B. and Wiemann, S.)
Unpublished (2001)
Contact: Ottenswaelder B

JOURNAL
COMMENT MIPs
Am Kiofepspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the CDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKEFZ686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES
Source Location/Qualifiers
1..544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKEFZ686E1728"
/clone_1lb="686 (synonym: hlc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pT7-riplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

BASE COUNT 192 a 94 c 110 g 148 t

ORIGIN
Query Match 4.3%; Score 87; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 4.9e-13;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAAGAAAAAGAGATGCTAAATCTCTTGAAGAACGAAATCCAGAACAGACTTAAG 1140
|||||
Db 432 AAAGAAAAAGAGATGCTAAATCTCTTGAAGAACGAAATCCAGAACAGACTTAAG 491
|||||

QY 1141 CTGACATCAGAGAGAGAGTCAAGG 1167
|||||
Db 492 CTGACATCAGAGAGAGAGTCAAGG 518
|||||

RESULT 12
BI461255/c 279 bp mRNA linear EST 21-AUG-2001
LOCUS 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
DEFINITION mRNA sequence.
ACCESSION BI461255
VERSION BI461255.1 GI:15251911
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 279)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1687 row: 9 column: 21
High quality sequence, stop: 236.
Location/Qualifiers
1..279
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5272364"
/clone_1lb="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.2 kb and
normalized to ROP 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 87 a 87 c 60 g 45 t

ORIGIN

Query Match 4.0%; Score 79; DB 13; Length 279;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTGGTTGAGGTGATTCATGCCGCTGCTTCGTGGAAGACCAATTTGGTTC 60
 |||||||
 DB 84 AAGTGGTTGAGGTGATTCATGCCGCTGCTTCGTGGAAGACCAATTTGGTTC 25
 |||||||
 QY 61 AGGACCAAGATGGCAAGT 79
 |||||||
 DB 24 AGGACCAAGATGGCAAGT 6

RESULT 13

LOCUS A0063365 385 bp DNA linear GSS 31-JUL-1998
 DEFINITION CIT-HSP-2348P17.TR CIT-HSP Homo sapiens genomic clone 2348P17, DNA sequence.

ACCESSION A0063365
 VERSION A0063365
 KEYWORDS GSS.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

ADAMS,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuza,H.,
 Simon,M. and Venter,J.C.
 Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)

JOURNAL

Unpublished (1998)
 Other-GSS: CIT-HSP-2348P17.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdamas@tigr.org
 Clones are available from Research Genetics (Info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse

FEATURES

Class: BAC ends.
 Location/Qualifiers
 1..385
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_11b="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelBAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT

ORIGIN 118 a 53 c 79 g 135 t

Query Match 3.6%; Score 73; DB 17; Length 385;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1408 AAGATTGGCAATTAATTTCTGACTACAAAGAAAACAGATGCCAAATTAATCTTTGAA 1467
 |||||||
 DB 189 AAGATTGGCAATTAATTTCTGACTACAAAGAAAACAGATGCCAAATTAATCTTTGAA 248
 |||||||

QY 1468 AACAGCAACCCAG 1480
 |||||||
 DB 249 AACAGCAACCCAG 261

RESULT 14

AG045796/c

AG045796 707 bp DNA linear GSS 02-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-024N04.R, genomic survey sequence.

ACCESSION AG045796
 VERSION AG045796.1 GI:16582688
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
 BAC library clone:PTB-024N04.R.
 ORGANISM Pan troglodytes

REFERENCE

1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 BAC end sequences of library PTB

JOURNAL

Unpublished
 2 (bases 1 to 707)
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission

COMMENT

Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
 1-7-22 Suenho-cho,Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9110)
 Clones are derived from the chimpanzee BAC library PTB r11s BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: M13rev
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.

FEATURES

Location/Qualifiers
 1..707
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-024N04.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_11b="PTB Chimpanzee Male BAC library"

BASE COUNT

ORIGIN 233 a 145 c 85 g 237 t

Query Match 2.9%; Score 59; DB 17; Length 707;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1911 GGAAGAAATTCATGCTAAGACTGAGCTAGACACATGAACATCAGACGCTAA 1969
 |||||||
 DB 226 GGAAGAAATTCATGCTAAGACTGAGCTAGACACATGAACATCAGACGCTAA 168
 |||||||

RESULT 15

B48260/c 607 bp DNA linear GSS 08-APR-1999
 DEFINITION RPi111-6K4.TV RPi1-11 Homo sapiens genomic clone RPi1-11-6K4, DNA
 sequence.

ACCESSION B48260
 VERSION B48260.1 GI:2600497
 KEYWORDS GSS.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 607)
 Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
 ,J.C., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter

Use of BAC End Sequences for Sequence-Ready Map Building
 Unpublished (1997)
 Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://inforesgen.com>). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..607
/organism="Homo sapiens"
/db_xref="GDB:7502163"
/db_xref="taxon:9606"
/clone="RPCI-11-6K4"
/clone_1id="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT
186 a 131 c 109 g 181 t

ORIGIN

Query Match 2.9%; Score 57; DB 17; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 TGCTGACAGACGATGTCACCTATGCTTCCTGACACAAAGAGACAGCTCTGA 631
|||||
Db 148 TGCTGACAGACGATGTCACCTATGCTTCCTGACACAAAGAGACAGCTCTGA 92
|||||

RESULT 16
BF329652 380 bp mRNA linear EST 22-NOV-2000
LOCUS RC6-BN0276-160600-011-F12 BN0276 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BF329652
VERSION BF329652.1 GI:11300400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 380)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., deOliveira,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&ct2=RC6-BN0276-160600-011-F12&ts=2000-06-16&tt=1>
Seq primer: puc 18 forward
High quality sequence start: 99

High quality sequence stop: 379.
FEATURES
source
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1id="BN0276"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
80 a 106 c 109 g 85 t

ORIGIN

Query Match 2.6%; Score 52; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GCAAGTGTGCTGCACGCTTCCCTGCTGACAGGGAGCGGACAGACAA 347
|||||
Db 202 GCAAGTGTGCTGCACGCTTCCCTGCTGACAGGGAGCGGACAGACAA 151
|||||

RESULT 17
AO372700 592 bp DNA linear GSS 20-MAY-1999
LOCUS RPCI11-14712-TV RPCI-11 Homo sapiens genomic clone RPCI-11-14712,
DEFINITION
DNA sequence.
ACCESSION AO372700
VERSION AO372700.1 GI:4343723
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 592)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: RPCI11-14712-TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://inforesgen.com>). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1..592
/organism="Homo sapiens"
/db_xref="GDB:7556257"
/db_xref="taxon:9606"
/clone="RPCI-11-14712"
/clone_1id="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT
199 a 87 c 99 g 207 t

Query Match 2.5%; Score 50; DB 17; Length 592;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 AATGAAGATTAATTAATGCGCAAGACACTGCTATATATGTCGTGATAT 794
 |||||||
 |||||||

RESULT 18
 A0469831/c 495 bp DNA linear GSS 23-APR-1999
 LOCUS CITBI-E1-2588F5.TF CITBI-E1 Homo sapiens genomic clone 2588F5, DNA
 DEFINITION sequence.
 ACCESSION A0469831.1 GI:4653485
 VERSION A0469831.1 GI:4653485
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
 Venter, J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other-GSSs: CITBI-E1-2588F5.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org
 Clones are available from Research Genetics (Info@resgen.com). BAC
 end search page:
 http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..495
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588F5"
 /clone_1lb="CITBI-E1"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelOBAC11; Site_1: ECORI; Site_2: ECORI;
 Caltech Human BAC Library D"
 BASE COUNT 179 a 75 c 67 g 174 t
 ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1196 AGAAATGCTCTCAAGACCAAGAAATTAATAGATGCTGATAGAGAGT 1244
 |||||||
 |||||||

Db 194 AGAAATGCTCTCAAGACCAAGAAATTAATAGATGCTGATAGAGAGT 146
 |||||||
 |||||||

RESULT 19
 A0469663/c 557 bp DNA linear GSS 23-APR-1999
 LOCUS CITBI-E1-2588M24.TF CITBI-E1 Homo sapiens genomic clone 2588M24,
 DEFINITION DNA sequence.
 ACCESSION A0469663.1 GI:4653317
 VERSION A0469663.1 GI:4653317
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
 Venter, J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other-GSSs: CITBI-E1-2588M24.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org
 Clones are available from Research Genetics (Info@resgen.com). BAC
 end search page:
 http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..557
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588M24"
 /clone_1lb="CITBI-E1"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelOBAC11; Site_1: ECORI; Site_2: ECORI;
 Caltech Human BAC Library D"
 BASE COUNT 201 a 83 c 74 g 199 t
 ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1196 AGAAATGCTCTCAAGACCAAGAAATTAATAGATGCTGATAGAGAGT 1244
 |||||||
 |||||||

Db 194 AGAAATGCTCTCAAGACCAAGAAATTAATAGATGCTGATAGAGAGT 146
 |||||||
 |||||||

RESULT 20
 AG156382/c 667 bp DNA linear GSS 09-JAN-2002
 LOCUS AG156382
 DEFINITION Pan troglodytes DNA, clone: RP43-020P19.TJ, genomic survey
 sequence.
 ACCESSION AG156382
 VERSION AG156382.1 GI:16686060
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphocytes DNA, clone_1lb:RPCI-43 Chimpanzee
 Male BAC Library clone:RP43-020P19.TJ.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chumpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
 end was generated during the RAD process and may have higher chance
 of clone tracking errors.

PRIMERS
Sequencing: TJ
LIBRARY
Vector : PBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. 667
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-020P19.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT 235 a 110 c 98 g 224 t
ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 667;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCAAGAACCAATAATAAGATGCTGATAGAGCT 1244
Db 212 AGAAATGCTCAAGAACCAATAATAAGATGCTGATAGAGCT 164
|||||

RESULT 21
A0030113/C 697 bp DNA linear GSS 14-APR-1999
LOCUS
DEFINITION
A0030113
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 697)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.F., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,U.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSS: RPCI11-39K18.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pierre@jeong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. 697
/organism="Homo sapiens"
/db_xref="GDB:751484"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: PBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 253 a 120 c 101 g 222 t 1 others
ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCAAGAACCAATAATAAGATGCTGATAGAGCT 1244
Db 167 AGAAATGCTCAAGAACCAATAATAAGATGCTGATAGAGCT 119
|||||

RESULT 22
BE069869 187 bp mRNA linear EST 09-JUN-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 187)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ft-CM1-BT0397-201>)
299-073-alleles-1999-12-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 141.
Location/Qualifiers
1. 187
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0397"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 66 a 45 c 34 g 42 t
ORIGIN

Query Match 2.4%; Score 47; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 GATATCGATCAAAAACCAACGATGCGCTCACACACTGTACTTGG 836
Db 91 GATATCGATCAAAAACCAACGATGCGCTCACACACTGTACTTGG 137
|||||

RESULT 23

A0057106 400 bp DNA linear GSS 30-JUL-1998
 LOCUS CIT-HSP-2335J19.TF CIT-HSP Homo sapiens genomic clone 2335J19, DNA
 DEFINITION sequence.
 ACCESSION A0057106
 VERSION A0057106.1 GI:3353632
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M. and Venter,J.C.
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other_GSSs: CIT-HSP-2335J19.TR
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source 1..400
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_11b="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 124 a 61 c 83 g 132 t
 ORIGIN

Query Match 2.3%; Score 46; DB 17; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1056 AATTGCGCAGTACTTCTGACTACAAAGAAAACAGATGCTAATAA 1101
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 219 AATTGCGCAGTACTTCTGACTACAAAGAAAACAGATGCTAATAA 264

RESULT 24
 BF675049 894 bp mRNA linear EST 21-DEC-2000
 LOCUS BF675049 602136643P1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4273139 5',
 DEFINITION mRNA sequence.
 ACCESSION BF675049
 VERSION BF675049.1 GI:11948944
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 894)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1088 row: e column: 12
 High quality sequence start: 6
 High quality sequence stop: 576.

FEATURES
 source 1..894
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4273139"
 /clone_11b="NIH_MGC_83"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-L1B (Clontech);
 Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggccatcagcc
); 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATATGCCC-3' and 3' adaptor
 sequence: 5'-ATCTAGAGAGCCGCGCCGCGCATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

BASE COUNT 239 a 186 c 208 g 261 t
 ORIGIN

Query Match 2.2%; Score 45; DB 12; Length 894;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 651 GGAAGATGATGCGCTTATGTTGCTGGAACATGCACATGAC 695
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 46 GGAAGATGATGCGCTTATGTTGCTGGAACATGCACATGAC 90

RESULT 25
 A0360298 460 bp DNA linear GSS 06-MAR-1999
 LOCUS HS_5035_A2_C08_SPEE RPC111 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate-611 Col-16 Row-E, DNA sequence.
 ACCESSION A0360298
 VERSION A0360298.1 GI:4209174
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 460)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380588
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 611 row: E column: 16
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 460.

FEATURES
 source 1..460
 /organism="Homo sapiens"

```
/db_xref="taxon:9606"
/clone="Plate-611 Col-16 Row-E"
/clone_lib="RPC11 Human Male BAC Library"
/sex="male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; RPC11 Human Male BAC Library"
BASE COUNT      144 a      79 c      95 g      141 t      1 others
ORIGIN

Query Match      2.1%; Score 41; DB 17; Length 460;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 AGAAGAGACAGACCTGAAAGCCAGCAATTCCTGACACTGA 1715
|||||
Db 335 AGAAGAGACAGACCTGAAAGCCAGCAATTCCTGACACTGA 378

RESULT 26
AQ392059      476 bp      DNA      linear      GSS 06-MAR-1999
LOCUS      CITBI-E1-2555J3.TR CITBI-E1 Homo sapiens genomic clone 2555J3, DNA
DEFINITION      sequence.
ACCESSION      AQ392059
VERSION      AQ392059.1 GI:4363082
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 476)
AUTHORS      Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE      Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL      Unpublished (1997)
COMMENT      Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
Source      Location/Qualifiers
1..476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2555J3"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT      170 a      75 c      65 g      166 t
ORIGIN

Query Match      2.1%; Score 41; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 TCTCAGACACGAAATTAATAGATGTCATAGAGAGGT 1244
|||||
Db 201 TCTCAGACACGAAATTAATAGATGTCATAGAGAGGT 161

RESULT 27
AG165908
LOCUS      AG165908      710 bp      DNA      linear      GSS 09-JAN-2002
```

```
DEFINITION      Pan troglodytes DNA, clone: RP43-033106.TJ, genomic survey
sequence.
ACCESSION      AG165908
VERSION      AG165908.1 GI:16695586
KEYWORDS      GSS.
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPC1-43 Chimpanzee
Male BAC Library clone:RP43-033106.TJ.
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE      1
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoxi,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of library RPC1-43
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 710)
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoxi,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the chimpanzee BAC library RPC1-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY      Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
Source      Location/Qualifiers
1..710
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-033106.TJ"
/sex="male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-43 Chimpanzee Male BAC Library"
BASE COUNT      218 a      121 c      111 g      258 t      2 others
ORIGIN

Query Match      2.1%; Score 41; DB 17; Length 710;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 754 AAATTATGCCAAGACACCTCTTATATGTCGTGATAT 794
|||||
Db 221 AAATTATGCCAAGACACCTCTTATATGTCGTGATAT 261

RESULT 28
AM302924      184 bp      mRNA      linear      EST 18-JAN-2000
LOCUS      x186907.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767068 3',
DEFINITION      mRNA sequence.
ACCESSION      AM302924
VERSION      AM302924.1 GI:6712604
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 184)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
cDNA Library Preparation: David B. Kitzman, Ph.D.
```

cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco
High quality sequence stop: 136.

FEATURES

source

1. 184

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2767068"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung

adenocarcinoma tissue, cDNA made by oligo-dT priming.

directionally cloned. Size-selected on agarose gel,

average insert size 500 bp. Primary library,

non-amplified."

BASE COUNT 92 a 35 c 33 g 24 t

ORIGIN

Query Match 2.0%; Score 40; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2000
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 150

RESULT 29

AM302925

LOCUS

xr86g08.x1 NCI-CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767070 3',
199 bp mRNA linear EST 18-JAN-2000

DEFINITION

AM302925
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 199)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco.

FEATURES

source

1. 199

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2767070"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung

adenocarcinoma tissue, cDNA made by oligo-dT priming.

directionally cloned. Size-selected on agarose gel,

average insert size 500 bp. Primary library,

non-amplified."

BASE COUNT 93 a 38 c 40 g 28 t

ORIGIN

Query Match 2.0%; Score 40; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2000
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 150

RESULT 30

AI344928

LOCUS

tb01a04.x1 NCI-CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052270 3',
224 bp mRNA linear EST 30-DEC-1998

DEFINITION

AI344928
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 224)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco.

FEATURES

source

1. 224

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2052270"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung

adenocarcinoma tissue, cDNA made by oligo-dT priming.

directionally cloned. Size-selected on agarose gel,

average insert size 500 bp. Primary library,

non-amplified."

BASE COUNT 119 a 40 c 36 g 29 t

ORIGIN

Query Match 2.0%; Score 40; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2000
Db 128 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 167

RESULT 31

AI336592

LOCUS

ta94d12.x1 NCI-CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2051735 3',
232 bp mRNA linear EST 16-FEB-1999

DEFINITION

AI336592
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.lnl.gov/bdrp/image/image.html
Insert length: 302 Std Error: 0.00
Seq primer: -40UP from GIBCO
High quality sequence stop: 225.
Location/Qualifiers
1. 232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2051735"
/clone_id="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming,
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 44 c 40 g 29 t
ORIGIN
Query Match 2.0%; Score 40; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1961 GCCAGCTAAAAA
Db 134 GCCAGCTAAAAA
RESULT 32 239 bp mRNA linear EST 16-FEB-1999
AI344933
LOCUS tb01a11.x1 NCI-CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052284 3',
DEFINITION mRNA sequence.
ACCESSION AI344933
VERSION AI344933.1 GI:4082139
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.lnl.gov/bdrp/image/image.html
Insert length: 291 Std Error: 0.00
Seq primer: -40UP from GIBCO.
Location/Qualifiers

source
1. 239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052284"
/clone_id="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming,
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN
Query Match 2.0%; Score 40; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1961 GCCAGCTAAAAA
Db 146 GCCAGCTAAAAA
RESULT 33 239 bp mRNA linear EST 30-DEC-1998
AI344936
LOCUS tb01b03.x1 NCI-CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052269 3',
DEFINITION mRNA sequence.
ACCESSION AI344936
VERSION AI344936.1 GI:4082142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.lnl.gov/bdrp/image/image.html
Seq primer: -40UP from GIBCO.
Location/Qualifiers
1. 239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052269"
/clone_id="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming,
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN
Query Match 2.0%; Score 40; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1961 GCCAGCTAAAAA
Db 146 GCCAGCTAAAAA

```

Db      146 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 185
RESULT 34
LOCUS   A1335449      250 bp      mRNA      linear      EST 29-DEC-1998
DEFINITION tb9f03.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2060573 3',
mRNA sequence.
ACCESSION A1335449
VERSION   A1335449.1 GI:4072376
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 250)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            CDNA Library Preparation: David B. Krizman, Ph.D.
            CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.lnl.gov/bbrp/image/image.html
            Seq primer: -400P from Gibco
            High quality sequence stop: 240.
FEATURES
source    Location/Qualifiers
            1..250
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2060573"
            /clone_1lb="NCI_CGAP_Lu26"
            /tissue_type="invasive adenocarcinoma"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Organ: lung; Vector: PAMPI; mRNA made from lung
            adenocarcinoma tissue, CDNA made by oligo-dr priming.
            Directionally cloned. Size-selected on agarose gel,
            average insert size 500 bp. Primary library,
            non-amplified."
BASE COUNT      136 a      43 c      41 g      30 t
ORIGIN
Query Match      2.0%; Score 40; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 134 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 173
RESULT 35
LOCUS   A1494279      360 bp      mRNA      linear      EST 17-MAR-1999
DEFINITION qy98c11.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2020052 3',
similar to WP:B0432.3 CE07741 ;, mRNA sequence.
ACCESSION A1494279
VERSION   A1494279.1 GI:4395282
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 360)
AUTHORS   NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project

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JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.lnl.gov/bbrp/image/image.html
            Insert length: 645 Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 318.
FEATURES
source    Location/Qualifiers
            1..360
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2020052"
            /clone_1lb="NCI_CGAP_Brn25"
            /tissue_type="anaplastic oligodendroglioma"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pRTT3D-Pac (Pharmacia) with a
            modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
            strand CDNA was primed with a Not I - oligo(dT) primer (5'
            TGTTCACATCTGAAGTGGAGCGCGCCACATGCTTTTCTTTTCTTTT
            T 3'); double-stranded CDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pRTT3 vector.
            Library is normalized, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
BASE COUNT      69 a      84 c      97 g      110 t
ORIGIN
Query Match      2.0%; Score 40; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 41 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 36
LOCUS   AA766864      367 bp      mRNA      linear      EST 18-MAR-1998
DEFINITION ocr87g12.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1356742 3',
similar to TR:P90993 P90993 CODED FOR BY C. ELEGANS CDNA YK187H7.5.
ACCESSION AA766864
VERSION   AA766864.1 GI:2818102
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 367)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

```


www.bio.lnl.gov/brp/image/image.html
 Insert Length: 626 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 218.
 Location/Qualifiers

FEATURES

source

1.367

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1356742"

/clone_1lb="NCI CGAP GCBI"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - Oligo(dT) primer

15'-TGTTCACATCTGAAGTGGAGCGCGCCCTCATTTTTTTTTTTT-3'

]. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pRT3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonadio."

BASE COUNT 61 a 88 c 106 g 111 t 1 others

ORIGIN

Query Match 2.0%; Score 40; DB 9; Length 367;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1961 GCCAGCTAAAAA
 Db 51 GCCAGCTAAAAA
 12

RESULT 37
 BQ230307 421 bp mRNA linear EST 02-MAY-2002
 LOCUS BQ230307
 DEFINITION AGENCOURT_7567202 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060433
 5', mRNA sequence.

ACCESSION BQ230307
 VERSION BQ230307.1 GI:20411707
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 421)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM1338 row: 1 column: 02
 High quality sequence stop: 420.
 Location/Qualifiers

FEATURES

source

1.421

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6060433"

/clone_1lb="NIH MGC 68"

/tissue_type="large cell carcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: PCMV-SPORT6; site_1: NotI;

BASE COUNT

155 a 106 c 99 g 61 t

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."

ORIGIN

155 a 106 c 99 g 61 t

Query Match 2.0%; Score 40; DB 14; Length 421;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1961 GCCAGCTAAAAA
 Db 323 GCCAGCTAAAAA
 362

RESULT 38
 BQ127207 442 bp mRNA linear EST 19-APR-2002
 LOCUS BQ127207
 DEFINITION BQ127207.y1 Melton Normalized Mixed Mouse Pancreas 1 NI-MMS1 Mus
 musculus cDNA clone IMAGE:5945796 5' similar to TR:088306 O88306
 DJ-1.; mRNA sequence.

ACCESSION BQ127207
 VERSION BQ127207.1 GI:20201118
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 442)
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
 M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T.,
 Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@bioh.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through LNL. Please contact the IMAGE
 Consortium (info@image.lnl.gov) for further information
 Putative full length read
 vector to vector length is 443
 Seq primer: -40RP from Gibco.

FEATURES

source

1.442

/organism="Mus musculus"

/strain="ICR"

/db_xref="taxon:10090"

/clone="IMAGE:5945796"

/clone_1lb="Melton Normalized Mixed Mouse Pancreas 1

NI-MMS1"

/sex="Both for embryonic & newborn, male for adult and

adult islet"

/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,

adult, mixed"

/lab_host="DH10B"

/note="Vector: pSPORT1. Site_1: Not I; Site_2: Sal I; Five

libraries representing E10.5/12.5 pancreatic bud, E16.5

pancreas, newborn pancreas, adult pancreas, and adult

islets of langerhans were separately constructed using

Superscript Plasmid library kit (Life Technologies). cDNA

was made by oligo-dT priming and size-selected by column

fractionation. Libraries were amplified once on solid

support and plasmid DNA from each library was prepared

and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 137 a 113 c 115 g 77 t

Query Match 2.0%; Score 40; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAA
DB 402 GCCAGCTAAAAA

RESULT 39
LOCUS B55862 503 bp DNA linear GSS 20-JUN-1998
DEFINITION CIT-HSP-2005F16.TF CIT-HSP Homo sapiens genomic clone 2005F16, DNA sequence.

ACCESSION B55862
VERSION B55862.1 GI:2610196
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams M.D., Rounsley S.D., Field C.E., Bass S., Linher K., Golden K., Berry K., Granger D., Sun E., Wible C., Shizuya H., Simon M. and Venter J.C.
TITLE Use of a random BAC End Sequence Database for sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSS: CIT-HSP-2005F16.TF

CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (Info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES
source Location/Qualifiers

1..503
/organism="Homo sapiens"
/db_xref="GDB:7039242"
/db_xref="taxon:9606"
/clone="2005F16"
/clone_11b="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 152 a 116 c 87 g 148 t

Query Match 2.0%; Score 40; DB 17; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1087 AACGAGATGCTAAATCTCTTCTGAAACAGCAATCCAG 1126
DB 502 AACGAGATGCTAAATCTCTTCTGAAACAGCAATCCAG 463

RESULT 40

LOCUS BF968779

DEFINITION BF968779 560 bp mRNA linear EST 22-JAN-2001
602270486F1 NIH-MGC_84 Homo sapiens cDNA clone IMAGE:4358564 5', mRNA sequence.

ACCESSION BF968779
VERSION BF968779.1 GI:12335994
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 560)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.

CONTACT: Robert Strausberg, Ph.D.
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM9996 row 1 column: 21
High quality sequence stop: 155.

FEATURES
source Location/Qualifiers

1..560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4358564"
/clone_11b="NIH-MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo dT primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 261 a 64 c 112 g 123 t

Query Match 2.0%; Score 40; DB 12; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAA
DB 57 GCCAGCTAAAAA

RESULT 41
LOCUS BG491207 616 bp mRNA linear EST 27-MAR-2001
DEFINITION 602535247F1 NIH-MGC_41 Homo sapiens cDNA clone IMAGE:4654258 5', mRNA sequence.
ACCESSION BG491207
VERSION BG491207.1 GI:13452719
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP


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RESULT 44
BM919526      1024 bp      mRNA      linear      EST 12-MAR-2002
LOCUS      AGENCOURT.6761896 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748822
DEFINITION      5', mRNA sequence.
ACCESSION      BM919526
VERSION      BM919526.1 GI:19369905
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgapbs-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://lmage.llnl.gov
              Plate: LLM12777 row: d column: 07
              High quality sequence stop: 606.
              Location/Qualifiers
                1..1024
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_image="5748822"
                /clone_lib="NIH_MGC_120"
                /lab_host="DH10B"
                /note="Organ: pooled pancreas and spleen; Vector:
                PCMV-SPORT6; Site_1: Not; Site_2: EcoRV (destroyed); RNA
                source anonymous pool of spleen and pancreas from 28 yo
                male. Library is oligo-dT primed and directionally cloned
                (EcoRV site is destroyed upon cloning). Average insert
                size 1.5 kb, insert size range 1-2.5 kb. Library is
                normalized and enriched for full-length clones and was
                constructed by C. Gruber (Invitrogen). Research Genetics
                tracking code 025. Note: this is a NIH_MGC library."
BASE COUNT      290 a      262 c      305 g      161 t      6 others
ORIGIN
Query Match      2.0%; Score 40; DB 14; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 577 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 616

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JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              cDNA Library Preparation: David B. Krizman, Ph.D.
              cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/dbp/image/image.html
              Seq primer: 40up from Gibco.
              Location/Qualifiers
                1..160
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_image="1996637"
                /clone_lib="NCI_CGAP_Ov33"
                /sex="female"
                /tissue_type="borderline ovarian carcinoma"
                /dev_stage="adult"
                /lab_host="DH10B"
                /note="Organ: ovary; Vector: pAMP1; mRNA made from
                borderline ovarian carcinoma, cDNA made by oligo-dT
                priming. Directionally cloned. Size-selected on agarose
                gel, average insert size 500 bp. Primary library,
                non-amplified."
BASE COUNT      59 a      38 c      35 g      26 t      2 others
ORIGIN
Query Match      1.9%; Score 39; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1999
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 149

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Search completed: November 8, 2002, 13:32:45
Job time : 2546.85 secs

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RESULT 45
A1305627      160 bp      mRNA      linear      EST 09-DEC-1998
LOCUS      qw72f03.x1 NCI_CGAP_Ov33 Homo sapiens cDNA clone IMAGE:1996637 3',
DEFINITION      mRNA sequence.
ACCESSION      A1305627
VERSION      A1305627.1 GI:3990518
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE      Tumor Gene Index

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 13:01:09 ; Search time 88.8713 Seconds
(without alignments)
8143.939 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgttgatgttgc.....aaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size: 15

Total number of hits satisfying chosen parameters: 20466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCrUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2040	100.0	2040	10 US-09-825-301-7	Sequence 7, Appl1
2	2040	100.0	2040	10 US-09-759-143-375	Sequence 375, App
3	2040	100.0	2040	10 US-09-780-669-375	Sequence 375, App
4	2040	100.0	2040	10 US-09-810-936-303	Sequence 303, App
5	2040	100.0	2040	10 US-09-822-827-375	Sequence 375, App
6	2040	100.0	2040	10 US-09-429-755-303	Sequence 303, App
7	1551	76.0	2000	10 US-09-825-301-6	Sequence 6, Appl1
8	1551	76.0	2000	10 US-09-759-143-374	Sequence 374, App
9	1551	76.0	2000	10 US-09-780-669-374	Sequence 374, App
10	1551	76.0	2000	10 US-09-810-936-302	Sequence 302, App
11	1551	76.0	2000	10 US-09-822-827-374	Sequence 374, App
12	1551	76.0	2000	10 US-09-429-755-302	Sequence 302, App
13	1128	55.3	1155	10 US-09-825-301-5	Sequence 5, Appl1
14	1128	55.3	1155	10 US-09-759-143-373	Sequence 373, App
15	1128	55.3	1155	10 US-09-780-669-373	Sequence 373, App
16	1128	55.3	1155	10 US-09-810-936-301	Sequence 301, App
17	1128	55.3	1155	10 US-09-822-827-373	Sequence 373, App
18	1128	55.3	1155	10 US-09-429-755-301	Sequence 301, App
19	1044	51.2	1590	10 US-09-810-936-323	Sequence 323, App

20	975	47.8	1155	10	US-09-810-936-328	Sequence 328, App
21	491	24.1	1512	10	US-09-759-143-368	Sequence 368, App
22	491	24.1	1512	10	US-09-780-669-368	Sequence 368, App
23	491	24.1	1512	10	US-09-810-936-294	Sequence 294, App
24	491	24.1	1512	10	US-09-822-827-368	Sequence 368, App
25	491	24.1	1512	10	US-09-429-755-294	Sequence 294, App
26	252	12.4	1853	10	US-09-759-143-369	Sequence 369, App
27	252	12.4	1853	10	US-09-780-669-369	Sequence 369, App
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32	120	5.9	879	10	US-09-780-669-531	Sequence 531, App
33	120	5.9	879	10	US-09-810-936-314	Sequence 314, App
34	120	5.9	879	10	US-09-822-827-531	Sequence 531, App
35	120	5.9	879	10	US-09-429-755-314	Sequence 314, App
36	120	5.9	1059	10	US-09-759-143-372	Sequence 372, App
37	120	5.9	1059	10	US-09-780-669-372	Sequence 372, App
38	120	5.9	1059	10	US-09-810-936-298	Sequence 298, App
39	120	5.9	1059	10	US-09-822-827-372	Sequence 372, App
40	120	5.9	1059	10	US-09-429-755-298	Sequence 298, App
41	120	5.9	1851	10	US-09-825-301-1	Sequence 1, Appl1
42	120	5.9	1851	10	US-09-759-143-366	Sequence 366, App
43	120	5.9	1851	10	US-09-780-669-366	Sequence 366, App
44	120	5.9	1851	10	US-09-810-936-291	Sequence 291, App
45	120	5.9	1851	10	US-09-810-936-292	Sequence 292, App

ALIGNMENTS

RESULT 1
US-09-825-301-7
Sequence 7, Application US/09825301
Patent No. US2002009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jianshun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
TITLE OF INVENTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-825-301-7

Query Match 100.0% Score 2040: DB 10: Length 2040:
Best Local Similarity 100.0% Pred. No. 0:
Matches 2040: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ATGTGTGTGAGTGTGATTCATGCGGCTGCTTCTGTGAAGACCATTTGCTC 60
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DB 1 ATGTGTGTGAGTGTGATTCATGCGGCTGCTTCTGTGAAGACCATTTGCTC 60
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QY 61 AGGACCAAGATGGCAAGTGTGCTGCGTTCCTCCCTGCTGAGGAGCGGCAAG 120
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DB 61 AGGACCAAGATGGCAAGTGTGCTGCGTTCCTCCCTGCTGAGGAGCGGCAAG 120
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QY 121 AGCAACGTGGGACCTTGTGAGACCAACGACTGTGATGAACACTGAGGCAAG 180
|||||
DB 121 AGCAACGTGGGACCTTGTGAGACCAACGACTGTGATGAACACTGAGGCAAG 180
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QY 181 ATGGCAAGTGTGCGGCACTGCTCCCTGCTGAGGAGGTGCAAGCAACTG 240
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Db 241 GGGCTTCTTGAGAGCAGCAGACTGTGCTATGAGACACTCAGAAACAAGATGGGCAAG 300
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Db 301 TGGTGTGCCACTGTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
OY 361 GGGAGCTAGCATGACAGTGTCTTCAATGAGCCAGGATCCAGCTCCGTGGAGAGATCTTG 420
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Db 361 GGGAGCTAGCATGACAGTGTCTTCAATGAGCCAGGATCCAGCTCCGTGGAGAGATCTTG 420
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Db 721 AACACTGTGACAGCTATCTATTAATGAAGATTAATTAAGGCAAGAGACAGCTCTTA 780
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Db 1021 GCCAGAGAGATATCTGTTTCTACTCATCATCATGTAATTTTCCAGTTACTTCTGACTAC 1080
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Db 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCAAAAGGCAAGTGAATAAGCCAGCCAGAGAA 1200
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Db 1381 CTTGACACAGCAAAAGTGAAGATATCACAGATTTGGCAATTTACTTTCTGACTCAAAAGAA 1440
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Db 1501 TCAGAGAGAGAGTCCAAAGAGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
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Db 1681 ACTGTGCGCAATGCTGATGATTAATTTCTTCAAGAGAGAGCAAGACACCTGAAAGC 1740
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Db 1741 CAGCAATTTCTGACACTGAGATGAAAGATATCACAGTACCAACAAATTTGATCTACAG 1800
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RESULT 2
US-09-759-143-375
: Sequence 375, Application US/09759143
: Patent No. US200202248A1
: GENERAL INFORMATION:
: APPLICANT: Xu, JIANGCHUN
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, YUQU
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrik
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

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;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C23
;; CURRENT APPLICATION NUMBER: US/09/759,143
;; CURRENT FILING DATE: 2001-01-12
;; NUMBER OF SEQ ID NOS: 934
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 375
;; LENGTH: 2040
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGCTTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGCTTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
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DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATAGAGAGTTGAAGAAATGAAG 1260
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DB 1321 AATGGTAAATGGAATTAATTCCTCAAGAGAGAGCAACCTGAAATCGCAATTT 1380
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DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
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QY 1801 AAGCAATTTTGTGAAGAAAGAACTGGAATTTACAGAGATGAGATTTCTGATTCATGAA 1860
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QY 1861 GAAAGCAGATGAAGTGTGAAGAAATGAATTCGACTTCTGTTAGTTAGTAAAGAA 1920
DB 1861 GAAAGCAGATGAAGTGTGAAGAAATGAATTCGACTTCTGTTAGTTAGTAAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAATATAGTACGTTGCGGAAGAAATTCATGCTTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGCATGAAATATAGTACGTTGCGGAAGAAATTCATGCTTAAGACTG 1980

Db 1921 GAAAAAGACATCTTGATGATAAATAGTACGTTGGGGAGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAATGAACAATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTAGACACAATGAACAATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 3

US-09-780-669-375
; Sequence 375, Application US/09780669
; Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780, 669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-375

Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTGATTCATGCGCGCTGCTCTTGTGAAGAACCATTTGATCTC 60
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QY 1261 AAGCATGAAAGATTAATTAATGTTGGGATTAATGAAACCTGATATGCTGCTGAGC 1320
Db 1261 AAGCATGAAAGATTAATTAATGTTGGGATTAATGAAACCTGATATGCTGCTGAGC 1320
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Db 1321 AATGTCATTAATGATTAATTTCTCAAGAGAGAGCAAGCACTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGGTATCACAGAAATTTGCAATTTAGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGGTATCACAGAAATTTGCAATTTAGTTCTGACTCAAGAA 1440
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Db 1441 AACAGATGCCCCAAATACCTCTCTGAAACACACCAGAACAGACTTAAAGCTGACA 1500
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Db 1501 TCAGAGAGAGTCCACAAAGGCTTGAGGGCAGTGAAGAGGCGACGACAGAGAAAGATCT 1560
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Db 1561 CAGAAGCAGAAATTAATTAAGGATGCTGATAGAGAGCTGAGAAATTTTATGCTATCGAA 1620
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Db 1621 GAAATGAGAGACGAGGAAAGTACTGATGCTGATTCGCCAGAAACCTGACTAATGCTGCC 1680
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Db 1681 ACTGCTGCAATGATGATGATGATGATTAATTCCTCCAGAGAAAGCAGAAACCTGAAAGC 1740
OY 1741 CAGCAATTTCTGACACTGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 1800
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RESULT 4
US-09-810-936-303
; Sequence 303, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-303

Query Match 100.0% Score 2040: DB 10: Length 2040:
Best Local Similarity 100.0%: Pred. No. 0;
Matches 2040: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGCTTGAGCTGATTCATGCCGCTGCTCTTCTGTGAAGAGCAATTTGCTCTC 60

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Db 1441 AAACAGATGCGAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAGGCTGACA 1500
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Db 1621 GAATGAAGAGAGAGCGGAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAGGCTG 1680
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Db 1921 GAAAGAGACATCTTGCATGAAAAATAGTACTGCGGAGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACAAATGAAGACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACAAATGAAGACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 5

US-09-822-827-375
; Sequence 375, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827

; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-375
Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGTGTTGAGGTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
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Dp	901	CTGGATATGATATGGAAGGACTGCTCTCAACTGCTGATATGTTGGATGACAGAACTATA	960
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Dp	961	GTGAGCCTTACTGTGAGCAAAATATGATATGATATGCTCAAGATCTATGCGACAGCG	1020
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Dp	1021	GCCAGAGATGATGCTGTTTCTAGTCATCATATGTAATTTGGCATTACTTTCTGACATAC	1080
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Dp	1081	AAAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATTCAGAACAGACTTAAAG	1140
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Dp	1141	CTGACATCAGAGGAAGGCTCACAAAGGTTCAAAAGCAGTGAATAATGCCAGCGACAGAAA	1200
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Dp	1201	ATGCTCAAGAACACAGAAATAATTAAGCATGGTGATAGAGAGTTGAAGAAGAAATGAG	1260
QY	1261	AAGCATGAAGTAAATAATGTGGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC	1320
Dp	1261	AAGCATGAAGTAAATAATGTGGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC	1320
QY	1321	AATGCTATATATGATTAATTTCTCTCAAGGAAGCAGAACCTGAAAATTCAGCAATT	1380
Dp	1321	AATGCTATATATGATTAATTTCTCTCAAGGAAGCAGAACCTGAAAATTCAGCAATT	1380
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Dp	1381	CCTGACACAGAAAGTGAAGATATCAACAATTTGGCAATTAGTTTCTGATCAGCAAGAA	1440
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QY	1561	CAAGAACACAGAAATAATTAAGATGGTGATAGAGACTTGAATAATTTATGGCTATCGAA	1620
Dp	1561	CAAGAACACAGAAATAATTAAGATGGTGATAGAGACTTGAATAATTTATGGCTATCGAA	1620
QY	1621	GAATATGAAGAAGCAGGAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC	1680
Dp	1621	GAATATGAAGAAGCAGGAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC	1680
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Dp	1741	CAGCAATTTCTGCACTGGAATGAAGATACACAGTGAAGCAAAATGATCTCAG	1800
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Dp	1801	AAGCAATTTTGTGAAGAACAGAACTGGAATTTACACAGATGAGATTTCTGATTCATGAA	1860
QY	1861	GAAGAAGCATAGAGTGTGTAAGAAATGAAATTCGACACTTCTTCTTATGTTTAAGAA	1920
Dp	1861	GAAGAAGCATAGAGTGTGTAAGAAATGAAATTCGACACTTCTTCTTATGTTTAAGAA	1920
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Db      1981 GAGCTGACACATCATGAAACATCAGAGCCAGCTTAAAAAAAAAAAAAAAAAAAAA 2040
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RESULT 6
US-09-429-755-303
; Sequence 303, Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misner, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303
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			Indels	0
			Gaps	0
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1	ATGGTGTGATGAGTTGATTCATGCGCGGCTGCTTCTGTGAAGACGATTTGGTCTC	60		
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61	AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGGCAG	120		
121	AGCAACGTGGGACATTCTTGAGACCAACGACGACTCTGCTATGAACACTCGAGAGCAAG	180		
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601	GTCTCTGACAAACAAAAGAGACAGCTGATTAAGGCGCTCAATGGCAGGAATATA	660		

Db 601 GTCTTGGACACAAAAAGAGACAGCTGTATAAGGCCCTACAAATCCAGAGAAATGAA 660
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Db 1681 ACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAGAGCAACCTGAAAGC 1740

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QY 1741 CAGCAATTTCTCTGACATGAGAAATGAAGAGTATCACAGTACGACGAAATGATTAATCAG 1800
Db 1741 CAGCAATTTCTCTGACATGAGAAATGAAGAGTATCACAGTACGACGAAATGATTAATCAG 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGAGATTTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGAGATTTGATTCATGAA 1860
QY 1861 GAAAGAGATAGAGAGTGTGAAAAATGAATTCAGGCTTCTTACTGTGAAGAA 1920
Db 1861 GAAAGAGATAGAGAGTGTGAAAAATGAATTCAGGCTTCTTACTGTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATGATACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAAAATGATACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAATGAAGATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACACAATGAAGATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 7
US-09-825-301-6
; Sequence 6, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehntner, Barbara
; APPLICANT: Pershing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825, 301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-6

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTGAATTCATGCGGCTGCTCTTCTGAAAGAACCAATTTGGTCTC 60
Db 1 ATGGTGGTGGAGTGAATTCATGCGGCTGCTCTTCTGAAAGAACCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACATCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACATCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGT 240
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QY 241 GCGCTTCTGAGACACAGACACTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300
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QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGCAAGTGGCGCTTGG 360

Db 301 TGTGTGTCACACTGCTTCCCTCCCTGCTGTCAGGGGGAGCGGCAGAGCAAGGTGGCCCTTGG 360
Oy 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCCAGTCCGCTGGAGAAATCTGG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCCAGTCCGCTGGAGAAATCTGG 420
Oy 421 GACAAAGCTCCACAGAGTGCCTGCTGGGGTAAAGTCCCGAGAAAGATCTCATCTCATG 480
Db 421 GACAAAGCTCCACAGAGTGCCTGCTGGGGTAAAGTCCCGAGAAAGATCTCATCTCATG 480
Oy 481 CTCAGGGACACTGACGTACACAGAGGACAAAGAGAGAGTCTCTACATCTGGCC 540
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Db 601 GTCCCTTGACAAACAAAAGAGAGAGACAGTCTGATAAAGCCGCTACATGCGAGAGATGAA 660
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Db 661 TGTGCGTAAATGTTGCTGGAGACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Oy 721 AACACTGCACTACGCTATCTATATGAGTAATTAATTAATGAGCCAAAGCATGCTCTTA 780
Db 721 AACACTGCACTACGCTATCTATATGAGTAATTAATTAATGAGCCAAAGCATGCTCTTA 780
Oy 781 TATGCTGCTGATATGATCAAAAACAAAGCATGCTGACACAGCTGTTACTTGTGTA 840
Db 781 TATGCTGCTGATATGATCAAAAACAAAGCATGCTGACACAGCTGTTACTTGTGTA 840
Oy 841 CATGACGCAAAACACAGAGTGTGTAATTTTATCAAGAAAAACGAATTTAAATGCA 900
Db 841 CATGACGCAAAACACAGAGTGTGTAATTTTATCAAGAAAAACGAATTTAAATGCA 900
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Oy 1261 AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACCTGACTAATGCTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACCTGACTAATGCTGCTGGC 1320
Oy 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGAGCAGAAACCTGAAATATGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGAGCAGAAACCTGAAATATGCAATTT 1380
Oy 1381 CCTGCAACAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGCAACAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440

Oy 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAAAGTCAACAAAGGCTTAGAGGAGGAGTGAATATGAGCAGAGAG 1551
Db 1501 TCAGAGAGAAAGTCAACAAAGGCTTAGAGGAGGAGTGAATATGAGCAGAGAG 1551

RESULT 8
US-09-759-143-374
; Sequence 374, Application US/09759143
; Patent No. US2002002248A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Wang, Aljun
; APPLICANT: Li, Samuel
; APPLICANT: Hepler, William
; APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: Pasted for windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGCTGTGAGTGTGATTCATGCGCGGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTGAGTGTGATTCATGCGCGGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
Oy 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCTCCCTGTCAGAGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCTCCCTGTCAGAGAGAGCGCGCAAG 120
Oy 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGATTAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGATTAAGACACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCGCGCACCTGCTCCCTCTGAGGGGAGTGGCAAGCAAGCTG 240
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Oy 241 GGCCTTCTGAGACACAGACACTCTGATTAAGACACTCAGAGCAAGTGGGCAAG 300
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Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGGCGCTTGG 360


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Db 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
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QY 961 GTGAGCTTCTACTGTGAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAC 1020
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Db 961 GTGAGCTTCTACTGTGAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAC 1020
QY 1021 GCCAGAGAGATGCTGTTCTAGCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
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Db 1021 GCCAGAGAGATGCTGTTCTAGCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
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Db 1081 AAAGAAAAACAGATGCTTAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
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RESULT 9
US-09-780-669-374
; Sequence 374, Application US/09780669
; Patent No. US2002051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780, 669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-780-669-374

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGTGATTCATGCGCGCTGCTCTTGTGAAAGAACCATTTGTCTC 60
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QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGTCAGGAGAGAGCGGCAAG 120
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Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGTCAGGAGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGGAGACACAGAGACTGCTTGAAGACACTCAGAGACAG 180
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QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGTCAGGAGAGAGTGGCAAGACGTG 240
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Db 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGTCAGGAGAGAGTGGCAAGACGTG 240
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QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTCGTAGAAGATCTG 420
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DB 421 GACAAGCTCCACAGAGTGCCTGGTAAAGTCCCGACAGAAAGATCTCATGCTCATG 480
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QY 661 TGTGCGTTAATGTGCTGGACATGGCAGTCCAAATATTCAGATGAGATGGAAT 720
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DB 721 ACCACTGCACTACGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTCTTA 780
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DB 781 TATGCTGCTGATATGCAATCAAAAAACAAGATGGCTCACACCACTGTACTGTGCTA 840
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DB 901 CTGCTAGATATGGAAGAGTGCCTCTACTGCTGATGTTGGATCAGACAGTATA 960
QY 961 GTCAAGCCTTCTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGGACAGC 1020
DB 961 GTCAAGCCTTCTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGGACAGC 1020
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DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCCAGAACAAAGACTTAAG 1140
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DB 1201 ATGCTCAAGAACCGAAATTAATTAAGATGCTGATAGAGGTTGAAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGAGGATTTACTAGAAAACTGACTAATAGGTTGCTCTGGC 1320
DB 1261 AAGCATGAAGATTAATTAATGAGGATTTACTAGAAAACTGACTAATAGGTTGCTCTGGC 1320
QY 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGACAGAACCTGAAATAATGCAATTT 1380
DB 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGACAGAACCTGAAATAATGCAATTT 1380
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QY 1441 AAACAGATCCCAAAATACTCTTGTGAAAAACAGAACCCAGAAACAGACTTAAGCTGACA 1500
DB 1441 AAACAGATCCCAAAATACTCTTGTGAAAAACAGAACCCAGAAACAGACTTAAGCTGACA 1500
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DB 1501 TCAGAGGAAGAGTCAACAAGCTTTAGAGGCACTGAAATTTGGCCAGCCAGAG 1551

RESULT 10
US-09-810-936-302
; Sequence 302, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Skelky, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-810-936-302

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCTTGTGAGTGTGATTCATGCGCGCTGCTCTTCTGTGAAGAACGCAATTTGGTCTC 60
DB 1 ATGCTGCTTGTGAGTGTGATTCATGCGCGCTGCTCTTCTGTGAAGAACGCAATTTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGCTGCGCTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGACCAAGATGGGCAAGTGTGCTGCGCTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAACCAACGACGACTGCTGATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAACCAACGACGACTGCTGATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTCTCTCAGAGGGGAGTGGCAAGAACGCTG 240
DB 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTCTCTCAGAGGGGAGTGGCAAGAACGCTG 240
QY 241 GCGCTTCTGGAACCAACGACGACTGCTGATGAAGACACTCAGAAACAAGTGGGCAAG 300
DB 241 GCGCTTCTGGAACCAACGACGACTGCTGATGAAGACACTCAGAAACAAGTGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTTG 360
DB 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTTG 360
QY 361 GGAGACTACAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTCGTAGAAGATCTG 420
DB 361 GGAGACTACAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTCGTAGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGTGCCTGGTAAAGTCCCGACAGAAAGATCTCATGCTCATG 480
DB 421 GACAAGCTCCACAGAGTGCCTGGTAAAGTCCCGACAGAAAGATCTCATGCTCATG 480

Db 721 ACCACTGTGCACCTAGCTATCTATATGAGATTAATTAATGCGCCAAAGCACTGCTCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACCACTGTTACTTGSTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACCACTGTTACTTGSTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
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Db 901 CTGATATATATGGAAGACGCTCTCATCTGCTATATGTTGGATCAGCAAGTATA 960
Qy 961 GTGACCTCTTACTGAGCAAAATATGATGATCTTCCAAAGATCTATCTGGAGAGAG 1020
Db 961 GTGACCTCTTACTGAGCAAAATATGATGATCTTCCAAAGATCTATCTGGAGAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTGGCACTTCTTCTGACTAC 1080
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Qy 1081 AAAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATAGAGGAAGAGCTCAAAAGGTTCAAGGCACTGAAAAATAGCCAGCCAGAGAA 1200
Db 1141 CTGACATAGAGGAAGAGCTCAAAAGGTTCAAGGCACTGAAAAATAGCCAGCCAGAGAA 1200
Qy 1201 ATGCTCAAGAACAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATTAATGTTGGATTAAGAAACCTGACTAATGTTGCTGCTGCGC 1320
Db 1261 AAGCATGAAGATTAATTAATGTTGGATTAAGAAACCTGACTAATGTTGCTGCTGCGC 1320
Qy 1321 AATGGTGAATGATGATTAATTCCTCAAGGAAGAGACAGAACCCCGAAATATAGCAATTT 1380
Db 1321 AATGGTGAATGATGATTAATTCCTCAAGGAAGAGACAGAACCCCGAAATATAGCAATTT 1380
Qy 1381 CCTGACAAGAAAGTGAAGATATCAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAGAAAGTGAAGATATCAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
Qy 1441 AAACGATGCCAAATTAATCTTTCTGAAAAACAGCAACCAAGAAAGAAAGTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATTAATCTTTCTGAAAAACAGCAACCAAGAAAGAAAGTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATGGCCAGCCAGAG 1551

RESULT 12

US-09-429-755-302
Sequence 302, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.41966
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302
Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGCTTGAAGTGAATTCATGCCGGCTGCTCTTCTGTGAGAGAGCAATTTGCTCTC 60
Db 1 ATGTGCTTGAAGTGAATTCATGCCGGCTGCTCTTCTGTGAGAGAGCAATTTGCTCTC 60
Qy 61 AGGACCAAGATGGGAAGGGTGGCGCTGCTCCCTGCTGAGGGAAGGAGGAGGCGCAAG 120
Db 61 AGGACCAAGATGGGAAGGGTGGCGCTGCTCCCTGCTGAGGGAAGGAGGAGGCGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCGTTCTGGAGACCAAGCACTCTGCTATGAAAGCACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCGTTCTGGAGACCAAGCACTCTGCTATGAAAGCACTCAGAGCAAGTGGGCAAG 300
Qy 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTTGG 360
Qy 361 GGAAGTACAGATGACAGTGCCTTCAAGAGCCAGGATACCAAGTGGGAGAGATCTG 420
Db 361 GGAAGTACAGATGACAGTGCCTTCAAGAGCCAGGATACCAAGTGGGAGAGATCTG 420
Qy 421 GACAAAGCTTCCAGAGAGTGGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTCATG 480
Db 421 GACAAAGCTTCCAGAGAGTGGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTCATG 480
Qy 481 CTCAGGACACTGAGAGTGAAGCAAGAGCAAGCAAGAGAGTCTTACATCTGCGC 540
Db 481 CTCAGGACACTGAGAGTGAAGCAAGAGCAAGCAAGAGAGTCTTACATCTGCGC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Qy 601 GTCCCTTGACAAAAAAGAGACAGTCTGATTAAGGCGCTGCAATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAAAAAGAGAGACAGTCTGATTAAGGCGCTGCAATGCCAGAAATGAA 660
Qy 661 TGTGGCTTAATGTTGCTGGAACATGGACACTGATCCAAATATTCAGATGATGATGAAT 720
Db 661 TGTGGCTTAATGTTGCTGGAACATGGACACTGATCCAAATATTCAGATGATGATGAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATTAATTAATTAATTAATTAAT 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATTAATTAATTAATTAATTAAT 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACCACTGTTACTTGSTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACCACTGTTACTTGSTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATATATGGAAGACGCTCTCATCTGCTATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATATATGGAAGACGCTCTCATCTGCTATATGTTGGATCAGCAAGTATA 960

Qy	961	GTGACGCTTCTACTGTAGGCAAATATTGATGTRATCTTCTCAAGATCTATCTGACACAGC	1020
Db	961	GTGACGCTTCTACTGTAGGCAAATATTGATGTRATCTTCTCAAGATCTATCTGACACAGC	1020
Qy	1021	GCCAGAGATGTGCTGTTTCTAGTCATCATATGTAATTGGCAGTTACTTTCATCACC	1080
Db	1021	GCCAGAGATGTGCTGTTTCTAGTCATCATATGTAATTGGCAGTTACTTTCATCACC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGGAAAGGTGACCAAGGTTCAAAAGCAGTGAATAATAGCCAGCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAAGGTGACCAAGGTTCAAAAGCAGTGAATAATAGCCAGCAGAGAA	1200
Qy	1201	ATGCTCTAAGACACAGAAATTAATTAAGATGGTGATGATGAGAGGTTGAAGAAGAAATGAG	1260
Db	1201	ATGCTCTAAGACACAGAAATTAATTAAGATGGTGATGATGAGAGGTTGAAGAAGAAATGAG	1260
Qy	1261	AAGCATGAAAGTAAATGATGGGATTACTAGAAAACTGACTAATGGTGCTCACTGCTGC	1320
Db	1261	AAGCATGAAAGTAAATGATGGGATTACTAGAAAACTGACTAATGGTGCTCACTGCTGC	1320
Qy	1321	AATGCTGATTAATGGATTAATTTCTCTCAAAGSAGACGAGAACCCTGAAAATTCAGCAATTT	1380
Db	1321	AATGCTGATTAATGGATTAATTTCTCTCAAAGSAGACGAGAACCCTGAAAATTCAGCAATTT	1380
Qy	1381	CCTGACAACGAAATGGAAGATATCACAGAAATTTGGGATTAAGTTTCTGATCTACCAAGAA	1440
Db	1381	CCTGACAACGAAATGGAAGATATCACAGAAATTTGGGATTAAGTTTCTGATCTACCAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTCTTTCTGAAAAACGACAAACCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTTCTGAAAAACGACAAACCAGAACAGACTTAAAGCTGACA	1500
Qy	1501	TCACAGGAAGAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1551
Db	1501	TCACAGGAAGAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1551

```

RESULT 13
US-09-825-301-5
Sequence 5, Application US/09825301
Patent No. US20020009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jiangchun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
FILE OF INVENTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: fastseq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 1155
TYPE: DNA
ORGANISM: Homo sapien
US-09-825-301-5

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Query Match	55.3%	Score 1128:	DB 10:	Length 1155:
Similarity	100.0%	Pred. No. 0:		
Best Local				
Matches 1128:	Conservative	0:	Mismatches	0: Indels
				Gaps 0:
QY	1	ATGCGTGTGAGGTTGATTCATGCGCGGCGTCTTCTGTGTAAGACGCAATTTGGTCTC	60	
db	1	ATGCGGTGTGAGGTTGATTCATGCGCGGCGTCTTCTGTGTAAGACGCAATTTGGTCTC	60	

QY	61	AGGACAGATGGCCAGTGGTGTCTGGCGTTCTTCCCTGCTGCGAGGGAGACGGCGAAG	120
Db	61	AGGAGCAAGATGGGGCAAGTGGTGTCTGGCGTTCTTCCCTGCTGCGAGGGAGACGGCGAAG	120
QY	121	AGCAACGTGGGCACTTCTTGGAGACACAGACACTCTGCTATGAAGCACTACAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTTGGAGACACAGACACTCTGCTATGAAGCACTACAGAGCAAG	180
QY	181	ATGGGCAATGGTGGCGGCGACACTGCTTCCCTGTCGACAGGGGAGTGGCAAGCACTG	240
Db	181	ATGGGCAATGGTGGCGGCGACACTGCTTCCCTGTCGACAGGGGAGTGGCAAGCACTG	240
QY	241	GGCGTTCTTGGAGCCAGACGACTGCTGCTATGAAGCACTCAGGAACAATGGGCAAG	300
Db	241	GGCGTTCTTGGAGCCAGACGACTGCTGCTATGAAGCACTCAGGAACAATGGGCAAG	300
QY	301	TGGTGTCCCACTCTTCCCTGTCTGCGAGGGGAGGGCAAGCAAGGTGGGCGCTTGG	360
Db	301	TGGTGTCTCCACTCTTCCCTGTCTGCGAGGGGAGGGCAAGCAAGGTGGGCGCTTGG	360
QY	361	GGAGACTACGATGACATGGCTTTCATGAGACCCAGGTACCACTGCTGTGGAGAAATCTG	420
Db	361	GGAGACTACGATGACATGGCTTTCATGAGACCCAGGTACCACTGCTGTGGAGAAATCTG	420
QY	421	GACAAGCTCCACAGAGCTGCGTGGTGGGTAAAGTCCCGAAGAAAGATCTCATCTCATG	480
Db	421	GACAAGCTCCACAGAGCTGCGTGGTGGGTAAAGTCCCGAAGAAAGATCTCATCTCATG	480
QY	481	CTCAGGCACTGACGTGTAACAGAGAGCAGCAAAAAGACACTGCTACATCTGGCC	540
Db	481	CTCAGGGAACACTGACGTGAACAGAGAGCAGCAAAAAGACACTGCTACATCTGGCC	540
QY	541	TCTGCAATGGGAATTCAGAAATGATGATTAACCTCTGCTGACAGAGATGCTCAACTTAT	600
Db	541	TCTGCAATGGGAATTCAGAAATGATGATTAACCTCTGCTGACAGAGATGCTCAACTTAT	600
QY	601	GTCCTTGACAACAAAAAGAGACAGCTGTGATAAAGGCGCTACATGCCAGGAGATGAA	660
Db	601	GTCCTTGACAACAAAAAGAGACAGCTGTGATAAAGGCGCTACATGCCAGGAGATGAA	660
QY	661	TGTGCGTTAATGTTGTCGTAACATGGGACACTGATCCAAATTTCCAGATGATGATGAAT	720
Db	661	TGTGCGTTAATGTTGTCGTAACATGGGACACTGATCCAAATTTCCAGATGATGATGAAT	720
QY	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATAAATTAATGAGCAACACTGCTTAA	780
Db	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATAAATTAATGAGCAACACTGCTTAA	780
QY	781	TATGTGCTGATATCGAATCAAAAACAGACATGCGCTCACACACTGTTACTTGGTGA	840
Db	781	TATGTGCTGATATCGAATCAAAAACAGACATGCGCTCACACACTGTTACTTGGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGACTGCTCTCATCTTGCTATGTTGGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGACTGCTCTCATCTTGCTATGTTGGATCAGCAAGTATA	960
QY	961	GTCAGCCTTACACTTGGAGCAAAATATTGATGATTTCTTCAAGATCTATCTGGAACAGG	1020
Db	961	GTCAGCCTTACACTTGGAGCAAAATATTGATGATTTCTTCAAGATCTATCTGGAACAGG	1020
QY	1021	GCCAGAGATGTGCTGTTTCTAGCATCATCATGTAATTTGGCAGTAACTTCTGATCAC	1080
Db	1021	GCCAGAGATGTGCTGTTTCTAGCATCATCATGTAATTTGGCAGTAACTTCTGATCAC	1080
QY	1081	AAAGAAAAACAGATGCTPAAAAATCTCTTGTGAAAACAGCAATCTCAGAA	1128
Db	1081	AAAGAAAAACAGATGCTPAAAAATCTCTTGTGAAAACAGCAATCTCAGAA	1128

```
RESULT 14
US-09-759-143-373
; Sequence 373, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-373

Query Match      55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGTGGTTGAGTGTGATTCATGCCGGCTCTTCTGTGAAGAAGCCATTGGTTC 60
DB      1  ATGGTGGTTGAGTGTGATTCATGCCGGCTCTTCTGTGAAGAAGCCATTGGTTC 60
QY      61  AGGAGCAAGATGGGCAAGTGGTGGCTGGCTGCTCCCTGCGAGGAGAGCCGCAAG 120
DB      61  AGGAGCAAGATGGGCAAGTGGTGGCTGGCTGCTCCCTGCGAGGAGAGCCGCAAG 120
QY      121  AGCAACGTGGGCACTTCTGGAGACGACGACGACTGTCTATGAAGACACTCAGAGCAAG 180
DB      121  AGCAACGTGGGCACTTCTGGAGACGACGACGACTGTCTATGAAGACACTCAGAGCAAG 180
QY      181  ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
DB      181  ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
QY      241  GCGGCTTGGGAGACGACGACTGTCTATGAAGACGACGACGAAAGATGGGCAAG 300
DB      241  GCGGCTTGGGAGACGACGACTGTCTATGAAGACGACGACGAAAGATGGGCAAG 300
QY      301  TGGTGGTGGCACTGCTTCCCTGCTGTCAGAGGGGAGCGGCAAGAGCAAGTGGCGCTTG 360
DB      301  TGGTGGTGGCACTGCTTCCCTGCTGTCAGAGGGGAGCGGCAAGAGCAAGTGGCGCTTG 360
QY      361  GGAGACTAGAGTACAGTGGCTTTCATGAGCCAGTACAGTCCGCTGGAGAAATCTG 420
DB      361  GGAGACTAGAGTACAGTGGCTTTCATGAGCCAGTACAGTCCGCTGGAGAAATCTG 420
QY      421  GACAAGCTCCACAGAGCTCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCTAG 480
DB      421  GACAAGCTCCACAGAGCTCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCTAG 480
QY      481  CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGACTGCTACATCTGGCC 540
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DB      481  CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGACTGCTACATCTGGCC 540
QY      541  TCTGCCAATGGGAATTCAGAAATGTAATTAATCTCTCTGAGACAGAGATGTCACTTAAT 600
DB      541  TCTGCCAATGGGAATTCAGAAATGTAATTAATCTCTCTGAGACAGAGATGTCACTTAAT 600
QY      601  GTCCCTGACACAAAAGAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGGAATGAA 660
DB      601  GTCCCTGACACAAAAGAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGGAATGAA 660
QY      661  TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTAAAT 720
DB      661  TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTAAAT 720
QY      721  ACCACTGCTACAGCTTCTATATATGAAGATTAATTAATGGCCAAAGACAGCTCTTA 780
DB      721  ACCACTGCTACAGCTTCTATATATGAAGATTAATTAATGGCCAAAGACAGCTCTTA 780
QY      781  TATGGTGTGATATGAATCAAAAACAGCATGGCTCACACCACTGTACTTGGTGA 840
DB      781  TATGGTGTGATATGAATCAAAAACAGCATGGCTCACACCACTGTACTTGGTGA 840
QY      841  CATGACCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAACGAATTTAAATGCA 900
DB      841  CATGACCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAACGAATTTAAATGCA 900
QY      901  CTGGATATATGAAGAGACTGCTCATACTTCTGTATGTTGGATCAGCAATATA 960
DB      901  CTGGATATATGAAGAGAGACTGCTCATACTTCTGTATGTTGGATCAGCAATATA 960
QY      961  GTGAGCTCTCTAGTGAATAATATGATGATCTTCAAGATATATCTGGACAGAG 1020
DB      961  GTGAGCTCTCTAGTGAATAATATGATGATCTTCAAGATATATCTGGACAGAG 1020
QY      1021  GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTGCCAGTTCTGACTAC 1080
DB      1021  GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTGCCAGTTCTGACTAC 1080
QY      1081  AAGAAAAACAGATGCTAAATCTTCTTGAAGACGACATTCAGAA 1128
DB      1081  AAGAAAAACAGATGCTAAATCTTCTTGAAGACGACATTCAGAA 1128

RESULT 15
US-09-780-669-373
; Sequence 373, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurlal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
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;; CURRENT FILING DATE: 2001-02-09
;; NUMBER OF SEQ ID NOS: 943
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 373
;; LENGTH: 1155
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-780-669-373

Query Match 55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTGGTGTAGGTTGATTCATCCGCGCTCTCTGTGAAGAAGCCATTGGCTC 60
Db 1 ATGTGGTGTAGGTTGATTCATCCGCGCTCTCTGTGAAGAAGCCATTGGCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGCGCAAG 120

QY 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGTATGAAGACATCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGTATGAAGACATCAGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240

QY 241 GGGCGCTTCTGAGACACAGAGACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGCTTCTGAGACACAGAGACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300

QY 301 TGGGCGCCACAGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGGGCGCCACAGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

QY 361 GGAAGTACATGATGACATGCTTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 420
Db 361 GGAAGTACATGATGACATGCTTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 420

QY 421 GACAAAGTCCACAGAGTGGCTGGTGGGATGAAGTCCCAAGAAAGATCTCATGCTATG 480
Db 421 GACAAAGTCCACAGAGTGGCTGGTGGGATGAAGTCCCAAGAAAGATCTCATGCTATG 480

QY 481 CTCAGGCACTGACGTGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGCACTGACGTGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 541 TCTGCAATGGAATGAGAAATGATTAAGTCTGCTGCAAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TCTGCAATGGAATGAGAAATGATTAAGTCTGCTGCAAGAGAGAGAGAGAGAGAGAGAG 600

QY 601 GTCCCTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCCCTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

QY 661 TGTGCGTAAATGTTGGTGAACATGAGCACTGATCCAATATATTCAGATGATGAGAAAT 720
Db 661 TGTGCGTAAATGTTGGTGAACATGAGCACTGATCCAATATATTCAGATGATGAGAAAT 720

QY 721 ACCACTGTGACATGCTATCTATATGAAGATTAATGAAGCAAGCAAGCAAGCAAGCAAG 780
Db 721 ACCACTGTGACATGCTATCTATATGAAGATTAATGAAGCAAGCAAGCAAGCAAGCAAG 780

QY 781 TATGCTCTGATATGATCAATCAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 TATGCTCTGATATGATCAATCAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

QY 841 CATGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 CATGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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QY 901 CTGATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 CTGATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

QY 961 GTGAGCTTCTACTGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

QY 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080

QY 1081 AAAGAAAAAGAGATGATTAATCTCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
Db 1081 AAAGAAAAAGAGATGATTAATCTCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
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RESULT 16
US-09-810-936-301
; Sequence 301, Application US/09810936
; Patent No. US2002006825A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-301

Query Match 55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTGGTGTAGGTTGATTCATCCGCGCTCTCTGTGAAGAAGCCATTGGCTC 60
Db 1 ATGTGGTGTAGGTTGATTCATCCGCGCTCTCTGTGAAGAAGCCATTGGCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGGAGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGGAGCGCAAG 120

QY 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGTATGAAGACATCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGTATGAAGACATCAGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240

QY 241 GGGCGCTTCTGAGACACAGAGACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGCTTCTGAGACACAGAGACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300

QY 301 TGGGCGCCACAGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGGGCGCCACAGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
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QY 361 GGAGACTAGATGACAGTCCCTTCATGAGACCAGGTACACGCTCCGTGAGAAATCTG 420
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Db 361 GGAGACTAGATGACAGTCCCTTCATGAGACCAGGTACACGCTCCGTGAGAAATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGGGGTAAAGTCCCGAGAAAGATCTCATGTCANG 480
    |||
Db 421 GACAGCTCCACAGAGCTGCTGGGGTAAAGTCCCGAGAAAGATCTCATGTCANG 480
QY 481 CTCAGGAGACCTGAGCTGAAACAAGAGACAAACAAGAGCTCTCATCTGGGCC 540
    |||
Db 481 CTCAGGAGACCTGAGCTGAAACAAGAGACAAACAAGAGCTCTCATCTGGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATCTCACTTAAT 600
    |||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATCTCACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
    |||
Db 601 GTCTCTTGACAAACAAAAGAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
QY 661 TGTGGCTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTTCCAGATGATGAAAT 720
    |||
Db 661 TGTGGCTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTTCCAGATGATGAAAT 720
QY 721 ACCACTCTGACACTACGCTATCTTAATGAAGATTAATTAATGAGCAAGACACTGCTTA 780
    |||
Db 721 ACCACTCTGACACTACGCTATCTTAATGAAGATTAATTAATGAGCAAGACACTGCTTA 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
    |||
Db 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTCGTAATTTTATCAAGAAAAACGAAATTTAATGCA 900
    |||
Db 841 CATGAGCAAAAACAGCAAGCTCGTAATTTTATCAAGAAAAACGAAATTTAATGCA 900
QY 901 CTGAGATAGATGGAAGAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGATA 960
    |||
Db 901 CTGAGATAGATGGAAGAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGATA 960
QY 961 GTACAGCTTCTACTTGAGCAAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
    |||
Db 961 GTACAGCTTCTACTTGAGCAAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATGATGCTGTTCTACTCATCATCATGTAATTTGCCAGTACTTGTGACTAC 1080
    |||
Db 1021 GCCAGAGATGATGCTGTTCTACTCATCATCATGTAATTTGCCAGTACTTGTGACTAC 1080
QY 1081 AAGAAGAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
    |||
Db 1081 AAGAAGAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 17
US-09-822-827-373
; Sequence 373, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.53AC1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-373
Query Match 55.3%; Score 1128; DB 10; Length 1155;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTGGAGGTTAATTCATATGCCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
    |||
Db 1 ATGTGGTGGAGGTTAATTCATATGCCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCGTGCAGGGGAGACGGGCAAG 120
    |||
Db 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCGTGCAGGGGAGACGGGCAAG 120
QY 121 AGCAAGTGGGGCACTTCTGGAGACACAGACAGATCTGCTTAAGACACTCAGAGCAAG 180
    |||
Db 121 AGCAAGTGGGGCACTTCTGGAGACACAGACAGATCTGCTTAAGACACTCAGAGCAAG 180
QY 181 ATGSGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
    |||
Db 181 ATGSGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
QY 241 GGGCCTTCTGGAGACACAGACAGCTGCTTAAGACACTCAGAGCAAGATGGGCAAG 300
    |||
Db 241 GGGCCTTCTGGAGACACAGACAGCTGCTTAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGTGCTGCGACACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGGCGCTTGG 360
    |||
Db 301 TGTGCTGCGACACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTCCCTTCATGAGACCAGGTACACGCTCCGTGAGAAATCTG 420
    |||
Db 361 GGAGACTAGATGACAGTCCCTTCATGAGACCAGGTACACGCTCCGTGAGAAATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCANG 480
    |||
Db 421 GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCANG 480
QY 481 CTCAGGAGACACTGAGCTGAAACAAGAGACAAACAAGAGAGCTCTCATCTGAGCC 540
    |||
Db 481 CTCAGGAGACACTGAGCTGAAACAAGAGACAAACAAGAGAGCTCTCATCTGAGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGAGAGATCTCACTTAAT 600
    |||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGAGAGATCTCACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
    |||
Db 601 GTCTCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
QY 661 TGTGGCTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTTCCAGATGATGAAAT 720
    |||
Db 661 TGTGGCTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTTCCAGATGATGAAAT 720
QY 721 ACCACTCTGACACTACGCTATCTTAATGAAGATTAATTAATGAGCAAGACACTGCTTA 780
    |||
Db 721 ACCACTCTGACACTACGCTATCTTAATGAAGATTAATTAATGAGCAAGACACTGCTTA 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
    |||
Db 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTCGTAATTTTATCAAGAAAAACGAAATTTAATGCA 900
    |||
Db 841 CATGAGCAAAAACAGCAAGCTCGTAATTTTATCAAGAAAAACGAAATTTAATGCA 900
QY 901 CTGAGATAGATGGAAGAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGATA 960
    |||
Db 901 CTGAGATAGATGGAAGAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGATA 960
QY 961 GTACAGCTTCTACTTGAGCAAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
    |||
Db 961 GTACAGCTTCTACTTGAGCAAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATGATGCTGTTCTACTCATCATCATGTAATTTGCCAGTACTTGTGACTAC 1080
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Dh 1021 GCCAGAGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTCTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Dh 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 18

US-09-429-755-301
; Sequence 301, Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-301

Query Match 55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTGTTGAGTTGATTCATCCGCGCTCTCTTCTGGAAGAACCCATTGGTCTC 60
Dh 1 ATGTTGTTGAGTTGATTCATCCGCGCTCTCTTCTGGAAGAACCCATTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTCTGAGGAGGAGGCGCAAG 120
Dh 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTCTGAGGAGGAGGCGCAAG 120
Qy 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTGCTATGAAGACACTGAGGCAAG 180
Dh 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTGCTATGAAGACACTGAGGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGTCGAGGGGAGTGGCAAGCAAGCTG 240
Dh 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGTCGAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGCGCTTCTGAGACACAGACACTGCTATGAAGACACTGAGAAACAGATGGGCAAG 300
Dh 241 GGCGCTTCTGAGACACAGACACTGCTATGAAGACACTGAGAAACAGATGGGCAAG 300
Qy 301 TGTGTTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
Dh 301 TGTGTTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTGTGCTTATGAGAGCCGATACCAAGTCCGCGGAGAAAGTGTG 420
Dh 361 GGAAGCTACGATGACAGTGTGCTTATGAGAGCCGATACCAAGTCCGCGGAGAAAGTGTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGTTGGGTTAAATCCCAAGAAAGATCTATGCTCATG 480
Dh 421 GACAAGCTCCACAGAGCTGCTGTTGGGTTAAATCCCAAGAAAGATCTATGCTCATG 480
Qy 481 CTCAGGGACACTGACGTGAACAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
Dh 481 CTCAGGGACACTGACGTGAACAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
Qy 541 TCTTCCATGGGAATTGAAAGTGTAAATCTCTGCTGACAGACATGTCAACTTAAT 600
Dh 541 TCTTCCATGGGAATTGAAAGTGTAAATCTCTGCTGACAGACATGTCAACTTAAT 600

Dh 541 TCTTCCATGGGAATTGAAAGTGTAAATCTCTGCTGACAGACATGTCAACTTAAT 600
Qy 601 GTCTTTCACACAAAAGAGAGACAGCTCTGATTAAGGCCCTGACATGCGAGAGATGAA 660
Dh 601 GTCTTTCACACAAAAGAGAGACAGCTCTGATTAAGGCCCTGACATGCGAGAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTCAGATGAGTATGAAAT 720
Dh 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTCAGATGAGTATGAAAT 720
Qy 721 ACCACTGTCACACTACGCTATATATGAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780
Dh 721 ACCACTGTCACACTACGCTATATATGAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780
Qy 781 TATGTTGCTGATATGCAATCAAAAACAGATGAGCCCTCACACACAGTTTACTGGTGA 840
Dh 781 TATGTTGCTGATATGCAATCAAAAACAGATGAGCCCTCACACACAGTTTACTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Dh 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATGATATGGAAGAGAGCTGCTCATACTGCTGATAGTTGGATGACAGATATA 960
Dh 901 CTGATGATATGGAAGAGAGCTGCTCATACTGCTGATAGTTGGATGACAGATATA 960
Qy 961 GTCAAGCTTCTACTGTGAGCAAAATATGATATCTCTCAAGATCTATCTGACAGACG 1020
Dh 961 GTCAAGCTTCTACTGTGAGCAAAATATGATATCTCTCTCAAGATCTATCTGACAGACG 1020
Qy 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Dh 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Dh 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 19

US-09-810-936-323
; Sequence 323, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 323
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-323

Query Match 51.2%; Score 1044; DB 10; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 34 TCTTCTGGAAGAACCCATTGGTCTCAGAGCAAGTGGCAAGTGGTGGCGCTTGC 93
Dh 34 TCTTCTGGAAGAACCCATTGGTCTCAGAGCAAGTGGCAAGTGGTGGCGCTTGC 93

Db 469 TCTTCTGTGAAGACCATTTGGTCTCAGAGACAGATGGGCAAGTGGTCTGCCGTTGC 528
QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGGCACTTCTGAGACAGACGAC 153
Db 529 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGGCACTTCTGAGACAGACGAC 568
QY 154 TCTGCTATGAAGACACTCAGAGACAGATGGGCAAGTGGTGGCCACTGCTTCCCTGC 213
Db 589 TCTGCTATGAAGACACTCAGAGACAGATGGGCAAGTGGTGGCCACTGCTTCCCTGC 648
QY 214 TCGAGGGGGAGTGGCAAGACAGTGGGCGCTTCTGAGACAGACAGACTTGTCTATG 273
Db 649 TCGAGGGGGAGTGGCAAGACAGTGGGCGCTTCTGAGACAGACAGACTTGTCTATG 708
QY 274 AAGACACTCAGGAACAAATGGGCAAGTGGTGGCTGCACTGCTTCCCTGCTCAGGGGG 333
Db 709 AAGACACTCAGGAACAAATGGGCAAGTGGTGGCTGCACTGCTTCCCTGCTCAGGGGG 768
QY 334 ACGGGCAAGACAGAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCAATGAGCC 393
Db 769 ACGGGCAAGACAGAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCAATGAGCC 828
QY 394 AGGTACACAGTCCGTGGAAGACAGTCTGACACAGCTCCAGAGCTCCCTGGGTAAA 453
Db 829 AGGTACACAGTCCGTGGAAGACAGTCTGACACAGCTCCAGAGCTCCCTGGGTAAA 888
QY 454 GTCCCAAGAAAGGATCTCATGCTCATGCTCAGGGACACTGAGCTGAACAAAGAGCAAG 513
Db 889 GTCCCAAGAAAGGATCTCATGCTCATGCTCAGGGACACTGAGCTGAACAAAGAGCAAG 948
QY 514 CAAAAGAGGACTGCTTACATCTGCGCTTGGCAATGGAAATCAGAAAGTAAACTC 573
Db 949 CAAAAGAGGACTGCTTACATCTGCGCTTGGCAATGGAAATCAGAAAGTAAACTC 1008
QY 574 CTGCTGAGACAGAGTGTCACTTAATGTCTTGACACAAAAAGAGCAGCTGTGAT 633
Db 1009 CTGCTGAGACAGAGTGTCACTTAATGTCTTGACACAAAAAGAGCAGCTGTGAT 1068
QY 634 AAGGCGCTCAATGGCAGAGATGAAATGGCTTAATGGTGAACATGGCACTGAT 693
Db 1069 AAGGCGCTCAATGGCAGAGATGAAATGGCTTAATGGTGAACATGGCACTGAT 1128
QY 694 CCAAAATATTCAGATGAGTATGGAATACACTCTGACTACGCTATTAATGAAGAT 753
Db 1129 CCAAAATATTCAGATGAGTATGGAATACACTCTGACTACGCTATTAATGAAGAT 1188
QY 754 AAATTAATGCGCAAGCACTGCTTATATATGTGTGATATGGAATCAAAAAAGCAT 813
Db 1189 AAATTAATGCGCAAGCACTGCTTATATATGTGTGATATGGAATCAAAAAAGCAT 1248
QY 814 GGGCTCAGCACTGTTACTTGGTGTACATGAGCAAAAAAGCAAGTCCGTGAATTTTA 873
Db 1249 GGGCTCAGCACTGTTACTTGGTGTACATGAGCAAAAAAGCAAGTCCGTGAATTTTA 1308
QY 874 ATCAAGAAAAAAGCGAATTTAAATGACATGATATGAAAGGAGCTGCTCATACT 933
Db 1309 ATCAAGAAAAAAGCGAATTTAAATGACATGATATGAAAGGAGCTGCTCATACT 1368
QY 934 GCTGATGTGTGATCAGCAAGTATAGTACGCTTCTACTTGAAGCAAAATATGATGA 993
Db 1369 GCTGATGTGTGATCAGCAAGTATAGTACGCTTCTACTTGAAGCAAAATATGATGA 1428
QY 994 TCTTTCAGATCTATCTGAGACAGAGGCGAGAGTATGCTTCTAGTCAATCAT 1053
Db 1429 TCTTTCAGATCTATCTGAGACAGAGGCGAGAGTATGCTTCTAGTCAATCAT 1488
QY 1054 GTAAATTTGCACTTCTGACTCAAAAGAAAAAGATGCTAAATTTCTTTGAA 1113
Db 1489 GTAAATTTGCACTTCTGACTCAAAAGAAAAAGATGCTAAATTTCTTTGAA 1548
QY 1114 AACAGCAATCCAGAA 1128
Db 1549 AACAGCAATCCAGAA 1563

RESULT 20
US-09-810-936-328
; Sequence 328, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Al-jun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-328

Query Match 47.8%; Score 975; DB 10; Length 1155;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTGATTCATCCAGCCGCTGCTTCTGTGGAAGACCATTTGCTTC 60
Db 1 ATGCTGTTGAGGTGATTCATCCAGCCGCTGCTTCTGTGGAAGACCATTTGCTTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGAGAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGAGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGGAGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGGAGAGTGGCAAGCAAGT 240
QY 241 GGGCTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
Db 241 GGGCTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGAGGAGGCGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGAGGAGGCGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGGCTTCAATGAGCCAGGTACCACTGCTGAGAGATCTG 420
Db 361 GGAGACTAGATGACAGTGGCTTCAATGAGCCAGGTACCACTGCTGAGAGATCTG 420
QY 421 GACAGCTCAGAGAGCTGCTGAGAGGAGTAAAGTCCCAAGAGATCTCATCTCAT 480
Db 421 GACAGCTCAGAGAGCTGCTGAGAGGAGTAAAGTCCCAAGAGATCTCATCTCAT 480
QY 481 CTGAGGAGCACTGCTGAGAGGAGCAAGCAAGAGAGAGTCTGCTCATCTCAT 540
Db 481 CTGAGGAGCACTGCTGAGAGGAGCAAGCAAGAGAGAGTCTGCTCATCTCAT 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGAGAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGAGAGAGATGTCAACTTAAT 600

Oy	601	GTTGTGCAACAAAAGAGACAGCGCTGGATGAAGCCGTCACAAATGCCAGGAACATAA	660
Oy	601	GTTGTGCAACAAAAGAGACAGCGCTGGATGAAGCCGTCACAAATGCCAGGAACATAA	660
Dd	601	GTTCTTGACAACAAAAGAGACAGCGCTGGATGAAGCCGTCACAAATGCCAGGAACATAA	660
Oy	661	TGTGCATTAAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTCACAGTAGTATGAAT	720
Dd	661	TGTGCATTAAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTCACAGTAGTATGAAT	720
Oy	721	ACCAGCTGTGCAGCTACGCTATCTATTAATGAAGAATAAATTATATGGCCAAAGACTGCTTTA	780
Dd	721	ACCAGCTGTGCAGCTACGCTATCTATTAATGAAGAATAAATTATATGGCCAAAGACTGCTTTA	780
Oy	781	TATGTGCTGTATATGCAATCAAAAAAACAGCATGGCGCTCACACACACTGTTACTTGGTGA	840
Dd	781	TATGTGCTGTATATGCAATCAAAAAAACAGCATGGCGCTCACACACACTGTTACTTGGTGA	840
Oy	841	CATGAGCAAAAAACGCAAGTCGTGAATTTTTATCAAGAAAAAAAGCGAATTTAAATGCA	900
Dd	841	CATGAGCAAAAAACGCAAGTCGTGAATTTTTATCAAGAAAAAAAGCGAATTTAAATGCA	900
Oy	901	CTGGATGGATATGGAAGAGCTGCGTCATACCTTGCTGTATGTTGGAGTACACAGATATA	960
Dd	901	CTGGATGGATATGGAAGAGCTGCGTCATACCTTGCTGTATGTTGGAGTACACAGATATA	960
Oy	961	GTCAGCCTTCTACTTGGACAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG	1020
Dd	961	GTCAGCCTTCTACTTGGACAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG	1020
Oy	1021	GCCAGAGAGTATGCTGTTTCTTACATCATCATCATGTAATTTGGCAGTACTTCTGACTAC	1080
Dd	1021	GCCAGAGAGTATGCTGTTTCTTACATCATCATCATGTAATTTGGCAGTACTTCTGACTAC	1080
Oy	1081	AAGAGAAAAACAGATGCTTAAATCTCTTCTGAAACAGCAATCCAGAA	1128
Dd	1081	AAGAGAAAAACAGATGCTTAAATCTCTTCTGAAACAGCAATCCAGAA	1128
 RESULT 21 US-09-759-143-368 ; Sequence 368, Application US/09759143 ; Patent NO. US2002002248A1 ; GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqul APPLICANT: Henderson, Robert A. APPLICANT: Kalos, Michael D. APPLICANT: Fanger, Gary R. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darriek APPLICANT: Li, Samuel APPLICANT: Wang, Aljun APPLICANT: Skelley, Yasir A.W. APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE: 210121.4ZJC23 CURRENT APPLICATION NUMBER: US/09/759,143 NUMBER OF SEQ ID NOS: 934 SOFTWARE: FastSeq for Windows Version 3.0 SEQ ID NO 368 LENGTH: 1512 TYPE: DNA ORGANISM: Homo sapien US-09-759-143-368			

Query Match	24.1%	Score 491;	DB 10;	Length 1512;
Best Local Similarity	99.4%;	Pred. No. 8e-180;		
Matches 691;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

OY	34	TCCTCTGTGAAGAAAGCCATTGGTCTCAGAGACAAAGATGGGCAAGTGGTCTGCGCTTGC	93
Db	256	TCCTTCTGTGAAGAAAGCCATTGGTCTCAGAGACAAAGATGGGCAAGTGGTCTGCGCTTGC	31.5
OY	94	TTCCCTCTCTCAGGAGAAAGCGGCAAGAGCAACGTGGGCACTTCTTGAGACCAAGAC	15.3
Db	316	TTCCCTCTCTCAGGAGAAAGCGGCAAGAGCAACGTGGGCACTTCTTGAGACCAAGAC	37.5
OY	154	TCCTCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCTTCCCTTCCCTGC	21.3
Db	376	TCCTCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCTTCCCTTCCCTGC	43.5
OY	214	TGCAGGGGAGCTGGCAAGACAGTGGGCGCTTCGAGACCAAGCACTGCTATG	27.3
Db	436	TGCAGGGGAGCTGGCAAGACAGTGGGCGCTTCGAGACCAAGCACTGCTATG	49.5
OY	274	AAGACACTCAGAGAAACAGATGGGCAAGTGTGTCCACTGCTTCCCTCTGCAAGGGG	33.3
Db	496	AAGACACTCAGAGAAACAGATGGGCAAGTGTGTCCACTGCTTCCCTCTGCAAGGGG	55.5
OY	334	AGCGGCAAGACCAAGTGGGCGCTTGGGAGACTACGATGACAGTGGCTTCATGAGAGCC	39.3
Db	556	AGCGCAAGACCAAGTGGGCGCTTGGGAGACTACGATGACAGTGGCTTCATGAGAGCC	61.5
OY	394	AGGTACCAAGTCCGTGGGAGAAAGATCTGTGACCAAGCTCCACAGAGCTGCTGGTGGGATAA	45.3
Db	616	AGGTACCAAGTCCGTGGGAGAAAGATCTGTGACCAAGCTCCACAGAGCTGCTGGTGGGATAA	67.5
OY	454	GTCCCCAAGAAAGATCTATCTGTATGCTCAGAGGACACTGACGTGAACAAGAGACAAAG	51.3
Db	676	GTCCCCAAGAAAGATCTATCTGTATGCTCAGAGGACACTGACGTGAACAAGAGACAAAG	73.5
OY	514	CAAAAGAGAGACTGCTCTCATCTGTGACCTCTCCAAATGGGAATTGAGAAATGATAAACTC	57.3
Db	736	CAAAAGAGAGACTGCTCTCATCTGTGACCTCTCCAAATGGGAATTGAGAAATGATAAACTC	79.5
OY	574	CTGTGTGACAGACAGATGTCAACTTAATGTCTTGAACAACAAAAAGAGACAGCTCTGATA	63.3
Db	796	STGCTGTGACAGACAGATGTCAACTTAATGTCTTGAACAACAAAAAGAGACAGCTCTGATA	85.5
OY	634	AAGGCGGACAAATGCGCAGAGAAAGATGAATGCGTTAATGTTGCGGAAACATGGCACATGAT	69.3
Db	856	AAGGCGGACAAATGCGCAGAGAAAGATGAATGCGTTAATGTTGCGGAAACATGGCACATGAT	91.5
OY	694	CCAAATATTCAGATGAGATGAGAAATACCACTCT	728
Db	916	CCAAATATTCAGATGAGATGAGAAATACCACTCT	950
RESULT 22			
US-09-780-669-368			
Sequence 368, Application US/09780669			
Patent No. US2002005197A1			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Davin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan L.			
APPLICANT: Jiang, Yuyu			
APPLICANT: Henderson, Robert A.			
APPLICANT: Kalos, Michael D.			
APPLICANT: Fanger, Gary R.			
APPLICANT: Retter, Marc W.			
APPLICANT: Stolk, John A.			
APPLICANT: Day, Craig H.			
APPLICANT: Vedvick, Thomas S.			
APPLICANT: Carter, Darrick			
APPLICANT: Li, Samuel			
APPLICANT: Wang, Aljun			

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 368
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-368

Query Match 24.1%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTGTGGAAGAACCCATTGGTCTCAGAGCAAGATGGCAAGTGGTCTGCCGTTGC 93
DB 256 TCTTGTGGAAGAACCCATTGGTCTCAGAGCAAGATGGCAAGTGGTCTGCCGTTGC 315
QY 94 TTCCCTGCTGAGGAGAGGCGGCAAGCAAGTGGGCACTTCTGGAGACCAGCAGAC 153
DB 316 TTCCCTGCTGAGGAGAGGCGGCAAGCAAGTGGGCACTTCTGGAGACCAGCAGAC 375
QY 154 TCTGTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 213
DB 376 TCTGTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTCTGTATG 495
QY 274 AAGCACTCAGGACAAAGATGGGCAAGTGGTGGCCACTGTTCCCTGCTGCAAGGGG 333
DB 496 AAGCACTCAGGACAAAGATGGGCAAGTGGTGGCCACTGTTCCCTGCTGCAAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCC 615
QY 394 AGTACCACTGCTCCGTGGAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 453
DB 616 AGTACCACTGCTCCGTGGAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 675
QY 454 GTCCCGCAAGAGATGTCATGTATGTCTCAGGGCACTGACGTGAACAAGAGCAAG 513
DB 676 GTCCCGCAAGAGATGTCATGTATGTCTCAGGGCACTGACGTGAACAAGAGCAAG 735
QY 514 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTGAATAACTC 573
DB 736 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTGAATAACTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGAACAACAAAAGAGAGACGCTGTGATA 633
DB 796 CTGCTGACAGACGATGTCAACTTAATGTCTTGAACAACAAAAGAGAGACGCTGTGATA 855
QY 634 AAGGCCGTACAAATGCCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 693
DB 856 AAGGCCGTACAAATGCCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 915
QY 694 CCAATATTCAGATGAGTATGAAATACCACTCT 728
DB 916 CCAATATTCAGATGAGTATGAAATACCACTCT 950

RESULT 23
US-09-810-936-294

Sequence 294, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 294
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-294

Query Match 24.1%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTGTGGAAGAACCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCTGCCGTTGC 93
DB 256 TCTTGTGGAAGAACCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCTGCCGTTGC 315
QY 94 TTCCCTGCTGAGGAGAGGCGGCAAGCAAGTGGGCACTTCTGGAGACCAGCAGAC 153
DB 316 TTCCCTGCTGAGGAGAGGCGGCAAGCAAGTGGGCACTTCTGGAGACCAGCAGAC 375
QY 154 TCTGTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 213
DB 376 TCTGTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTCTGTATG 495
QY 274 AAGCACTCAGGACAAAGATGGGCAAGTGGTGGCCACTGTTCCCTGCTGCAAGGGG 333
DB 496 AAGCACTCAGGACAAAGATGGGCAAGTGGTGGCCACTGTTCCCTGCTGCAAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCC 615
QY 394 AGTACCACTGCTCCGTGGAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 453
DB 616 AGTACCACTGCTCCGTGGAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 675
QY 454 GTCCCGCAAGAGATGTCATGTATGTCTCAGGGCACTGACGTGAACAAGAGCAAG 513
DB 676 GTCCCGCAAGAGATGTCATGTATGTCTCAGGGCACTGACGTGAACAAGAGCAAG 735
QY 514 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTGAATAACTC 573
DB 736 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTGAATAACTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGAACAACAAAAGAGAGACGCTGTGATA 633
DB 796 CTGCTGACAGACGATGTCAACTTAATGTCTTGAACAACAAAAGAGAGACGCTGTGATA 855
QY 634 AAGGCCGTACAAATGCCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 693
DB 856 AAGGCCGTACAAATGCCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 915

QY 694 CCAAAATATTCAGATGATGGAATACCACTCT 728
|
Db 916 CCAAAATATTCAGATGATGGAATACCACTCT 950

RESULT 24

US-09-822-827-368
; Sequence 368, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-368

Query Match 24.1%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGTGCTCAGAGCAAGATGGGCAAGTGTCTGCGCTTGC 93
|
Db 256 TCTTCTGTGAAGAGCCATTGTGCTCAGAGCAAGATGGGCAAGTGTCTGCGCTTGC 315
|
QY 94 TTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACAGAGAGC 153
|
Db 316 TTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACAGAGAGC 375
|
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGGCACTTCCCTGC 213
|
Db 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGGCACTTCCCTGC 435
|
QY 214 TCGAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTGCTATG 273
|
Db 436 TCGAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTGCTATG 495
|
QY 274 AAGACACTCAGAAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
|
Db 496 AAGACACTCAGAAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
|
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGTGCTTATGAGGCC 393
|
Db 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGTGCTTATGAGGCC 615
|
QY 394 AGGTACCACTGCTGAGAGCAAGTGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 453
|
Db 616 AGGTACCACTGCTGAGAGCAAGTGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 675
|
QY 454 GTCCCGAAGAAAGATGTCATGCTGAGGAGCACTGAGTGAACAAGAGAGCAAG 513
|
Db 676 GTCCCGAAGAAAGATGTCATGCTGAGGAGCACTGAGTGAACAAGAGAGCAAG 755
|
QY 514 CAAAAGAGAGTCTGCTACATCTGGGCTTGGCAATGGGAATTCAGAAAGTAAACTC 573
|
Db 736 CAAAAGAGAGTCTGCTACATCTGGGCTTGGCAATGGGAATTCAGAAAGTAAACTC 795
|
QY 574 CTGCTGAGAGAGATGTCATTAATGTCTTGAACAACAAAAGAGAGAGAGCTGTGATA 633
|
Db 796 CTGCTGAGAGAGATGTCATTAATGTCTTGAACAACAAAAGAGAGAGAGCTGTGATA 855
|
QY 634 AAGGCGTCAATGGAGAGAGATGATGCGTTAATGTGGAACAATGGCACTGAT 693
|
Db 856 AAGGCGTCAATGGAGAGAGATGATGCGTTAATGTGGAACAATGGCACTGAT 915
|

QY 694 CCAAAATATTCAGATGATGGAATACCACTCT 728
|
Db 916 CCAAAATATTCAGATGATGGAATACCACTCT 950

RESULT 25

US-09-429-755-294
; Sequence 294, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 294
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-294

Query Match 24.1%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGTGCTCAGAGCAAGATGGGCAAGTGTCTGCGCTTGC 93
|
Db 256 TCTTCTGTGAAGAGCCATTGTGCTCAGAGCAAGATGGGCAAGTGTCTGCGCTTGC 315
|
QY 94 TTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACAGAGAGC 153
|
Db 316 TTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACAGAGAGC 375
|
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGGCACTTCCCTGC 213
|
Db 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGTGCGGCACTTCCCTGC 435
|
QY 214 TCGAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTGCTATG 273
|
Db 436 TCGAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGCACTGCTATG 495
|
QY 274 AAGACACTCAGAAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
|
Db 496 AAGACACTCAGAAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
|
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGTGCTTATGAGGCC 393
|
Db 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGTGCTTATGAGGCC 615
|
QY 394 AGGTACCACTGCTGAGAGCAAGTGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 453
|
Db 616 AGGTACCACTGCTGAGAGCAAGTGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 675
|
QY 454 GTCCCGAAGAAAGATGTCATGCTGAGGAGCACTGAGTGAACAAGAGAGCAAG 513
|
Db 676 GTCCCGAAGAAAGATGTCATGCTGAGGAGCACTGAGTGAACAAGAGAGCAAG 755
|
QY 514 CAAAAGAGAGTCTGCTACATCTGGGCTTGGCAATGGGAATTCAGAAAGTAAACTC 573
|
Db 736 CAAAAGAGAGTCTGCTACATCTGGGCTTGGCAATGGGAATTCAGAAAGTAAACTC 795
|
QY 574 CTGCTGAGAGAGATGTCATTAATGTCTTGAACAACAAAAGAGAGAGAGCTGTGATA 693
|
Db 796 CTGCTGAGAGAGATGTCATTAATGTCTTGAACAACAAAAGAGAGAGAGCTGTGATA 855
|

QY 634 AAGCCGTACATGCGCAGGAAGATGTCGTTAATGTCGTGACACTGAT 693
| | | | |
DB 856 AAGCGGTACATGCGCAGGAAGATGTCGTTAATGTCGTGACACTGAT 915
QY 694 CCAATATTCAGATGATGGAATACACTCT 728
| | | | |
DB 916 CCAATATTCAGATGATGGAATACACTCT 950

RESULT 26

US-09-759-143-369
; Sequence 369, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 369
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-369

Query Match 12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGTCCTCAGAGCAGATGGGCAAGTGGTGCCTGTC 93
| | | | |
DB 256 TCTTCTGTGAAGAGCCATTGTCCTCAGAGCAGATGGGCAAGTGGTGCCTGTC 315
QY 94 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAAGTGGCACTTCTGAGACCAAGAGCAG 153
| | | | |
DB 316 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAAGTGGCACTTCTGAGACCAAGAGCAG 375
QY 154 TCTGCTATGAGAGCACTCAGAGAGCAAGATGGCAAGTGGTCCCGCACTGCTTCCCTG 213
| | | | |
DB 376 TCTGCTATGAGAGCACTCAGAGAGCAAGATGGCAAGTGGTCCCGCACTGCTTCCCTG 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGAGTGGGCGCTTCTGAGACCAAGAGCAAGTGGTATG 273
| | | | |
DB 436 TGCAGGGGAGTGGCAAGAGCAAGAGTGGGCGCTTCTGAGACCAAGAGCAAGTGGTATG 495
QY 274 AAGACACTCAGAGAGCAAGATGGGCAAGTGGTCTGCACTGCTTCCCTGTCAGAGGGG 333
| | | | |
DB 496 AAGACACTCAGAGAGCAAGATGGGCAAGTGGTCTGCACTGCTTCCCTGTCAGAGGGG 555
QY 334 AGC 336
| | |
DB 556 AGC 558

RESULT 27

US-09-780-669-369
; Sequence 369, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 369
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-369

Query Match 12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGTCCTCAGAGCAGATGGGCAAGTGGTGCCTGTC 93
| | | | |
DB 256 TCTTCTGTGAAGAGCCATTGTCCTCAGAGCAGATGGGCAAGTGGTGCCTGTC 315
QY 94 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAAGTGGCACTTCTGAGACCAAGAGCAG 153
| | | | |
DB 316 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAAGTGGCACTTCTGAGACCAAGAGCAG 375
QY 154 TCTGCTATGAGAGCACTCAGAGAGCAAGATGGCAAGTGGTCCCGCACTGCTTCCCTG 213
| | | | |
DB 376 TCTGCTATGAGAGCACTCAGAGAGCAAGATGGCAAGTGGTCCCGCACTGCTTCCCTG 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGAGTGGGCGCTTCTGAGACCAAGAGCAAGTGGTATG 273
| | | | |
DB 436 TGCAGGGGAGTGGCAAGAGCAAGAGTGGGCGCTTCTGAGACCAAGAGCAAGTGGTATG 495
QY 274 AAGACACTCAGAGAGCAAGATGGGCAAGTGGTCTGCACTGCTTCCCTGTCAGAGGGG 333
| | | | |
DB 496 AAGACACTCAGAGAGCAAGATGGGCAAGTGGTCTGCACTGCTTCCCTGTCAGAGGGG 555
QY 334 AGC 336
| | |
DB 556 AGC 558

RESULT 28

US-09-810-936-295
; Sequence 295, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.

APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810.936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-295

Query Match 12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCGTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCGTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGCGGCAAGCAAGCTGGGCACTTCTGAGACCAAGAGAGC 153
DB 316 TTCCCTGTGTCAGAGGAGCGGCAAGCAAGCTGGGCACTTCTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGAGCACTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGAGCACTGCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGTCAGGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGTCAGGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 29
US-09-822-827-369
Sequence 369, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TREATMENT OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 369
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-822-827-369

Query Match 12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCGTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCGTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGCGGCAAGCAAGCTGGGCACTTCTGAGACCAAGAGAGC 153
DB 316 TTCCCTGTGTCAGAGGAGCGGCAAGCAAGCTGGGCACTTCTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGAGCACTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGAGCACTGCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGTCAGGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGTCAGGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 30
US-09-429-755-295
Sequence 295, Application US/09429755A
Patent No. US2002011167A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429.755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-295

Query Match 12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCGTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCGTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGCGGCAAGCAAGCTGGGCACTTCTGAGACCAAGAGAGC 153
DB 316 TTCCCTGTGTCAGAGGAGCGGCAAGCAAGCTGGGCACTTCTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGAGCACTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACCAAGAGCACTGCTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGTCAGGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTGTTCCCTGTCAGGGGG 555

QY 334 AGC 336
|||
DB 556 AGC 558

RESULT 31
US-09-759-143-531

; Sequence 531, Application US/09759143
; Patent No. US20020022248A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-531

Query Match 5.9%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
|||
DB 333 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 392
|||
QY 567 AAAAAGCTCGTGGAGAGAGATGTCACCTTAATGCTTGCACACAAAAGAGAGACAGC 626
|||
DB 393 AAAAAGCTCGTGGAGAGAGATGTCACCTTAATGCTTGCACACAAAAGAGAGACAGC 452
|||
QY 627 TCTGATTAAGGCCGTACATATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
|||
DB 453 TCTGATTAAGGCCGTACATATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 512
|||
QY 687 CACTGATCCAAATATTCAGATGAGTGAATATCCACTCT 728
|||
DB 513 CACTGATCCAAATATTCAGATGAGTGAATATCCACTCT 554
|||

RESULT 32
US-09-780-669-531

; Sequence 531, Application US/09780669

; Patent No. US20020051977A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-531

Query Match 5.9%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
|||
DB 333 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 392
|||
QY 567 AAAAAGCTCGTGGAGAGATGTCACCTTAATGCTTGCACACAAAAGAGAGACAGC 626
|||
DB 393 AAAAAGCTCGTGGAGAGATGTCACCTTAATGCTTGCACACAAAAGAGAGACAGC 452
|||
QY 627 TCTGATTAAGGCCGTACATATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
|||
DB 453 TCTGATTAAGGCCGTACATATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 512
|||
QY 687 CACTGATCCAAATATTCAGATGAGTGAATATCCACTCT 728
|||
DB 513 CACTGATCCAAATATTCAGATGAGTGAATATCCACTCT 554
|||

RESULT 33
US-09-810-936-314

; Sequence 314, Application US/09810936

; Patent No. US20020068285A1

GENERAL INFORMATION:

; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 314
; LENGTH: 879
; TYPE: DNA

```

; ORGANISM: Homo sapiens
US-09-810-936-314

Query Match          5.9%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0

OY 507 GGACAGCAAGCAAAAGAGACGCTCTCFACATCTGGCCCTCTGCGCAATGGGAATTCCAGAACTAGT 566
DB 333 GGACAGCAAGCAAAAGAGACGCTCTCFACATCTGGCCCTCTGCGCAATGGGAATTCCAGAACTAGT 392
OY 567 AAAACTCCTGCTGACAGACGATGTCACCTTAATGTCTTGACAACAAAAGAGACAGC 626
DB 393 AAAACTCGGCTGGACAGACGATGTCACCTTAATGTCTTGACAACAAAAGAGACAGC 452
OY 627 TCTGATTAAGGCGGACATGCGCAGAGATGAATGTGGTTAATGTCTGGAACATGG 686
DB 453 TCTGCAAAAGGCGGACATGCGCAGAGATGAATGAATGTGGTTAATGTCTGGAACATGG 512
OY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
DB 513 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 554

RESULT 34
US-09-822-827-531
; Sequence 531, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-531

Query Match          5.9%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0

OY 507 GGACAGCAAGCAAAAGAGACGCTCTCFACATCTGGCCCTCTGCGCAATGGGAATTCCAGAACTAGT 566
DB 333 GGACAGCAAGCAAAAGAGACGCTCTCFACATCTGGCCCTCTGCGCAATGGGAATTCCAGAACTAGT 392
OY 567 AAAACTCCTGCTGACAGACGATGTCACCTTAATGTCTTGACAACAAAAGAGACAGC 626
DB 393 AAAACTCGGCTGGACAGACGATGTCACCTTAATGTCTTGACAACAAAAGAGACAGC 452
OY 627 TCTGATTAAGGCGGACATGCGCAGAGATGAATGTGGTTAATGTCTGGAACATGG 686
DB 453 TCTGCAAAAGGCGGACATGCGCAGAGATGAATGAATGTGGTTAATGTCTGGAACATGG 512
OY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
DB 513 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 554

RESULT 35
US-09-429-755-314
; Sequence 314, Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda

```

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 314
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-429-755-314

Query Match          5.9%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2,3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGACGAAAAGAGGAGCGCTCTACATCTTGCGCCCTCTGCCATGGGAATTCAGAGTGT 566
    |||||||
Db 333 GGACAGACGAAAAGAGGAGCGCTCTACATCTTGCGCCCTCTGCCAATGGGAATTCAGAGTGT 392
    |||||||

QY 567 AAAATCTCGTGGAGACAGACGATGTCACCTTAATGTCTTGACACAAAAGAGACAGC 626
    |||||||
Db 393 AAAATCTCGTGGAGACAGACGATGTCACCTTAATGTCTTGACACAAAAGAGACAGC 452
    |||||||

QY 627 TCTGTATAAAGCGCGGTACATGCCAGAGAGATGTGGCTTAAATGTGCTGGAACATGG 686
    |||||||
Db 453 TCTGTACAAAGCGCGGTACATGCCAGAGAGATGTGGCTTAAATGTGCTGGAACATGG 512
    |||||||

QY 687 CACGTATCCAAATATATCCAGATGATATAGGAATACCACTCT 728
    |||||||
Db 513 CACTGATCCAAATATATCCAGATGATATAGGAATACCACTCT 554
    |||||||

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RESULT 36
US-09-759-143-372
; Sequence 372, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-372

Query Match          5.9%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2,3e-37;

```


Query Match 5.9%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGGAATTGCAAGTAGT 566
DB 276 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGGAATTGCAAGTAGT 335
QY 567 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 395
QY 627 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 396 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
DB 456 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 497

RESULT 40

US-09-429-755-298
Sequence 298, Application US/09429755A
Patent No. US2002011467A1

GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 298
LENGTH: 1059
TYPE: DNA
ORGANISM: Homo sapien

Query Match 5.9%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGGAATTGCAAGTAGT 566
DB 276 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGGAATTGCAAGTAGT 335
QY 567 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 395
QY 627 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 396 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
DB 456 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 497

RESULT 41

US-09-825-301-1/C
Sequence 1, Application US/09825301
Patent No. US20020009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, Davin C.

APPLICANT: Molesch, David A.
APPLICANT: Xu, Jianshun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1851
TYPE: DNA
ORGANISM: Homo sapien

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGGAATTGCAAGTAGT 566
DB 791 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGGAATTGCAAGTAGT 732
QY 567 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 626
DB 731 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
DB 611 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 570

RESULT 42

US-09-759-143-366/C
Sequence 366, Application US/09759143
Patent No. US2002022248A1

GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 366
LENGTH: 1851
TYPE: DNA
ORGANISM: Homo sapien

US-09-759-143-366

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 566
|||||
DB 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 732

QY 567 AAAACTCGTGGAGACAGATGTCACACTTAATGCTGTGACCAAAAAGAGACAGC 626
|||||
DB 731 AAAACTCGTGGAGACAGATGTCACACTTAATGCTGTGACCAAAAAGAGACAGC 672

QY 627 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 686
|||||
DB 671 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 612

QY 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
|||||
DB 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 43
US-09-780-669-366/c
; Sequence 366, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: JIang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-366

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 566
|||||
DB 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 732

QY 567 AAAACTCGTGGAGACAGATGTCACACTTAATGCTGTGACCAAAAAGAGACAGC 626
|||||
DB 731 AAAACTCGTGGAGACAGATGTCACACTTAATGCTGTGACCAAAAAGAGACAGC 672

QY 627 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 686
|||||
DB 611 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 686

DB 671 TCTGCAAAAGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 612
QY 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
|||||
DB 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 44
US-09-810-936-291/c
; Sequence 291, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 291
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-291

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 566
|||||
DB 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 732

QY 567 AAAACTCGTGGAGACAGATGTCACACTTAATGCTGTGACCAAAAAGAGACAGC 626
|||||
DB 731 AAAACTCGTGGAGACAGATGTCACACTTAATGCTGTGACCAAAAAGAGACAGC 672

QY 627 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 686
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DB 671 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATG 612

QY 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
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RESULT 45
US-09-810-936-292/c
; Sequence 292, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-292

FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 292
LENGTH: 1851
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-292

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 731 AAAACTGCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 672
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QY 687 CACTGATCAAAATATTCAGATGAGTATGGAATACCACTCT 728
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Job time : 115.871 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Perfect score: 2040
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Scoring table: ORIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Result				SUMMARIES			
No.	Score	% Match	Query Length	ID	Description		
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2	2040	100.0	2040	16 US-09-288-946-375	Sequence 375, App		
3	2040	100.0	2040	16 US-09-289-198-303	Sequence 303, App		
4	2040	100.0	2040	18 US-09-429-755-303	Sequence 303, App		
5	2040	100.0	2040	18 US-09-443-686-375	Sequence 375, App		
6	2040	100.0	2040	18 US-09-483-672A-375	Sequence 375, App		
7	2040	100.0	2040	20 US-09-534-825A-303	Sequence 303, App		
8	2040	100.0	2040	20 US-09-536-857-375	Sequence 375, App		
9	2040	100.0	2040	22 US-09-568-100A-375	Sequence 375, App		
10	2040	100.0	2040	22 US-09-577-058B-303	Sequence 303, App		
11	2040	100.0	2040	22 US-09-590-583-303	Sequence 303, App		
12	2040	100.0	2040	22 US-09-593-793A-375	Sequence 375, App		
13	2040	100.0	2040	23 US-09-605-783A-375	Sequence 375, App		
14	2040	100.0	2040	24 US-09-636-215-375	Sequence 375, App		
15	2040	100.0	2040	25 US-09-651-236-375	Sequence 375, App		
16	2040	100.0	2040	25 US-09-657-279-375	Sequence 375, App		
17	2040	100.0	2040	26 US-09-679-272-375	Sequence 375, App		
18	2040	100.0	2040	26 US-09-679-426-375	Sequence 375, App		
19	2040	100.0	2040	27 US-09-685-166-375	Sequence 375, App		
20	2040	100.0	2040	27 US-09-685-166A-375	Sequence 375, App		
21	2040	100.0	2040	27 US-09-699-295-303	Sequence 303, App		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

22	2040	100.0	2040	28	US-09-759-129-375	Sequence 375, App
23	2040	100.0	2040	29	US-09-759-163-375	Sequence 375, App
24	2040	100.0	2040	30	US-09-780-669-375	Sequence 375, App
25	2040	100.0	2040	31	US-09-810-936-375	Sequence 303, App
26	2040	100.0	2040	31	US-09-822-827-375	Sequence 375, App
27	2040	100.0	2040	31	US-09-825-901-7	Sequence 7, App11
28	2040	100.0	2040	32	US-09-852-911-375	Sequence 375, App
29	2040	100.0	2040	33	US-09-895-793-375	Sequence 375, App
30	2040	100.0	2040	33	US-09-895-814-375	Sequence 375, App
31	2040	100.0	2040	34	US-09-924-400-303	Sequence 303, App
32	2040	100.0	2040	38	US-10-006-920-375	Sequence 375, App
33	2040	100.0	2040	38	US-10-010-940-375	Sequence 375, App
34	2040	100.0	2040	38	US-10-012-896-375	Sequence 375, App
35	2040	100.0	2040	39	US-10-079-1378-303	Sequence 303, App
36	2040	100.0	2040	40	US-10-144-6788-375	Sequence 375, App
37	2040	100.0	2040	42	US-10-212-679-303	Sequence 303, App
38	1551	76.0	2000	1	PCT-US02-24917-302	Sequence 302, App
39	1551	76.0	2000	16	US-09-588-946-374	Sequence 374, App
40	1551	76.0	2000	16	US-09-588-946-374	Sequence 374, App
41	1551	76.0	2000	18	US-09-429-755-302	Sequence 302, App
42	1551	76.0	2000	18	US-09-443-686-374	Sequence 374, App
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45	1551	76.0	2000	20	US-09-536-857-374	Sequence 374, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-303
; Sequence 303, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-303

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			Indels	Gaps
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Db	61	AGGACCAAGATGGCAAGTGTGTCCGCTTCCCTGCTGCAGGAGAGCGGCAAG	120	
QY	121	AGCAACGTGGGCACTTCTGTGAGACCAACGACGACTCGCATGAAGACACTCAGAGCAAG	180	
Db	121	AGCAACGTGGGCACTTCTGTGAGACCAACGACGACTCGCATGAAGACACTCAGAGCAAG	180	
QY	181	ATGGCAAGATGGTGCAGCCACTGCTTCCCTCTCTCAGAGGGAGTGGCAAGAGCAACGCTG	240	
Db	181	ATGGCAAGATGGTGCAGCCACTGCTTCCCTCTCTCAGAGGGAGTGGCAAGAGCAACGCTG	240	

QY	241	GAGCGTCTGGAGACCAACGACGACTGCTGTA	TATAAGACTACTAGAACACAGATGGGCAAG	300
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Db	301	TGCGTCACCACTGCTTCCCTCGTCGAGGGGGAGGGG	CAAGCAAGGTGGGCGCTTGG	360
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QY	601	GTCTTGGACCAACAAAAGAGGACAGCTCTGAT	AAAGGCGGTCAATTCGAGGAAGATGAA	660
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QY	661	TGTGCGTTAATGTTGCTGGGAACATGGCAGCT	GATCCAAATATTCACAGTAGATGTGAAT	720
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QY	721	ACCACTGCACTAGCGGTATCTAATGAAGAT	TAATGAATGATGGCCAAAGCACTGCTCTTA	780
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QY	841	CATGACGAAAAACGCAAGTCGTGAAATTTT	TATACAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGACGAAAAACGCAAGTCGTGAAATTTT	TATACAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGGATAGATATGGAAGAGACTGCTCATCT	CTGCTGATGTTGGATCAGCAAGTATA	960
Db	901	CTGGATAGATATGGAAGAGACTGCTCATCT	CTGCTGATGTTGGATCAGCAAGTATA	960
QY	961	GTCAAGCTTCTACTTGGACAAAAATATT	GATGTATCTTCAAGATCTATCTGGACAGCG	1020
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QY	1021	GCCAGAGATGCTGTTTCTAGTCATCATCAT	GTATATTGGCAGTACTTTCTGACATAC	1080
Db	1021	GCCAGAGATGCTGTTTCTAGTCATCATCAT	GTATATTGGCAGTACTTTCTGACATAC	1080
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QY 1561 CAAGAACCCAGAAATTAATTAAGATGTGTATAGAGAGTGTGAAGAAGTGTATAGGCTATGAGAA 1620
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QY 1621 GAAATGAAGAAGCAGGAAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGACC 1680
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Db 1681 ACTCTGGCAATGTGTATGATGATTAATTCCTCAAGAAAGAGCAGAACCCCTGAAAGC 1740
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QY 1801 AAGCAATTTTGTGAAGAAGCAGAACTGGAATATTACACGATGAGATTTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAAGCAGAACTGGAATATTACACGATGAGATTTGATTCATGAA 1860
QY 1861 GAAAAGCAGATAGAAAGTGTGAAAATAATCTGAGCTTTCTCTAGTTGTAAGAA 1920
Db 1861 GAAAAGCAGATAGAAAGTGTGAAAATAATCTGAGCTTTCTCTAGTTGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAATATAGCTTGGGGAAGAAATGGCAGTAAAGCTG 1980
Db 1921 GAAAAAGACATCTTGATGAAAATATAGCTTGGGGAAGAAATGGCAGTAAAGCTG 1980
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RESULT 3

US-09-289-198-303
Sequence 303, Application US/09289198

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Reed, Steven G.

APPLICANT: Misher, Lynda

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

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; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; EARLIER FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/991,789
; EARLIER FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: US 08/838,762
; EARLIER FILING DATE: 1997-04-09
; EARLIER APPLICATION NUMBER: PCT/US97/00485
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: US 08/700,014
; EARLIER FILING DATE: 1996-08-20
; EARLIER APPLICATION NUMBER: US 08/585,392
; EARLIER FILING DATE: 1996-01-01
; NUMBER OF SEQ. ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO: 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-289-198-303

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Best Local Similarity 100.0%; Pred. No. 2,7e+264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTGGTTAGAGTTGATTCATTCGCGGCTGCTCTCTCTGTGTAAGAGCCATTTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTGCTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTGCTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 ATGGGCAAGTGGTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GCGCCTTCTGAGAGCCAGCAGACTGCTATGAAGACACTGAGAGCAAGATGGGCAAG 300
Db 241 GCGCCTTCTGAGAGCCAGCAGACTGCTATGAAGACACTGAGAGCAAGATGGGCAAG 300
QY 301 TGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCTTGG 360
Db 301 TGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTATGAGAGCCAGTACACGTCGCTGGAGGAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGGCTTATGAGAGCCAGTACACGTCGCTGGAGGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGAGGTAAGATCCCAAGAAAGATCTATGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGAGGTAAGATCCCAAGAAAGATCTATGTCATG 480
QY 481 CTCAGGACACTGACGTGAACAGAGACAGCAAAAGAGAGTGTCTACATCTGGC 540
Db 481 CTCAGGACACTGACGTGAACAGAGACAGCAAAAGAGAGTGTCTACATCTGGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGTCGACAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGTCGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGACAGCTCTGATAAAGCCCTACATCCAGAGAAATGAA 660
Db 601 GTCTTGACAAACAAAAGAGAGACAGCTCTGATAAAGCCCTACATCCAGAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATGATGAAAT 720

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Db 661 TGTGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGAAAT 720
Oy 721 ACCACTGCACTACGCTATCTATTAAGAAATTAATGAGCCCAAGCACTGCTCTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAAGAAATTAATGAGCCCAAGCACTGCTCTTA 780
Oy 781 TATGCTGTGATATGCAATCAAAAAAACAAGCATGGCTCACACCACTGTACTGTGTA 840
Db 781 TATGCTGTGATATGCAATCAAAAAAACAAGCATGGCTCACACCACTGTACTGTGTA 840
Oy 841 CATGAGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Db 841 CATGAGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Oy 901 CTGGATATATATGGAAGAGCTGCTCATCTGCTGATGATGTTGGATGCAAGCAATTA 960
Db 901 CTGGATATATATGGAAGAGCTGCTCATCTGCTGATGATGTTGGATGCAAGCAATTA 960
Oy 961 GTCAGCCTTCTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAGCCTTCTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCACTTCTGACTAC 1080
Oy 1081 AAAAGAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCCAAGCAACTTAAG 1140
Db 1081 AAAAGAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCCAAGCAACTTAAG 1140
Oy 1141 CTGACATCAGAGAAAGCTCAAAAGTTCAAAAGCAGTGAATAATGACAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAAAGCTCAAAAGTTCAAAAGCAGTGAATAATGACAGCAGAGAA 1200
Oy 1201 ATGCTCAAGAACCAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAATTAATTAATGCTGGGATTAAGTAAACCTGACTAATGCTGCTGCTGC 1320
Db 1261 AAGCATGAAATTAATTAATGCTGGGATTAAGTAAACCTGACTAATGCTGCTGCTGC 1320
Oy 1321 AATGGTAAATGATTAATTCCTCAAGAAAGAGCAGAACCCGGAATTAAGCAATTT 1380
Db 1321 AATGGTAAATGATTAATTCCTCAAGAAAGAGCAGAACCCGGAATTAAGCAATTT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTAAGTTCTGACTACAAAG 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTAAGTTCTGACTACAAAG 1440
Oy 1441 AAACGATGCGCAAAATACTCTTCTGAAAAACAGCAACCAAGAACAGCTTAAAGCTGCA 1500
Db 1441 AAACGATGCGCAAAATACTCTTCTGAAAAACAGCAACCAAGAACAGCTTAAAGCTGCA 1500
Oy 1501 TCAGAGAAAGTGCACAAAGGCTTGAGGCACTGAAATTTGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGTGCACAAAGGCTTGAGGCACTGAAATTTGGCCAGCAGAGAAAGATCT 1560
Oy 1561 CAAGAACAGAAATTAATTAAGATGCTGATAGAGATGAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGCTGATAGAGATGAGAAATTTATGCTATCGAA 1620
Oy 1621 GAATGAAAGAGCAGGAAAGTATCTATGCGATTCCTCAAGAAACCTGATATGCTGCC 1680
Db 1621 GAATGAAAGAGCAGGAAAGTATCTATGCGATTCCTCAAGAAACCTGATATGCTGCC 1680
Oy 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAAAGAGCAGAAACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAAAGAGCAGAAACCTGAAAGC 1740
Oy 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCACTGAGCAAAATGATACTGAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCACTGAGCAAAATGATACTGAG 1800

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Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCACTGAGCAAAATGATACTGAG 1800
Oy 1801 AAGCAATTTTGGAAAGACAGAAACCTGGAATTTACAGATGATGATTCGATGAA 1860
Db 1801 AAGCAATTTTGGAAAGACAGAAACCTGGAATTTACAGATGATGATTCGATGAA 1860
Oy 1861 GAAAGCAGATGAAAGTGGTGAATAAATGAAATTTCTGAGCTTCTCTAGTTGTAAGA 1920
Db 1861 GAAAGCAGATGAAAGTGGTGAATAAATGAAATTTCTGAGCTTCTCTAGTTGTAAGA 1920
Oy 1921 GAAAGACATCTTCATGAAATATGATAGTTCGCGGAGAAATTTCCATGCTAAGACTG 1980
Db 1921 GAAAGACATCTTCATGAAATATGATAGTTCGCGGAGAAATTTCCATGCTAAGACTG 1980
Oy 1981 GAGCTAGACACATGAATCATGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
Db 1981 GAGCTAGACACATGAATCATGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 4
US-09-429-755-303
; Sequence 303, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264; Indels 0; Gaps 0;
Matches 2040; Conservative 0; Mismatches 0;

Oy 1 AATGGTGGTGAAGTGAATTCATGCGGCTGCTCTCTGTAAGAAAGCAATTTGCTGTC 60
Db 1 AATGGTGGTGAAGTGAATTCATGCGGCTGCTCTCTGTAAGAAAGCAATTTGCTGTC 60
Oy 61 AAGACCAAGATGGCGCAAGTGTGCTGCGGTTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
Db 61 AAGACCAAGATGGCGCAAGTGTGCTGCGGTTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
Oy 121 AGCAAGCTGGGCACTTCTGAGACACGACGACCTGCTGATGAAGACACTCGAGGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACGACGACCTGCTGATGAAGACACTCGAGGCAAG 180
Oy 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTCAGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTCAGAGGGGAGTGGCAAGCAAGCTG 240
Oy 241 GCGCTTCTGAGAGCAGAGGACACTCTGCTATGAAGACACTAGAGAACAAATGCGCAAG 300
Db 241 GCGCTTCTGAGAGCAGAGGACACTCTGCTATGAAGACACTAGAGAACAAATGCGCAAG 300
Oy 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGTACACAGTCCGCTGGAGAAATG 420
Db 361 GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGTACACAGTCCGCTGGAGAAATG 420

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OY	421	GACAAAGCTCCACAGAGCGCGCTGGGGGTAAGTCCCGAAGAAAGATCTCAATCCGTCAG	480
Db	421	GACAAAGCTCCACAGAGCTGCGTGGGGTAAGTCCCGAAGAAAGATCTCAATCGTCAG	480
OY	481	CTCAGGAGCACTGACGTGAACAGAAAGACAAAGCAAAAGAGAGACTGCTTACATCTGGCC	540
Db	481	CTCAGGAGCACTGACGTGAACAGAAAGAGACAAAGCAAAAGAGAGACTGCTTACATCTGGCC	540
OY	541	TCTGCGCAATGGGAATTTCAGAAAGTAAAGTCTCTCTGTGACAGACAGATGTCAACTTAAT	600
Db	541	TCTGCGCAATGGGAATTTCAGAAAGTAAAGTCTCTCTGTGACAGAGATGTCAACTTAAT	600
OY	601	GTCCCTTGACAAACAAAAGAGAGACAGCTCTGTATAAAGCGCTACAAATGCCAGGAAGATGAA	660
Db	601	GTCCCTTGACAAACAAAAGAGAGACAGCTCTGTATAAAGCGCTACAAATGCCAGGAAGATGAA	660
OY	661	TGTGCGTTAATGTGTTGCTGGAAACATGGCAGCTGATCCAAATATTCAGATAGTATGGAAT	720
Db	661	TGTGCGTTAATGTGTTGCTGGAAACATGGCAGCTGATCCAAATATTCAGATAGTATGGAAT	720
OY	721	ACCACCTGCGACTACGCTATCTATATGAAGATTAATATGGCCAAACACACTGTCGCTTA	780
Db	721	ACCACCTGCGACTACGCTATCTATATGAAGATTAATATGGCCAAACACACTGTCGCTTA	780
OY	781	TATGGTGTGATATTCGAATCAAAAAMACAGCATGGCCTCACACACACTGTTACTTGGTGA	840
Db	781	TATGGTGTGATATTCGAATCAAAAAMACAGCATGGCCTCACACACACTGTTACTTGGTGA	840
OY	841	CATGAGCGAAAACGCAAGTCGGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCGAAAACGCAAGTCGGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
OY	901	CTGGATAGATATGGAAGAGCTGCTCTCATCTGCTATGTTGTGGATCAGCAGATATA	960
Db	901	CTGGATAGATATGGAAGAGAGCTGCTCTCATCTGCTATGTTGTGGATCAGCAGATATA	960
OY	961	GTACAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATCTGACAGACG	1020
Db	961	GTACAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATCTGACAGACG	1020
OY	1021	GCCAGAGAGATGCTGTTTCTAGCATCATCATGTAAATTTGCCAGTACTTTCTGATAC	1080
Db	1021	GCCAGAGAGATGCTGTTTCTAGCATCATCATGTAAATTTGCCAGTACTTTCTGATAC	1080
OY	1081	AAAGAAAAACAGATGCTPAAAAATCTCTTGAAACAGCAATCCAGACAGACTTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTPAAAAATCTCTTGAAACAGCAATCCAGACAGACTTTAAAG	1140
OY	1141	CTGACATCAGAGGAAGGTCCAAAGGTTCAAAAGGAGTGAATAATGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGGTCCAAAGGTTCAAAAGGAGTGAATAATGCCAGCCAGAGAA	1200
OY	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGGATGTGATAGAGAGGTGGAAGAAATAGAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGGATGTGATAGAGAGGTGGAAGAAATAGAG	1260
OY	1261	AAGCATGAAAGTAAATTAATGTGGGATTAATGAAGAACTGACTTAATGTCTCACTCTGGC	1320
Db	1261	AAGCATGAAAGTAAATTAATGTGGGATTAATGAAGAACTGACTTAATGTCTCACTCTGGC	1320
OY	1321	AATGGTGAATATGATTAATTTCTCTCAAGAGAGAGCGAGAACCTGTAAATATAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTTCTCTCAAGAGAGAGCGAGAACCTGTAAATATAGCAATTT	1380
OY	1381	CTTGACAAACGAAGTGAAGAGTATCACAGAAATTTGGCAATTAATGTTCTGACTACAAAGA	1440
Db	1381	CTTGACAAACGAAGTGAAGAGTATCACAGAAATTTGGCAATTAATGTTCTGACTACAAAGA	1440
OY	1441	AAACAGATGCCAAATATCTCTTGAAAGACAGAACCCAGAACAGACTTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTGAAAGACAGAACCCAGAACAGACTTTAAAGCTGACA	1500

QY	1501	TCGAGGAAAGAGTCACAAAGGCTTGAGGGCAGCGAATAATGGCCAGCCAGAGAAAAAGACT	1560
Db	1501	TCGAGGAAAGAGTCACAAAGGCTTGAGGGCAGCGAATAATGGCCAGCCAGAGAAAAAGACT	1560
QY	1551	CAAGAACCAGAAATTAATTAAGATGGTATAGAGAGCTAGAAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGACCCAGAAATTAATTAAGATGGTATAGAGAGACTAGAAAAATTTTATGGCTATCGAA	1620
QY	1621	GAATAGGAAGACGACGGAGACTACATCGATGTCGGATTCGCGAATAACCTGACTAATGGTCC	1680
Db	1621	GAATAGGAAGAGCAGCGAGAGTACTCATGTCCGATTCGCCAGAAACCTGACTAATGGTCC	1680
QY	1681	ACTGCTGGCAATGGTGTATGTATGTGATTAATTCCTCCCAAGGAAAGCAGAACACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGTATGTGATTAATTCCTCCCAAGGAAAGCAGAACACCTGAAAGC	1740
QY	1741	CAGCAATTTCTGACACTGAGAAATGGAAGATATCACAGTACGACGAACAAATGATCTCAG	1800
Db	1741	CAGCAATTTCTGACACTGAGAAATGGAAGATATCACAGTACGACGAACAAATGATCTCAG	1800
QY	1801	AAGCAATTTTCTGAGAGAAACAGAACACTGGAATTTACAGATGAGATTCGTATTCATGAA	1860
Db	1801	AAGCAATTTTCTGAGAGAAACAGAACACTGGAATTTACAGATGAGATTCGTATTCATGAA	1860
QY	1861	GAAAAAGCAGATAGAAAGTGTTGAAAAAATGSAATTTCTGACCTTCTCTTAATTGTTAAGAA	1920
Db	1861	GAAAAAGCAGATAGAAAGTGTTGAAAAAATGSAATTTCTGACCTTCTCTTAATTGTTAAGAA	1920
QY	1921	GAAAAAGCAGATTCGCATGAAAAATAGTACCTGCGGGAAGAAATTCGCATGCTAAGACTG	1980
Db	1921	GAAAAAGCAGATTCGCATGAAAAATAGTACCTGCGGGAAGAAATTCGCATGCTAAGACTG	1980
QY	1981	GAGCTAGACACATGAACATCTCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACATGAACATCTCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT	2040

```

US-09-443-686-375      RESULT 5
; Sequence 375, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: JIANG YUQU
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443,686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 551
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-375
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Query Match	100.0%	Score 2040:	DB 18:	Length 2040:
Best Local Similarity	100.0%	Pred. No. 2.7e-264:		
Matches 2040:	Conservative	0:	Mismatches 0:	Indels 0:
				Gaps 0:
QY	1	ATGTCGTTGACGTTGATTCATGCGCGGCTCTCTCTGTGACAGACCCATTGGTCTC	60	
Db	1	ATGGCGTTGACGTTGATTCATGCGCGGCTCTCTCTGTGACAGACCCATTGGTCTC	60	

QY	61	AGGAGCAAGATGGGGCAAGTGTGCTCCGCTTGCTTCCCTGCTGCAAGGGAAGCGGGCAAG	120
Dp	61	AGGAGCAAGATGGGGCAAGTGTGCTCCGCTTGCTTCCCTGCTGCAAGGGAAGCGGGCAAG	120
QY	121	AGCAACCTGGGGCACTTCTTGAGAGCCACAGACACTGCTGATGAACACTCAGGAGCAAG	180
Dp	121	AGCAACCTGGGGCACTTCTTGAGAGCCACAGACACTGCTGATGAACACTCAGGAGCAAG	180
QY	181	ATGGGGCAAGTGTGGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACTG	240
Dp	181	ATGGGGCAAGTGTGGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACTG	240
QY	241	GGCGCTTCTGGAAGCCACAGCACTGCTGATGAGACACTAGAACAGATGGGCAAG	300
Dp	241	GGCGCTTCTGGAAGCCACAGCACTGCTGATGAGACACTAGAACAGATGGGCAAG	300
QY	301	TGGTGTGGCCACTGTCCCTGCTGCAAGGGGAGCGCAAGCAAGTGGGGCCCTGG	360
Dp	301	TGGTGTGGCCACTGTCCCTGCTGCAAGGGGAGCGCAAGCAAGTGGGGCCCTGG	360
QY	361	GGAGACTAGCATGACAGTGGCTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAAAGATG	420
Dp	361	GGAGACTAGCATGACAGTGGCTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAAAGATG	420
QY	421	GACACGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTCATG	480
Dp	421	GACACGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTCATG	480
QY	481	CTCAGGGACACTACGCGAACAAGAGGACCAAGGACACGCTCTACTCTGGCC	540
Dp	481	CTCAGGGACACTACGCGAACAAGAGGACCAAGGACACGCTCTACTCTGGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAAGTAAACCTCTGCTGAGAGACGATGTCACATTAT	600
Dp	541	TCTGCCAATGGGAATTCAGAAAGTAAACCTCTGCTGAGAGACGATGTCACATTAT	600
QY	601	GTCCTTACACAACAAAAGAGGACAGCTGTGATTAAGGCCGTACCAATGCCAGGAAGATGA	660
Dp	601	GTCCTTACACAACAAAAGAGGACAGCTGTGATTAAGGCCGTACCAATGCCAGGAAGATGA	660
QY	661	TGTGCGTAATGTGGCGGAACAATGGCACTGATGCCAATATCCAGATGAGATGGAAT	720
Dp	661	TGTGCGTAATGTGGCGGAACAATGGCACTGATGCCAATATCCAGATGAGATGGAAT	720
QY	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTA	780
Dp	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTA	780
QY	781	TATGTGCTCATATTCGATATCAAAAAACAGCATGGCGCTCACACCACTGTACTGGTGTA	840
Dp	781	TATGTGCTCATATTCGATATCAAAAAACAGCATGGCGCTCACACCACTGTACTGGTGTA	840
QY	841	CATGAGCAAAAACAGCAAGTCGTAATTTAATCAAGAAAAAGCAATTTAATGCA	900
Dp	841	CATGAGCAAAAACAGCAAGTCGTAATTTAATCAAGAAAAAGCAATTTAATGCA	900
QY	901	CTGGATATGATATGGAAGCACTGCTGCTCATACTTGTGTTGGATACAGCAAGTATA	960
Dp	901	CTGGATATGATATGGAAGCACTGCTGCTCATACTTGTGTTGGATACAGCAAGTATA	960
QY	961	GTCAGCTTCTACTTGAGCAAAAATATATGATATCTTCAAGATCTATCTGGACAGC	1020
Dp	961	GTCAGCTTCTACTTGAGCAAAAATATATGATATCTTCAAGATCTATCTGGACAGC	1020
QY	1021	GCGCAGATGATGCTGTCTCTACTCATATCATATGTAATTTGGCAATTAATTTGACATAC	1080
Dp	1021	GCGCAGATGATGCTGTCTCTACTCATATCATATGTAATTTGGCAATTAATTTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG	1140
Dp	1081	AAAGAAAAACAGATGCTTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG	1140
QY	1141	CTGACATCAGAGAGAGTCCACAAAGCTTCAAAAGCAAGTGAATAATAGCCAGCCAGAGAA	1200

Db	1141	CTGACATCGAGGAAGAGTCACAAAGGTTCAAAAGGACAGTGAATAATGACGACAGAGAAA	1200
Qy	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGATGCGTGTATAGAGAGTGTGAAGAAGAAATTAAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGATGCGTGTATAGAGAGTGTGAAGAAGAAATTAAG	1260
Qy	1261	AAGCATGAAGAATTAATTAATGTGGGATTACTAGAAAACTGTACTAATGTGTCTACTGTGC	1320
Db	1261	AAGCATGAAGAATTAATTAATGTGGGATTACTAGAAAACTGTACTAATGTGTCTACTGTGC	1320
Qy	1321	AATGTGATAATAGTAAATTATTTCTCTCAAGAGAGACAGAACCCGTGAATAATCAGCAATTT	1380
Db	1321	AATGTGATAATAGTAAATTATTTCTCTCAAGAGAGACAGAACCCGTGAATAATCAGCAATTT	1380
Qy	1381	CCGTGCAACGAAAGTGAAGAGTATCATCAGAAATTTGCGAATTTGTTCTGACTACAAAGAA	1440
Db	1381	CCGTGCAACGAAAGTGAAGAGTATCATCAGAAATTTGCGAATTTGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATACTCTTCTGTAAGAACAGCAACCCAGAACANAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATACTCTTCTGTAAGAACAGCAACCCAGAACANAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGATCTACAAAGGCTTTAGAGGCATGAAAAATGGCCACGACAGAAAAAGACT	1560
Db	1501	TCAGAGGAAGATCTACAAAGGCTTTAGAGGCATGAAAAATGGCCACGACAGAAAAAGACT	1560
Qy	1561	CAGAAACCCGAATTAATTAAGATGGTGTATAGAGCTAGAAAAATTTATGGCTATCGAA	1620
Db	1561	CAGAAACCCGAATTAATTAAGATGGTGTATAGAGCTAGAAAAATTTATGGCTATCGAA	1620
Qy	1621	GAAATGAAAGACACACGGAAATCTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC	1680
Db	1621	GAAATGAAAGACACACGGAAATCTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC	1680
Qy	1681	ACTGCTGGCAATGATGATGATGATTAATTTCTCCAGAGGAAGAGAGAAACCTGTAAAGC	1740
Db	1681	ACTGCTGGCAATGATGATGATGATTAATTTCTCCAGAGGAAGAGAGAAACCTGTAAAGC	1740
Qy	1741	CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAACAAATGATACTCG	1800
Db	1741	CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAACAAATGATACTCG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAAACCTGGAATATTATACAGATGAGATTTCTGATTTATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAAACCTGGAATATTATACAGATGAGATTTCTGATTTATGAA	1860
Qy	1861	GAAAGACAGATGAAGTGGTTGAATAAATGAATTCGTGAGCTTCTCTTAAGTTGTAAAGAA	1920
Db	1861	GAAAGACAGATGAAGTGGTTGAATAAATGAATTCGTGAGCTTCTCTTAAGTTGTAAAGAA	1920
Qy	1921	GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
Db	1921	GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
Qy	1981	GAGCTATGACACATAAAGATATAGAGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTATGACACATAAAGATATAGAGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 6
US-09-483-672A-375
; Sequence 375, Application US/09483672A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocke, Susan Louise
; APPLICANT: Jiang Yuyui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.


```

: APPLICANT: Solk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Wang, Aljun
: APPLICANT: Meagher, Madeleine
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE REFERENCE: 210121.42711C11
: CURRENT APPLICATION NUMBER: US/09/483,672A
: CURRENT FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 590
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-483-672A-375

Query Match      100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATAGTGTGAGGTGATTCCATGCGCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60
DB      1  ATGGTGTGAGGTGATTCCATGCGCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60

QY      61  AGGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTGTCAGAGGAGCGGCAAG 120
DB      61  AGGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTGTCAGAGGAGCGGCAAG 120

QY      121  AGCAAGCTGGGCACTTTGTGAGACACAGACACTGTGTAAGACACTCAGAGCAAG 180
DB      121  AGCAAGCTGGGCACTTTGTGAGACACAGACACTGTGTAAGACACTCAGAGCAAG 180

QY      181  ATGGCAAGTGGTGGCCGCTGCTCCCTGCTGTCAGAGGAGGAGTGGCAAGCAAGT 240
DB      181  ATGGCAAGTGGTGGCCGCTGCTCCCTGCTGTCAGAGGAGGAGTGGCAAGCAAGT 240

QY      241  GGGGCTTCTGGAGACCAAGCAAGCTGTGTAAGACACTCAGAAACAAGATGGGCAAG 300
DB      241  GGGGCTTCTGGAGACCAAGCAAGCTGTGTAAGACACTCAGAAACAAGATGGGCAAG 300

QY      301  TGTGCTGCCACTGCTTCCCTGCTGTCAGAGGAGGAGGAGGAGCAAGTGGGCGCTTGG 360
DB      301  TGTGCTGCCACTGCTTCCCTGCTGTCAGAGGAGGAGGAGGAGCAAGTGGGCGCTTGG 360

QY      361  GGAGACTAGAGTAGAGTGGCTTCATGAGGCCAGGTACACGCTCGGTGAGAAAGATCTG 420
DB      361  GGAGACTAGAGTAGAGTGGCTTCATGAGGCCAGGTACACGCTCGGTGAGAAAGATCTG 420

QY      421  GACAACTCCACAGAGCTGCTGCTGGTAAAGTCCGCCAGAAAGATCTCATCTGATG 480
DB      421  GACAACTCCACAGAGCTGCTGCTGGTAAAGTCCGCCAGAAAGATCTCATCTGATG 480

QY      481  CTCAGGGAACACTGAGCTGAACAAGAACAGCAAAAGAGACTCTCTACATCTGGCC 540
DB      481  CTCAGGGAACACTGAGCTGAACAAGAACAGCAAAAGAGACTCTCTACATCTGGCC 540

QY      541  TCTGCCAATGGGAATTCAGAAAGTAGTAATAAATCTGCTGGACAGAGATGTCAACTTAAT 600
DB      541  TCTGCCAATGGGAATTCAGAAAGTAGTAATAAATCTGCTGGACAGAGATGTCAACTTAAT 600

QY      601  GTTCCTTGACAAACAAAAAGAGAGAGCTGTGATTAAGGCCGTACAAATGCGAGAAAGATGA 660
DB      601  GTTCCTTGACAAACAAAAAGAGAGAGCTGTGATTAAGGCCGTACAAATGCGAGAAAGATGA 660

QY      661  TGTGCTTAATGTGCTGGAACATGCGACTGATCAAAATATTCACAGATGATGGAAT 720
DB      661  TGTGCTTAATGTGCTGGAACATGCGACTGATCAAAATATTCACAGATGATGGAAT 720

QY      721  ACCACTCTGACACTAGGCTATCTATATGAAGAAATTAATGAGCCAAACAGCTGCTTGA 780
DB      721  ACCACTCTGACACTAGGCTATCTATATGAAGAAATTAATGAGCCAAACAGCTGCTTGA 780
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QY      781  TATGTGCTGATATCGAATCAAAAAACAGATGGCTCACACACTGTACTTGGTGA 840
DB      781  TATGTGCTGATATCGAATCAAAAAACAGATGGCTCACACACTGTACTTGGTGA 840

QY      841  CATGAGCAAAAAACAGCAAGTCGTAATTTTATATCAAAAAAGCAATTTAAATGCA 900
DB      841  CATGAGCAAAAAACAGCAAGTCGTAATTTTATATCAAAAAAGCAATTTAAATGCA 900

QY      901  CTGGATGATATGTAAGAGAGTGGCTCATCTGCTGATGATGTTGGATGAGCAAGTATA 960
DB      901  CTGGATGATATGTAAGAGAGTGGCTCATCTGCTGATGATGTTGGATGAGCAAGTATA 960

QY      961  GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCCAGATCTATCTGACAGAGC 1020
DB      961  GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCCAGATCTATCTGACAGAGC 1020

QY      1021  GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB      1021  GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080

QY      1081  AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB      1081  AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAG 1140

QY      1141  CTGACATCAGAGAGAGTGCACAAAGGTTCCAAAGGCAAGTGAATAAGCCAGCAAGAAA 1200
DB      1141  CTGACATCAGAGAGAGTGCACAAAGGTTCCAAAGGCAAGTGAATAAGCCAGCAAGAAA 1200

QY      1201  ATGTCTCAGAACCCAGAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
DB      1201  ATGTCTCAGAACCCAGAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260

QY      1261  AAGCATGAAGATTAATATGAGGATTAATCTGAAACCTGCTAATGCTGCTGCTGGC 1320
DB      1261  AAGCATGAAGATTAATATGAGGATTAATCTGAAACCTGCTAATGCTGCTGCTGGC 1320

QY      1321  AATGGTGAATGATTAATTTCTCAAAAGGAGAGCAAGAACCTGAAATAGCAATTT 1380
DB      1321  AATGGTGAATGATTAATTTCTCAAAAGGAGAGCAAGAACCTGAAATAGCAATTT 1380

QY      1381  CTTGACACAGAAAGTGAAGATATCACAGATTTGGCAATTTAGTTTCTGACTCAAGAA 1440
DB      1381  CTTGACACAGAAAGTGAAGATATCACAGATTTGGCAATTTAGTTTCTGACTCAAGAA 1440

QY      1441  AAACAGATGCGCAAAATACCTTCTGAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
DB      1441  AAACAGATGCGCAAAATACCTTCTGAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500

QY      1501  TCAGAGGAAGAGTCCACAAAGGCTTGAAGGCAAGTGAATGGCCAGAGAAAGATCT 1560
DB      1501  TCAGAGGAAGAGTCCACAAAGGCTTGAAGGCAAGTGAATGGCCAGAGAAAGATCT 1560

QY      1561  CAAGAACCCAGAAATTAATTAAGATGTGATAGAGACTGAGAAATTTTATGCTATCGAA 1620
DB      1561  CAAGAACCCAGAAATTAATTAAGATGTGATAGAGACTGAGAAATTTTATGCTATCGAA 1620

QY      1621  GAAATGAAGAGCAGGAAGTACTCATGTCGAGTTCCAGAAACCTGACTAATGGGCC 1680
DB      1621  GAAATGAAGAGCAGGAAGTACTCATGTCGAGTTCCAGAAACCTGACTAATGGGCC 1680

QY      1681  ACTGTGCGAATGTGATGATGATTAATTTCTCCAAAGGAAGAGCAAGCACTGGAAGC 1740
DB      1681  ACTGTGCGAATGTGATGATGATTAATTTCTCCAAAGGAAGAGCAAGCACTGGAAGC 1740

QY      1741  CAGCAATTTCTGACACTGAGAAAGTATCACAGTGAAGCAAAATGATTAATCTGAG 1800
DB      1741  CAGCAATTTCTGACACTGAGAAAGTATCACAGTGAAGCAAAATGATTAATCTGAG 1800

QY      1801  AAGCAATTTTGAAGAGCAAGAACTGGAATTTACAGATGAGATTTGATTCATGA 1860
DB      1801  AAGCAATTTTGAAGAGCAAGAACTGGAATTTACAGATGAGATTTGATTCATGA 1860
```


Db 1561 CAAGAACAGAAATTAATGAAGTGGTATAGAGAGCTAGAAAAATTTTATGCTATTCGAA 1620
Qy 1621 GAATGAGAAAGCAGGAACTACTCATGTCTGATTCAGAAAACTGACTAAATGGTGCC 1680
Db 1621 GAATGAGAAAGCAGGAACTACTCATGTCTGATTCAGAAAACTGACTAAATGGTGCC 1680
Qy 1681 ACTGTGGCAATGTGTATGATTTAATTCCTCCAGAGAGAGCAGACACCTGAAAGC 1740
Db 1681 ACTGTGGCAATGTGTATGATTTAATTCCTCCAGAGAGAGCAGACACCTGAAAGC 1740
Qy 1741 CACCAATTTCTCAGACTGAGATGAAGAGATATACAGATCAACAAATGATATACAG 1800
Db 1741 CACCAATTTCTCAGACTGAGATGAAGAGATATACAGATCAACAAATGATATACAG 1800
Qy 1801 AACCAATTTTGTAGAGAACAGAACTGGAATTTACACATGAGATTCGATTCATGAA 1860
Db 1801 AACCAATTTTGTAGAGAACAGAACTGGAATTTACACATGAGATTCGATTCATGAA 1860
Qy 1861 GAAAGCAGATAGAGTGGTTGAAAAAATGAAATTCGAGCTTCTCTTACTGTAAGAAA 1920
Db 1861 GAAAGCAGATAGAGTGGTTGAAAAAATGAAATTCGAGCTTCTCTTACTGTAAGAAA 1920
Qy 1921 GAAAAAGACATCTTGCATGAATAATAGTACCTTGCAGGAAAGAAATTCGATTAAGCTG 1980
Db 1921 GAAAAAGACATCTTGCATGAATAATAGTACCTTGCAGGAAAGAAATTCGATTAAGCTG 1980
Qy 1981 GACCTAGACACATGAATAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db 1981 GACCTAGACACATGAATAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 8

US-09-536-857-375

Sequence 375, Application US/09536857

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536, 857
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 592
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-375

Query Match 100.0%; Score 2040; DB 20; Length 2040;
Best Local Similarity 100.0%; Fred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTTGAGGTGATTCATGCGGCGCTCTTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGTGTTGAGGTGATTCATGCGGCGCTCTTCTGTAAGAACCATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGCAAGTGTCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGCAAGTGTCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTGTGAGACGAGACGACTGTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTGTGAGACGAGACGACTGTGCTATGAAGACACTCAGAGCAAG 180

Db 121 AGCAAGTGGGCACTTGTGAGACGAGACGACTGTGCTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACCAAGTGG 240
Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACCAAGTGG 240
Qy 241 GGGCGTTTGTGAGACCAAGCAAGCACTGTGCTATGAAGCACTCAGAAACAAGATGGCAAG 300
Db 241 GGGCGTTTGTGAGACCAAGCAAGCACTGTGCTATGAAGCACTCAGAAACAAGATGGCAAG 300
Qy 301 TGGTGGCGCCACGCTTCCCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
Db 301 TGGTGGCGCCACGCTTCCCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
Qy 361 GGAGACTACGATGACAGTGGCTTCATGAGACCCAGGATACAGCTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTGGCTTCATGAGACCCAGGATACAGCTCCGTGGAGAAATCTG 420
Qy 421 GACAAAGCTCCAGAGCTGCTGGTGGGTAAAGTCCCGAAGAAAGATCTCATCTGATG 480
Db 421 GACAAAGCTCCAGAGCTGCTGGTGGGTAAAGTCCCGAAGAAAGATCTCATCTGATG 480
Qy 481 CTGAGGGACACTGACGTGGAACAAGAAAGACAAACAAAGAGCACTGCTACATCTGGCC 540
Db 481 CTGAGGGACACTGACGTGGAACAAGAAAGACAAACAAAGAGCACTGCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCGCTGGACAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCGCTGGACAGAGATGCAACTTAAT 600
Qy 601 GTCCCTTGACAAACAAAGAGAGACGCTGTGATAAAGGCGCTACATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAGAGAGAGCAGCTGTGATAAAGGCGCTACATGCCAGAAATGAA 660
Qy 661 TGTGCGTTAATGTGTGCTGGAACATGGCAGCTGATCCAAATTTCAAGTGTATGGAAT 720
Db 661 TGTGCGTTAATGTGTGCTGGAACATGGCAGCTGATCCAAATTTCAAGTGTATGGAAT 720
Qy 721 ACCACTGTGCATCAGCTATCTAATAAGATAAATTAATGAGCCAAAGCAGCTCTTA 780
Db 721 ACCACTGTGCATCAGCTATCTAATAAGATAAATTAATGAGCCAAAGCAGCTCTTA 780
Qy 781 TATGTGCTGATATCGAATCAAAAACAGCATGGCCTCACACACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATCGAATCAAAAACAGCATGGCCTCACACACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGCGGGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGCGGGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGGATAGATATGGAAGGAGCTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGGAAGGAGCTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
Qy 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAGATCTATCTGGACAGAG 1020
Db 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy 1081 AAGGAAAAACAGATGCTAAATAATCTTCTGAAACAGCAATCCAAACAAAGACTTAAG 1140
Db 1081 AAGGAAAAACAGATGCTAAATAATCTTCTGAAACAGCAATCCAAACAAAGACTTAAG 1140
Qy 1141 CTGACATCAGAGGAGAGTTCAAAAGTTCAAAAGCAAGTGAATAATAGCCAGCAAGAAA 1200
Db 1141 CTGACATCAGAGGAGAGTTCAAAAGTTCAAAAGCAAGTGAATAATAGCCAGCAAGAAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATAGAGAGGTTGAAGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATAGAGAGGTTGAAGAAAGAAATGAAG 1260

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QY 1261 AAGCATGAAGTAATATGTGGATTACTAGAAAACCTGACTAATGTGTCTGCTGCGC 1320
    |||||||
Db 1261 AAGCATGAAGTAATATGTGGATTACTAGAAAACCTGACTAATGTGTCTGCTGCGC 1320
QY 1321 AATGGTGAATATGATTAATTCCTCAAGAGAGACAGACACCTGAAATATGCAATTT 1380
    |||||||
Db 1321 AATGGTGAATATGATTAATTCCTCAAGAGAGACAGACACCTGAAATATGCAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGAGATATACAGAAATTTGCAATTAAGTTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCTGACAAACGAAAGTGAAGAGATATACAGAAATTTGCAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACGATGCGCAAAATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
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Db 1441 AAACGATGCGCAAAATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAGAAAAGATCT 1560
    |||||||
Db 1501 TCAGAGAAAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAGAAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGAGTGTGATAGAGCTAGAAATTTTATGGCTATCGAA 1620
    |||||||
Db 1561 CAAGAACCAAGAAATTAATAGAGTGTGATAGAGCTAGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAGACAGAGAGTACTCATGTGCGGATTCAGAAAACCTGACTAATGCTGCC 1680
    |||||||
Db 1621 GAAATGAAGAGACAGAGAGTACTCATGTGCGGATTCAGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGTGTATGATGATTAATTCCTCCAGAGAGAGCAACACCTGAAAGC 1740
    |||||||
Db 1681 ACTGCTGCAATGTGTATGATGATTAATTCCTCCAGAGAGAGCAACACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTGCAGAAACAAATATATCTCAG 1800
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Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTGCAGAAACAAATATATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAGACAGAACTGAAATATTAACAGATGATTCCTGATTAATGAA 1860
    |||||||
Db 1801 AAGCAATTTTGAAGAGACAGAACTGAAATATTAACAGATGATTCCTGATTAATGAA 1860
QY 1861 GAAAAAGCAGATAGAAGTGTGAAAAATGAATTCCTGAGCTTCTTCTAGTTGTAAGAA 1920
    |||||||
Db 1861 GAAAAAGCAGATAGAAGTGTGAAAAATGAATTCCTGAGCTTCTTCTAGTTGTAAGAA 1920
QY 1921 GAAAAAGCAGATCTTCTGATGAAAAATGTACGTTGCGGAGAAATTCCTGCTAAGACTG 1980
    |||||||
Db 1921 GAAAAAGCAGATCTTCTGATGAAAAATGTACGTTGCGGAGAAATTCCTGCTAAGACTG 1980
QY 1981 GAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAA 2040
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Db 1981 GAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAA 2040

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RESULT 9
US-09-568-100A-375
Sequence 375. Application US/09568100A
GENERAL INFORMATION:

```

: APPLICANT: Xu, Jianshun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Reed, Steven G.
: APPLICANT: Kaios, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedrick, Thomas S.
: APPLICANT: Carter, Darriek
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun

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: APPLICANT: Skeiky, Yasir A.W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE REFERENCE: 210121.42713613
: CURRENT FILING DATE: 2000-05-09
: NUMBER OF SEQ ID NOS: 701
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-568-100A-375

Query Match      100.0%  Score 2040;  DB 22;  Length 2040;
Best Local Similarity 100.0%  Pred. No. 2,7e-264;
Matches 2040;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 ATGGTGTGAGTGTGATTCATGCGGCTGCGCTCTCTGTAAGAGCATTTGCTGC 60
    |||||||
Db 1 ATGGTGTGAGTGTGATTCATGCGGCTGCGCTCTCTCTGTAAGAGCATTTGCTGC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
    |||||||
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGACACTGCTATATGAACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGACACTGCTATATGAACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGGCACTGCTCCCTGCTCAGAGGAGAGTGGCAAGCAAGTG 240
    |||||||
Db 181 ATGGCAAGTGTGCGGCACTGCTCCCTGCTCAGAGGAGAGTGGCAAGCAAGTG 240
QY 241 GCGGCTTGTGAGACCAAGACACTGCTATATGAACACTCAGAGCAAGTGGGCAAG 300
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Db 241 GCGGCTTGTGAGACCAAGACACTGCTATATGAACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCTTGG 360
    |||||||
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCTTGG 360
QY 361 GGAGACTACAGTACAGAGTGTGCTGCTATGAAGACACTCAGAGCAAGTGGGCTTGG 420
    |||||||
Db 361 GGAGACTACAGTACAGAGTGTGCTGCTATGAAGACACTCAGAGCAAGTGGGCTTGG 420
QY 421 GACAAGCTTCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
    |||||||
Db 421 GACAAGCTTCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACACTGAGCTGAAACAAGAGCAAGCAAGAGAGAGTGTCTACATCTGGCC 540
    |||||||
Db 481 CTCAGGAGACACTGAGCTGAAACAAGAGCAAGCAAGAGAGAGTGTCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGATAAAATCTGCTGCTGCTGCTGCTGCTGCTGCT 600
    |||||||
Db 541 TCTGCCAATGGGAATTCAGAAATGATAAAATCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTCTTGAACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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Db 601 GTCTTGAACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCTTAAATTTCTGTAACATGCACTGATTCACAAATTTCCAGATGATGAAAT 720
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Db 661 TGTGCTTAAATTTCTGTAACATGCACTGATTCACAAATTTCCAGATGATGAAAT 720
QY 721 ACCACTGCACTACGATATCATATGAATGAATTAATTAATGAGAGAGAGAGAGAG 780
    |||||||
Db 721 ACCACTGCACTACGATATCATATGAATGAATTAATTAATGAGAGAGAGAGAGAG 780
QY 781 TATGCTGTGATATGAATCAAAAAACAAGATGAGCTCACACCACTGTACTGTGTGA 840
    |||||||
Db 781 TATGCTGTGATATGAATCAAAAAACAAGATGAGCTCACACCACTGTACTGTGTGA 840

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541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGACAGAGATGTCAACTTAAT 600
|||||
541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGACAGAGATGTCAACTTAAT 600
601 GTCTCTTGACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGGAAGTGA 660
601 GTCTCTTGACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGGAAGTGA 660
661 TGTGGTATATGTTGCTGGAAACATGGCAGTCCAAATATTCAGATAGTATGTAAT 720
661 TGTGGTATATGTTGCTGGAAACATGGCAGTCCAAATATTCAGATAGTATGTAAT 720
721 ACCACTCTGACATGCTATCTATATGAAGATTAATATGAGCCAAAGCAGCTGCTTA 780
721 ACCACTCTGACATGCTATCTATATGAAGATTAATATGAGCCAAAGCAGCTGCTTA 780
781 TATGCTGTATATGCAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
781 TATGCTGTATATGCAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
841 CATGACCAAAAACAGCAATCGTGAATTTTATATCAAGAAAAACGAATTTAAATGCA 900
841 CATGACCAAAAACAGCAATCGTGAATTTTATATCAAGAAAAACGAATTTAAATGCA 900
901 CTGGATAGATATGGAAGAGCTGCTCATCTGCTATGTTGTTGGATCAGCAAGTATA 960
901 CTGGATAGATATGGAAGAGCTGCTCATCTGCTATGTTGTTGGATCAGCAAGTATA 960
961 GTACAGCTTCTACTTGAGCAAAAATATGATGATCTTCTCAAGATCATCTGGACAGAG 1020
961 GTACAGCTTCTACTTGAGCAAAAATATGATGATCTTCTCAAGATCATCTGGACAGAG 1020
1021 GCCAGAGATATGCTCTTCTAGTCTCATCATGTTATTTGCCAGTTACTTTGTGACTAC 1080
1021 GCCAGAGATATGCTCTTCTAGTCTCATCATGTTATTTGCCAGTTACTTTGTGACTAC 1080
1081 AAGGAAAAACAGATGCTTAAAAATCTCTTCTGAAAAACAGCATCCAGAACAGCTTAAAG 1140
1081 AAGGAAAAACAGATGCTTAAAAATCTCTTCTGAAAAACAGCATCCAGAACAGCTTAAAG 1140
1141 CTGACATCAGAGAGAGAGTACAAAGGTTCAAAAGCAGTGAAGAAATGAGCCAGAGAAA 1200
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1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
1261 AAGCATGAAGATTAATTAAGGATTAAGAAACCTGACTAATGCTGACTGCTGGC 1320
1261 AAGCATGAAGATTAATTAAGGATTAAGAAACCTGACTAATGCTGACTGCTGGC 1320
1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACACTGAAAAATCGCAATTT 1380
1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACACTGAAAAATCGCAATTT 1380
1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGCGAATTTAGTTCTGACTCAAAAGAA 1440
1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGCGAATTTAGTTCTGACTCAAAAGAA 1440
1441 AAACAGATGCAAAATACTCTTCTGAAAAACAGAACCCAGAACCAAGACTTAAAGCTGACA 1500
1441 AAACAGATGCAAAATACTCTTCTGAAAAACAGAACCCAGAACCAAGACTTAAAGCTGACA 1500
1501 TCAGAGAGAGAGTACAAAGGCTTTGAGGGCAGTGAAGAAATGCGCAGAGAGAAAGATCT 1560
1501 TCAGAGAGAGAGTACAAAGGCTTTGAGGGCAGTGAAGAAATGCGCAGAGAGAAAGATCT 1560
1561 CAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGCTGAAAAATTTTATGCTATGAAA 1620
1561 CAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGCTGAAAAATTTTATGCTATGAAA 1620

1621 GAAATGAGAGACAGCAGAGTACTCATGTCGGATTCAGAAAAACCTGACTAATGCTGCC 1680
|||||
1621 GAAATGAGAGACAGCAGAGTACTCATGTCGGATTCAGAAAAACCTGACTAATGCTGCC 1680
1681 ACTGCTGGCAATGCTATGATGATTAATTTCTCCAAAGAGAGCAGAAACCTGAAAGC 1740
1681 ACTGCTGGCAATGCTATGATGATTAATTTCTCCAAAGAGAGCAGAAACCTGAAAGC 1740
1741 CAGCAATTTCCGACACTGAGAAATGAGATCAAGTGAAGCAGCAAAATGATTAATCAG 1800
1741 CAGCAATTTCCGACACTGAGAAATGAGATCAAGTGAAGCAGCAAAATGATTAATCAG 1800
1801 AAGCAATTTTGTGAAAGACAGAACTGGAATTTACAGATGAGATGCTGATTCATGAA 1860
1801 AAGCAATTTTGTGAAAGACAGAACTGGAATTTACAGATGAGATGCTGATTCATGAA 1860
1861 GAAAGCAGATGAGTGTGTAAGAAATGAAATTTGAGCTTTCTTTAGTTGTAAGAAA 1920
1861 GAAAGCAGATGAGTGTGTAAGAAATGAAATTTGAGCTTTCTTTAGTTGTAAGAAA 1920
1921 GAAAGACATCTTGATGAAATTAATGATGCTGGGGAAGAAATGCTAAGACTG 1980
1921 GAAAGACATCTTGATGAAATTAATGATGCTGGGGAAGAAATGCTAAGACTG 1980
1981 GAGCTGACACATGAAACATCAGACAGCTGAAAAACCTGAAAAACCTGAAAAACCTG 2040
1981 GAGCTGACACATGAAACATCAGACAGCTGAAAAACCTGAAAAACCTGAAAAACCTG 2040

RESULT 11
US-09-583-303
; Sequence 303, Application US/09590583
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C9
; CURRENT APPLICATION NUMBER: US/09/590,583
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-583-303
Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCTTGGTCTC 60
|||||
1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCTTGGTCTC 60
61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
121 AGCAAGTGGGCACTTCTGAGACCAAGAGATCTGCTATGAAGCACTCAGAGCAAG 180
121 AGCAAGTGGGCACTTCTGAGACCAAGAGATCTGCTATGAAGCACTCAGAGCAAG 180
181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTC 240
181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTC 240

QY 241 GGCCTTCTGGAGACACGAGACTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300
|||||
Db 241 GGCCTTCTGGAGACACGAGACTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300
QY 301 TGGTGTGCTCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
|||||
Db 301 TGGTGTGCTCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACCAGTCCGCTGGAGAGATCTG 420
|||||
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACCAGTCCGCTGGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
|||||
Db 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGATGCTCTCATCTGGCC 540
|||||
Db 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGATGCTCTCATCTGGCC 540
QY 541 TCTGCCATGGGAATTCAGAAGTAACTCCTGCTGACAGACGATGTCACATTAAT 600
|||||
Db 541 TCTGCCATGGGAATTCAGAAGTAACTCCTGCTGACAGACGATGTCACATTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGACAGCTCTGATAAGGCCGTACAAATGCCAGGAAGATGAA 660
|||||
Db 601 GTCTTGAACAACAAAGAGAGACAGCTCTGATAAGGCCGTACAAATGCCAGGAAGATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
|||||
Db 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTACGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTCTTA 780
|||||
Db 721 ACCACTGTGCACTACGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTCTTA 780
QY 781 TATGTGCTGATATGCAATCAAAAACAGCATGGCCTCACACCACTGTTACTTGTGTGA 840
|||||
Db 781 TATGTGCTGATATGCAATCAAAAACAGCATGGCCTCACACCACTGTTACTTGTGTGA 840
QY 841 CATGAGCAAAACAGCAAGCTGTAATTTTATCAAGAAAGAAAGGAATTTAAATGCA 900
|||||
Db 841 CATGAGCAAAACAGCAAGCTGTAATTTTATCAAGAAAGAAAGGAATTTAAATGCA 900
QY 901 CTGATGATATGAGAGAGACTGCTCTCATCTGCTGTATGTTGGATCGCAAGTATA 960
|||||
Db 901 CTGATGATATGAGAGAGACTGCTCTCATCTGCTGTATGTTGGATCGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAACAAATATGATGTATCTTCAAGATCTATCTGACAGACG 1020
|||||
Db 961 GTGAGCTTCTACTTGAACAAATATGATGTATCTTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTGTAGTCATCATCATGTAATTTGGCCGTAATCTTTCGACAC 1080
|||||
Db 1021 GCCAGAGATATGCTGTTTGTAGTCATCATCATGTAATTTGGCCGTAATCTTTCGACAC 1080
QY 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGAAGAAACAGCAATCCAGAAACAGACTTAAG 1140
|||||
Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGAAGAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGAGAGTGAATAATAGCCAGAGAGAA 1200
|||||
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGAGAGTGAATAATAGCCAGAGAGAA 1200
QY 1201 ATGCTCTAAGAGACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAAGAAATGAG 1260
|||||
Db 1201 ATGCTCTAAGAGACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAAGAAATGAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGGATTAATAAGAAACCTGACTAATGTTGCTACTGCTGC 1320
|||||
Db 1261 AAGCATGAAGATTAATATGTTGGGATTAATAAGAAACCTGACTAATGTTGCTACTGCTGC 1320

QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGACAGACACCTGAAATCAGCAATTT 1380
|||||
Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGACAGACACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGATATCACGAATTTGCCAATTAGTTTCTGACTACAAAGAA 1440
|||||
Db 1381 CCTGACAAACGAAAGTGAAGATATCACGAATTTGCCAATTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCGCAAAATACTCTTGAAGAACAGCAACCCAGAACAGATTAAAGCTGACA 1500
|||||
Db 1441 AAACAGATGCGCAAAATACTCTTGAAGAACAGCAACCCAGAACAGATTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAACAAAGCTTGAAGGACAGTGAATAATGGCCAGCCAGAGAAAAATCT 1560
|||||
Db 1501 TCAGAGAGAGAGTCAACAAAGCTTGAAGGACAGTGAATAATGGCCAGCCAGAGAAAAATCT 1560
QY 1561 CAAGACACGAAATTAATTAAGATGATGATGAGAGCTAGAGAAATTTATGCGTATGAA 1620
|||||
Db 1561 CAAGACACGAAATTAATTAAGATGATGATGAGAGCTAGAGAAATTTATGCGTATGAA 1620
QY 1621 GAAATGAAGAGACAGGAGTACTCATGTGCGATTCCAGAGAAACCTGACTAATGCTGCC 1680
|||||
Db 1621 GAAATGAAGAGACAGGAGTACTCATGTGCGATTCCAGAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGGTATGATGATGATTAATTCCTCAAGAGAGACAGACACCTGAAAGC 1740
|||||
Db 1681 ACTGCTGCAATGGTATGATGATGATTAATTCCTCAAGAGAGACAGACACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGCAATGAAGATATCACAGTGCAGCAAAATGATGACTCAG 1800
|||||
Db 1741 CAGCAATTTCTGACACTGAGCAATGAAGATATCACAGTGCAGCAAAATGATGACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGACACCTGGAATATTAACAGATGATGATTCATGATTA 1860
|||||
Db 1801 AAGCAATTTTGTGAAGAACAGACACCTGGAATATTAACAGATGATGATTCATGATTA 1860
QY 1861 GAAAAAGCAGATGAGAGTGTGTTAAAAATGCAATTCGACTTCTCTTAGTTGAAGAA 1920
|||||
Db 1861 GAAAAAGCAGATGAGAGTGTGTTAAAAATGCAATTCGACTTCTCTTAGTTGAAGAA 1920
QY 1921 GAAAAAGCAGATGAGAGTGTGTTAAAAATGCAATTCGACTTCTCTTAGTTGAAGAA 1980
|||||
Db 1921 GAAAAAGCAGATGAGAGTGTGTTAAAAATGCAATTCGACTTCTCTTAGTTGAAGAA 1980
QY 1981 GAGCTAGACACATGAACATCAGAGCCAGCTAAAAAGAAAAAGAAAAAGAAAAAG 2040
|||||
Db 1981 GAGCTAGACACATGAACATCAGAGCCAGCTAAAAAGAAAAAGAAAAAGAAAAAG 2040

RESULT 12
US-09-593-793A-375
Sequence 375, Application US/09593793A
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helper, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42715C15


```

CURRENT APPLICATION NUMBER US/09/593,793A
CURRENT FILING DATE: 2000-06-13
NUMBER OF SEQ. ID NOS. 814
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-593-793A-375

```

Query Match	100.0%	Score 2040:	DB 22;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 2,7e-264;		
Matches 2040:	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

OY		1	ATGGGTGTTAGGGTGAATTTCACATCGGGGGCCCTCTTGAGAAAGAAGCATTTGGTCTC	60
Db		1	ATGGGTGTTAGGGTGAATTTCATATCGGGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC	60
OY		61	AGAGACAAGATGGGCAAGTGGTGGCTGCCTTGGCTCCCTGCTGCAGAGGGAGACGGCCAG	120
Db		61	AGGAGACAAGATGGGCAAGTGGTGGCTGCCGTTGGCTCCCTGCTGCAGAGGGAGACGGCCAG	120
OY		121	AGCAACTGGGGCACCTTGTGGAGACACAGACGACTCTGTCTATGAAGACACTCAGAGACAAG	180
Db		121	AGCAACTGGGGCACCTTGTGGAGACACAGAGACGACTCTGTCTATGAAGACACTCAGAGACAAG	180
OY		181	ATGGGCAAGTGGTGGCCCCGCACTGCTCCCCTGCTGCAGGGGGAGTGGCAAGACCAACGTG	240
Db		181	ATGGGCAAGTGGTGGCCCCGCACTGCTCCCCTGCTGCAGGGGGAGTGGCAAGACCAACGTG	240
OY		241	GGGCGCTTCTGGAGACACAGACGACTGCTGTATGAAGACACTCAGGAACAAGATGGGCAAG	300
Db		241	GGCGCTTCTGGAGACACAGACGACTGCTGTATGAAGACACTCAGGAACAAGATGGGCAAG	300
OY		301	TGGGTGCGCACTGCTCCCTGCTGGAGGGGGAGGGGCAAGAACAGTGGGGCGTTGG	360
Db		301	TGGGTGCGCACTGCTCCCTGCTGGAGGGGGAGGGGCAAGAACAGTGGGGCGTTGG	360
OY		361	GGAGACTACGATGACAGTGGCTTTCATGAGAGCCCAAGTACCACGCTCCGTGGAGAAAGATCTG	420
Db		361	GGAGACTACGATGACAGTGGCTTTCATGAGAGCCCAAGTACCACGCTCCGTGGAGAAAGATCTG	420
OY		421	GACAAAGTCCACAGAGCTGGCTGGGGGTAAAGTCCCCGAAAAGGATCTCATCTGCTAAG	480
Db		421	GACAAAGTCCACAGAGCTGGCTGGGGGTAAAGTCCCCGAAAAGGATCTCATCTGCTAAG	480
OY		481	CTCAGGGACACTGCAGTAACAAGAAAGAAACAAGAGAGAGCTGCTACATCTGAGCC	540
Db		481	CTCAGGGACACTGCAGTAACAAGAAAGAAACAAGAGAGAGCTGCTACATCTGAGCC	540
OY		541	TCGTGCCAATGGGAATTTCAGAAAGTATAAACTCCTGCTGGACAGACAGATGTCAACTTAAT	600
Db		541	TCGTGCCAATGGGAATTTCAGAAAGTATAAACTCCTGCTGGACAGAGATGTCAACTTAAT	600
OY		601	GTCCTTACAACAAGAAAAAGAGACAGCTCTGATTAAGAGCCGTACAAATGCCAGGAAGTAGAA	660
Db		601	GTCCTTACAACAAGAAAAAGAGACAGCTCTGATTAAGAGCCGTACAAATGCCAGGAAGTAGAA	660
OY		661	TGTGCGTTAATGTTGCTGGAAACATGCGACTGATCCAATATTTCCAGATGAGTATGGAAT	720
Db		661	TGTGCGTTAATGTTGCTGGAAACATGCGACTGATCCAATATTTCCAGATGAGTATGGAAT	720
OY		721	AACCACTCTGCACCTACGCTATCTATTAATGAAGATTAATATGGCCAAAGCACCTGCTCTTA	780
Db		721	AACCACTCTGCACCTACGCTATCTATTAATGAAGATTAATATGGCCAAAGCACCTGCTCTTA	780
OY		781	TATGTCCTGATATATCGAATCAAAAAAACAACATGGCCCTCACACACACTGTACTTGGGTGA	840
Db		781	TATGTCCTGATATATCGAATCAAAAAAACAACATGGCCCTCACACACACTGTACTTGGGTGA	840
OY		841	CATAGCAAAAAACGCAAGTCGTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGCA	900
Db		841	CATAGCAAAAAACGCAAGTCGTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGCA	900

QY	901	CTGATATGATATGGAAGACGCTGCTCATCTACTGCTGATATGTTGGATACAGCAAGTATA	960
Db	901	CTGGATATGATATGGAAGACGCTGCTCATCTACTGCTGATATGTTGGATACAGCAAGTATA	960
QY	961	GTCACCTTCTACTGTTAGACCAAAATTTGATGATCTTCTCAAGATCTATCGGACAGACG	1020
Db	961	GTCACCTTCTACTGTTAGACCAAAATTTGATGATCTTCTCAAGATCTATCGGACAGACG	1020
QY	1021	GCCACAGAGTATGCTGTTTCTTAGTCATCATCATGTAATTTGCCACTTACTTTTGACTATC	1080
Db	1021	GCCACAGAGTATGCTGTTTCTTAGTCATCATCATGTAATTTGCCACTTACTTTTGACTATC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTTTCTGAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTTTCTGAAAACAGCAATCCAGAACAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAAGACTCACAAAGTTCAAAAGCAGTGAATAATGCCACGACAGAAA	1200
Db	1141	CTGACATCAGAGGAAGACTCACAAAGTTCAAAAGCAGTGAATAATGCCACGACAGAAA	1200
QY	1201	ATGCTCAAGAACCGAANAATTAATAGATGTTGATAGAGAGTGAAGGAAGAAATGAAG	1260
Db	1201	ATGCTCAAGAACCGAANAATTAATAGATGTTGATAGAGAGTGAAGGAAGAAATGAAG	1260
QY	1261	AAGCATGAAGAATTAATGTTGGATTACTAGAAAACTGACTAATGTTGTCACCTGCTGC	1320
Db	1261	AAGCATGAAGAATTAATGTTGGATTACTAGAAAACTGACTAATGTTGTCACCTGCTGC	1320
QY	1321	AATGTTGATATGATTAAATTTCTCAAAAGGAAGACAGACACCTGGAATAATCAGCAATTT	1380
Db	1321	AATGTTGATATGATTAAATTTCTCAAAAGGAAGACAGACACCTGGAATAATCAGCAATTT	1380
QY	1381	CCTGCAACGGAAGGAAGAGATATACAGAAATTTGCGAATTAAGTTTCTGACTACCAAGAA	1440
Db	1381	CCTGCAACGGAAGGAAGAGATATACAGAAATTTGCGAATTAAGTTTCTGACTACCAAGAA	1440
QY	1441	AAACGATGTCGCAAAATACTCTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA	1500
Db	1441	AAACGATGTCGCAAAATACTCTTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGACTCACAAAGGCTTGAGGGCACTGAAAAATGCCAGCCAGAGAAAAAGATCT	1560
Db	1501	TCAGAGGAAGACTCACAAAGGCTTGAGGGCACTGAAAAATGCCAGCCAGAGAAAAAGATCT	1560
QY	1561	CAAGAACCAAGAATTAATTAAGATGCTAATAGAGCTATGAAGAAATTTATGCTATCGAA	1620
Db	1561	CAAGAACCAAGAATTAATTAAGATGCTAATAGAGCTATGAAGAAATTTATGCTATCGAA	1620
QY	1621	GAAATGAAGAACACAGGAATCTACTGATCGGATTTCCAGAAAACTCAGTAATGCTGCC	1680
Db	1621	GAAATGAAGAACACAGGAATCTACTGATCGGATTTCCAGAAAACTCAGTAATGCTGCC	1680
QY	1681	ACTGCTGGCAATGTTGATGATGATTAATTTCCCTCCAGGAAGACAGAACACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGTTGATGATGATTAATTTCCCTCCAGGAAGACAGAACACCTGAAAGC	1740
QY	1741	CAGCAATTTCCCTGACACCTGAGAAATGAAGAGTTACACATGACGACGAACCAAAATCATCTCAG	1800
Db	1741	CAGCAATTTCCCTGACACCTGAGAAATGAAGAGTTACACATGACGACGAACCAAAATCATCTCAG	1800
QY	1801	AAGCAATTTTGAAGAACAGAAACCTGGAATATTACAGATGAGATTTCTGATTATGAA	1860
Db	1801	AAGCAATTTTGAAGAACAGAAACCTGGAATATTACAGATGAGATTTCTGATTATGAA	1860
QY	1861	GAAAGACAGATGAAGTGGTTGAAAAAATGAATTTCTGAGCTTTCTTAGTTGTAAGAAA	1920
Db	1861	GAAAGACAGATGAAGTGGTTGAAAAAATGAATTTCTGAGCTTTCTTAGTTGTAAGAAA	1920
QY	1921	GAAAAAGACATTTGTCATGAAAAATGTACGTTGCGGGAAGAAATGCCATGTAAGACTG	1980
Db	1921	GAAAAAGACATTTGTCATGAAAAATGTACGTTGCGGGAAGAAATGCCATGTAAGACTG	1980

QY 1981 GACGTAGACACATGAATGAACATGACAGCCAGCTAAAAA 2040
DB 1981 GACGTAGACACATGAATGAACATGACAGCCAGCTAAAAA 2040

RESULT 13

US-09-605-783A-375

Sequence 375, Application US/09605783A

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427016
CURRENT APPLICATION NUMBER: US/09/605,783A
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-783A-375

Query Match

Best Local Similarity 100.0%; Score 2040; DB 23; Length 2040;
Pred. Local Similarity 100.0%; Pred. No. 2.7e-264;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTGTGATTCATGCGCGCTGCTCTTGTGAAGAACCCATTTGCTC 60
DB 1 ATGGTGGTGGAGTGTGATTCATGCGCGCTGCTCTTGTGAAGAACCCATTTGCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACGAGACGCTGCTATGAAGACACACAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAGACACGAGACGCTGCTATGAAGACACACAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
QY 241 GGGGCTTGTGAGACACGAGACGCTGCTATGAAGACACACAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTGTGAGACACGAGACGCTGCTATGAAGACACACAGAGCAAGTGGCAAG 300
QY 301 TGTGTCGCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTGG 360
DB 301 TGTGTCGCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTGG 360
QY 361 GGAGACTACGATGACAGTGTGCTTATGAGACCCAGGATACAGCTCCCTGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGTGCTTATGAGACCCAGGATACAGCTCCCTGGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGTGTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAGCTCCACAGAGTGTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480

DB 421 GACAGCTCCACAGAGTGTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGACACTGACGTGAGACAAAGAGACAGCAAAAGAGAGTGTCTACATCTGCGC 540
DB 481 CTCAGGACACTGACGTGAGACAAAGAGAGACAGCAAAAGAGAGTGTCTACATCTGCGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGTGACAGAGAGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGTGACAGAGAGTCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGACAGCTGTATTAAGCCCTTACAAATCCGAGAAAGTGA 660
DB 601 GTCCCTTGACAAACAAAAGAGACAGCTGTATTAAGCCCTTACAAATCCGAGAAAGTGA 660
QY 661 TGTGCGTAAATGTTGTCGGAACATGGACATGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTAAATGTTGTCGGAACATGGACATGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACATACGCTATCTATATGAAGATTAATTAAGCCAAAGACAGCTCTCTTA 780
DB 721 ACCACTGTGACATACGCTATCTATATGAAGATTAATTAAGCCAAAGACAGCTCTCTTA 780
QY 781 TATGTCCTATATCCGAATCAAAAAACAGATGCGCTCACACACCTGTTACTGTGTA 840
DB 781 TATGTCCTATATCCGAATCAAAAAACAGATGCGCTCACACACCTGTTACTGTGTA 840
QY 841 CATGAGCAAAACAGCAAGTCGTAATTTTATCAAGAAAAAGCAATTTTAAATGA 900
DB 841 CATGAGCAAAACAGCAAGTCGTAATTTTATCAAGAAAAAGCAATTTTAAATGA 900
QY 901 CTGATGATATGGAAGAGAGTGTCTCATCTGCTGATATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATGATATGGAAGAGAGTGTCTCATCTGCTGATATGTTGTGATCAGCAAGTATA 960
QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATGTGACAGAC 1020
DB 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATGTGACAGAC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGATAC 1080
QY 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAGACAGCAATCCAGAACAGCTTAAG 1140
DB 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAGACAGCAATCCAGAACAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGCGATGAATAATGCCAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGCGATGAATAATGCCAGCCAGAGAAA 1200
QY 1201 ATGCTCAAGAACAGCAAAATTAATTAAGATGATGATGAAGAGTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACAGCAAAATTAATTAAGATGATGATGAAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATGTTGGATTACTAGAAAACCTGACTAATGCTGCTGCTG 1320
DB 1261 AAGCATGAAAGTAAATGTTGGATTACTAGAAAACCTGACTAATGCTGCTGCTGCTG 1320
QY 1321 AATGCTATTAATGATTAATTCCTCAAGAGAGAGCAAGACCTGAAATTCAGCAATTT 1380
DB 1321 AATGCTATTAATGATTAATTCCTCAAGAGAGAGCAAGACCTGAAATTCAGCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGATATACAGAAATTTGCAATTAATGTTCTGACTACAAAGAA 1440
DB 1381 CTTGACACAGAAAGTGAAGATATACAGAAATTTGCAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATTAATCTTCTGAAAGACAGAACCCAGAACAGCTTAAGCTGACA 1500
DB 1441 AAACAGATGCAAAATTAATCTTCTGAAAGACAGAACCCAGAACAGCTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTGCACAAAGCTTGAAGGAGAGTGAAGTGGCCAGCCAGAGAAAGATCT 1560
DB 1501 TCAGAGGAAGAGTGCACAAAGCTTGAAGGAGAGTGAAGTGGCCAGCCAGAGAAAGATCT 1560

Qy 1501 CAGAACGAGAAATTAATTAAGATGATAGAGAGCTAGAGAAATTTTATGGCTATCGAA 1620
|||
Db 1501 CAGAACGAGAAATTAATTAAGATGATAGAGAGCTAGAGAAATTTTATGGCTATCGAA 1620
Qy 1621 GAAATGAAGAAGCAGCGGAAGTACTCATGTCGGATTCCAGAGAAACCTGACTAATGTGCC 1680
|||
Db 1621 GAAATGAAGAAGCAGCGGAAGTACTCATGTCGGATTCCAGAGAAACCTGACTAATGTGCC 1680
Qy 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCCAGAGAGAGAGAACCTGAAAGC 1740
|||
Db 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCCAGAGAGAGAGAACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAGATGAGATATCATCAGTGACGAGCAAAATGATCTCAG 1800
|||
Db 1741 CAGCAATTTCTGACACTGAGAGATGAGATATCATCAGTGACGAGCAAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAAGCAGAACCTGGAATTTACAGCATGATCTGATGATGAA 1860
|||
Db 1801 AAGCAATTTTGTGAAGAAGCAGAACCTGGAATTTACAGCATGATCTGATGATGAA 1860
Qy 1861 GAAAAAGCAGATAGAAAGTGTGAAAAAATGAAATTCGACTTTCTTAGTTGAAGAA 1920
|||
Db 1861 GAAAAAGCAGATAGAAAGTGTGAAAAAATGAAATTCGACTTTCTTAGTTGAAGAA 1920
Qy 1921 GAAAAAGCAGATCTGACATGAAATATGATACGTTGCGGAGAAATTCGATGAGACTG 1980
|||
Db 1921 GAAAAAGCAGATCTGACATGAAATATGATACGTTGCGGAGAAATTCGATGAGACTG 1980
Qy 1981 GAGCTAGACACAATGAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
|||
Db 1981 GAGCTAGACACAATGAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 14

US-09-636-215-375
Sequence 375, Application US/09636215
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jlang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-375

Query Match 100.0%; Score 2040; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTCTCTCTGTGAAGAACCATTTGGTCTC 60

Db 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTCTCTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGACCAAGATGAGGCAAGTGGTGTGCGCTGCTTCCCTGTCGAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGAGGCAAGTGGTGTGCGCTGCTTCCCTGTCGAGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTGTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTGTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGATGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGATGCAAGCAAGCTG 240
Qy 241 GCGGCTTGGAGACACAGACACTGCTATGAAGACACTAGGAACAAGATGGGCAAG 300
Db 241 GCGGCTTGGAGACACAGACACTGCTATGAAGACACTAGGAACAAGATGGGCAAG 300
Qy 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGCAAGGTTGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGCAAGGTTGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGTCTTCAATGAGGCCAGGTACCAAGTGTGGTGAAGAATCTG 420
Db 361 GGAGACTACGATGACAGTGTCTTCAATGAGGCCAGGTACCAAGTGTGGTGAAGAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTCATGCTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTCATGCTCATG 480
Qy 481 CTGAGGACACTGAGCTGAACAAGAGCAACAAGAGCACTGCTTACATCTGGCC 540
Db 481 CTGAGGACACTGAGCTGAACAAGAGCAACAAGAGCACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGCAATTCAGAACTAGTAAATCTCTGCTGAGACAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGCAATTCAGAACTAGTAAATCTCTGCTGAGACAGATGTCAACTTAAT 600
Qy 601 GTGCTTGAACAAAAAGAGAGCTGCTGATAAAGGCGCTCAATGCCAGAGATGTA 660
Db 601 GTGCTTGAACAAAAAGAGAGCTGCTGATAAAGGCGCTCAATGCCAGAGATGTA 660
Qy 661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGCTTA 780
Qy 781 TATGGGCTGATATGCAATCAAAAAAAGCATGGGCTCACACCACTGTTACTGGTGA 840
Db 781 TATGGGCTGATATGCAATCAAAAAAAGCATGGGCTCACACCACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Qy 901 CTGATATGATATGAAGAGCTGCTCATCTTCTGATGTTGGTGGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAGAGCTGCTCATCTTCTGATGTTGGTGGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATTTGATGATCTTCCAGAGATCTATCTGAGACAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATTTGATGATCTTCCAGAGATCTATCTGAGACAG 1020
Qy 1021 GCCAGAGATATGCTTGTATGATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTTGTATGATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATCTTAAAAATCTCTGTGAAGAACAGCAATCCAGAACAGCTTAAAG 1140
|||

```

Db 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCCACAAAGTTCAAGGCGAGTGAATAGCCAGCCAGAGAA 1200
Db 1141 CTTGACATCAGAGAGAGTCCACAAAGTTCAAGGCGAGTGAATAGCCAGCCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTATAGAGAGTTGAGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTATAGAGAGTTGAGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTGGATTAATGAAAAACCTGACTAATGTGTGCTGCTGCC 1320
Db 1261 AAGCATGAAGATTAATATGTGGATTAATGAAAAACCTGACTAATGTGTGCTGCTGCC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 CCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 CCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 AAGCATGCGCAAAATATCTCTTGTGAAAAAGCAGACCCAGACAGACTTAAAGTGACA 1500
Db 1441 AAGCATGCGCAAAATATCTCTTGTGAAAAAGCAGACCCAGACAGACTTAAAGTGACA 1500
Qy 1501 TCAGAGAGAGAGTCCAGAAAGGCTTGAGGGGAGTGAATGGCCAGGAGAGAGAGAGTCT 1560
Db 1501 TCAGAGAGAGAGTCCAGAAAGGCTTGAGGGGAGTGAATGGCCAGGAGAGAGAGTCT 1560
Qy 1561 CAAGAACAGAAATTAATAGATGTGTATAGAGAGCTAGAGAAATTTATGGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATAGATGTGTATAGAGAGCTAGAGAAATTTATGGCTATCGAA 1620
Qy 1621 GAAATTAAGAGAGAGAGAGAGTCTGATGTCGAGTTTCCAGAGAAACCTGACTAATGTGCC 1680
Db 1621 GAAATTAAGAGAGAGAGAGTCTGATGTCGAGTTTCCAGAGAAACCTGACTAATGTGCC 1680
Qy 1681 ACTGCTGCAATGTGATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACTGCTGCAATGTGATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 CAGCAATTTCTGACACAGAGAGAGAGAGTATCAGAGTACAGAGAGAGAGAGAGAGAG 1800
Db 1741 CAGCAATTTCTGACACAGAGAGAGAGTATCAGAGTACAGAGAGAGAGAGAGAGAG 1800
Qy 1801 AAGCAATTTTGTGAAGAGAGAGAGAGAGTATGACAGATGATGATGATGATGATGATG 1860
Db 1801 AAGCAATTTTGTGAAGAGAGAGAGAGTATGACAGATGATGATGATGATGATGATG 1860
Qy 1861 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 GAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 GAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 GAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040

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RESULT 15

US-09-651-236-375

Sequence 375, Application US/09651236

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, David C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

```

? APPLICANT: Kalos, Michael D.
? APPLICANT: Fanger, Gary R.
? APPLICANT: Renter, Marc W.
? APPLICANT: Stolk, John A.
? APPLICANT: Day, Craig H.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Darrick
? APPLICANT: Li, Samuel
? APPLICANT: Wang, Aljun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Hepler, William
? TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
? FILE REFERENCE: 210121.42718C18
? CURRENT APPLICATION NUMBER: US/09/651,236
? NUMBER OF SEQ ID NOS: 865
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 375
? LENGTH: 2040
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-651-236-375

Query Match 100.0%; Score 2040; DB 25; Length 2040;
Best local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGTGCTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGGTCTGCGGCTGCTCCCTGCTGAGAGAGAGAGAGAGAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCGGCTGCTCCCTGCTGAGAGAGAGAGAGAGAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 ATGGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 ATGGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 241 GGGGCTTCTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGGGCTTCTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 TGGTGTGCGCAGTCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 TGGTGTGCGCAGTCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 421 GAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 CTCAGGAGACAGTACGTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACAGTACGTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 TCTGCAATGGGAATTCAGAAAGTAGTAAACTCTCTGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TCTGCAATGGGAATTCAGAAAGTAGTAAACTCTCTGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 GTCCCTGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCCCTGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TGTGCGTAAATGTTGCTGGAACAGTGCATGATCAAAATATTCAGATGATGAGAAAT 720

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Db 661 TGTGGTTAAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 AACACTGCACTACGCTATCATTAATGAAGATAATTAAGGCCAAAGCACTGCTTA 780
Db 721 AACACTGCACTACGCTATCATTAATGAAGATAATTAAGGCCAAAGCACTGCTTA 780
Oy 781 TATGCTGTGATATGCAATCAAAAACAAGCATGGCTCACACCACTGTTACTTGCTA 840
Db 781 TATGCTGTGATATGCAATCAAAAACAAGCATGGCTCACACCACTGTTACTTGCTA 840
Oy 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAAGCAATTTAAATGA 900
Oy 901 CTGGATATATATGGAAGAGCTGCTCATCTACTGATATGTTGGATCAGCAAGTAA 960
Db 901 CTGGATATATATGGAAGAGCTGCTCATCTACTGATATGTTGGATCAGCAAGTAA 960
Oy 961 GTCAAGCTTCTACTTGAGCAAAATATATGATGATCTTCAAGATCTATCTGGACAG 1020
Db 961 GTCAAGCTTCTACTTGAGCAAAATATATGATGATCTTCAAGATCTATCTGGACAG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
Oy 1081 AAAGAAAAAGATGCTTAAAAATCTCTCTGAAAACAGCAATCCCAAGCAACTTAAAG 1140
Db 1081 AAAGAAAAAGATGCTTAAAAATCTCTCTGAAAACAGCAATCCCAAGCAACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAGAGCAGTGAAGAAAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAGAGCAGTGAAGAAAGCCAGAGAAA 1200
Oy 1201 ATGCTCAGAAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAAGTGAAG 1260
Db 1201 ATGCTCAGAAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAAGTGAAG 1260
Oy 1261 AAGCATGAAGATTAATTAAGTGGGATTAAGTAAGAAACCTGAATATGCTGCTGCTGC 1320
Db 1261 AAGCATGAAGATTAATTAAGTGGGATTAAGTAAGAAACCTGAATATGCTGCTGCTGC 1320
Oy 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATATAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATATAGCAATTT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCAATTAAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCAATTAAGTTCTGACTACAAAGAA 1440
Oy 1441 AAACAGATGCCAAATTAATCTTCTAAAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTAAAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAGTCAAAAGGCTTGAAGGCACTGAATAATGGCCAGAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGTCAAAAGGCTTGAAGGCACTGAATAATGGCCAGAGAGAAAGATCT 1560
Oy 1561 CAAGAAGCAGAAATTAATTAAGATGCTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAAGCAGAAATTAATTAAGATGCTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
Oy 1621 GAAATGAAGAGCAGAGAGTACTCATGTCGATCCAGAAACCTGACTAATGGTGC 1680
Db 1621 GAAATGAAGAGCAGAGAGTACTCATGTCGATCCAGAAACCTGACTAATGGTGC 1680
Oy 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGCAACACTGAAAC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGCAACACTGAAAC 1740
Oy 1741 CAGCAATTTCTGACACTGAGAAAGATATCAAGTGAAGCAAAATATATCTAG 1800

```

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Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAAGTGAAGCAAAATGATCTAG 1800
Oy 1801 AAGCAATTTTCTGAGAGACAGAAACCTGGAATATTACAGATGATGATTCATGAA 1860
Db 1801 AAGCAATTTTCTGAGAGACAGAAACCTGGAATATTACAGATGATGATTCATGAA 1860
Oy 1861 GAAAGCAGATGAGAGTGTGAAAAATGAATTCAGACTTCTTATGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAGAGTGTGAAAAATGAATTCAGACTTCTTATGTTGAAGAA 1920
Oy 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTCCTGTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTCCTGTAAGACTG 1980
Oy 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040

```

RESULT 16

US-09-657-279-375

; Sequence 375; Application US/09657279

GENERAL INFORMATION:

```

; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqin
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kailos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-375

```

Query Match 100.0%; Score 2040; DB 25; Length 2040;

Best Local Similarity 100.0%; Pred. No. 2.7e-264;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 ATGCTGTTGAGGTGATTCATATGCCGCTGCTCTTCTGTGAAGAGCCATTTGGTCTC 60
Db 1 ATGCTGTTGAGGTGATTCATATGCCGCTGCTCTTCTGTGAAGAGCCATTTGGTCTC 60
Oy 61 AGGAGCAATGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 AGGAGCAATGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Oy 121 ACCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 ACCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCAGAGCAAG 180
Oy 181 ATGGCAAGTGTGCGCCGCTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGTGCGCCGCTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240

```

QY 241 GCGCTTCTGGAGACACGACGACTGCTATGAGACACTCAGAGAACAGATGGGCAAG 300
 Db 241 GGGGCTTCTGGAGACACGACGACTGCTATGAGACACTCAGAGAACAGATGGGCAAG 300
 QY 301 TGGTGGTCCACTGCTTCCCTGCTGAGGGGAGGGGCAAGAGAGAGGGGCGCTGG 360
 Db 301 TGGTGGTCCACTGCTTCCCTGCTGAGGGGAGGGGCAAGAGAGAGGGGCGCTGG 360
 QY 361 GGAGACTAGAGTACAGTGGCTTCTCATGAGGCCAGGTACACGCTCGGTGAGAGAGATCTG 420
 Db 361 GGAGACTAGAGTACAGTGGCTTCTCATGAGGCCAGGTACACGCTCGGTGAGAGAGATCTG 420
 QY 421 GACAACTCCACAGAGCTGCTGCTGGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
 Db 421 GACAACTCCACAGAGCTGCTGCTGGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
 QY 481 CTCAGGACACTGAGCTGGAACAGAAAGAGAACCAAGAGGAGCTGCTCATGCTCATG 540
 Db 481 CTCAGGACACTGAGCTGGAACAGAAAGAGAACCAAGAGGAGCTGCTCATGCTCATG 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCTGCTGAGACAGAGATGCTCAACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCTGCTGAGACAGAGATGCTCAACTTAAT 600
 QY 601 GTCTTTCACACAAACAAAGAGAGAGCTCTGATTAAGGCGCTACATGCGCAGAGATGAA 660
 Db 601 GTCTTTCACACAAACAAAGAGAGAGCTCTGATTAAGGCGCTACATGCGCAGAGATGAA 660
 QY 661 TGTGCTTATGTTGGTGGAGACATGGGACCTGATCCAAATTTCCATGATGATGAGAAAT 720
 Db 661 TGTGCTTATGTTGGTGGAGACATGGGACCTGATCCAAATTTCCATGATGATGAGAAAT 720
 QY 721 ACCACTCTGCACACTGCTATCTATTAATGAAGATTAATTAAGGCCAAAGCAGCTGCTTA 780
 Db 721 ACCACTCTGCACACTGCTATCTATTAATGAAGATTAATTAAGGCCAAAGCAGCTGCTTA 780
 QY 781 TATGCTGCTGATTCGAATTCACAAACAAAGCAGCTGCTGACACACTGTTACTTGGTGA 840
 Db 781 TATGCTGCTGATTCGAATTCACAAACAAAGCAGCTGCTGACACACTGTTACTTGGTGA 840
 QY 841 CATGACCAACAAACAGCAGCTGCTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 Db 841 CATGACCAACAAACAGCAGCTGCTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 QY 901 CTGGATAGATAGGAAGAGCTGCTCATATCTGCTGATGTTGTGGATCAGCAAGTATA 960
 Db 901 CTGGATAGATAGGAAGAGCTGCTCATATCTGCTGATGTTGTGGATCAGCAAGTATA 960
 QY 961 GTCAGGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 Db 961 GTCAGGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGATAGCTGTTCTAGTCAATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
 Db 1021 GCCAGAGATAGCTGTTCTAGTCAATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
 QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGATTCAGAACAGACTTAAAG 1140
 Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGATTCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAACAAAGGTTCAAGGCAAGGAAATAGCCAGCCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAACAAAGGTTCAAGGCAAGGAAATAGCCAGCCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATAGAGAGTTAAGAGAAATAGAG 1260
 Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATAGAGAGTTAAGAGAAATAGAG 1260
 QY 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 Db 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTT 1380

Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGATTT 1380
 QY 1381 CTTGACAAAGAAAGTGAAGATATCACAGATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 Db 1381 CTTGACAAAGAAAGTGAAGATATCACAGATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AAACAGATGCCAAATACTTCTGAAACAGCAACCCAGACAGATTAAGCTGACA 1500
 Db 1441 AAACAGATGCCAAATACTTCTGAAACAGCAACCCAGACAGATTAAGCTGACA 1500
 QY 1501 TCAGAGAGAGATCACAAAGGCTTGAAGGCGATGAAAGTGGCCAGCCAGAGAAATCT 1560
 Db 1501 TCAGAGAGAGATCACAAAGGCTTGAAGGCGATGAAAGTGGCCAGCCAGAGAAATCT 1560
 QY 1561 CAAGAACCCAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db 1561 CAAGAACCCAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1621 GAAATGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1621 GAAATGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 Db 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 QY 1741 CAGCAATTTCTGACACTGAGATGAGAGATGATGATGATGATGATGATGATGATGATGAT 1800
 Db 1741 CAGCAATTTCTGACACTGAGATGAGAGATGATGATGATGATGATGATGATGATGATGAT 1800
 QY 1801 AAGCAATTTTGTGAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Db 1801 AAGCAATTTTGTGAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 QY 1861 GAAAGACAGATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Db 1861 GAAAGACAGATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 QY 1921 GAAAAAGACATCTTGCATGAAATAGTACGTTGCGGAGAGAAATTTGCAATGCTAAGCTG 1980
 Db 1921 GAAAAAGACATCTTGCATGAAATAGTACGTTGCGGAGAGAAATTTGCAATGCTAAGCTG 1980
 QY 1981 GAGCTAGACACATGAAGATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 2040
 Db 1981 GAGCTAGACACATGAAGATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 2040

RESULT 17
 ; US-09-679-272-375
 ; Sequence 375, Application US/09679272
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Skelky, Yasir
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Cheever, Martin
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.534
 ; CURRENT APPLICATION NUMBER: US/09/679,272
 ; NUMBER OF SEQ ID NOS: 476
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 375
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-679-272-375

Query Match 100.0%; Score 2040; DB 26; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 2,76-264;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yashir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-375

Query Match 100.0%; Score 2040; DB 26; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTGTGATTCATGCGGGCTCTTCTGTGTGAAGAACATTTGGTCTC 60
DB 1 ATGGTGGTTGAGTGTGATTCATGCGGGCTCTTCTGTGTGAAGAACATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACGACGACTGTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACGACGACTGTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCACTTCCCTGCTGCTGCAAGGAGAGTGGCAAGACAGTGTG 240
DB 181 ATGGGCAAGTGGTGGGCACTTCCCTGCTGCTGCAAGGAGAGTGGCAAGACAGTGTG 240
QY 241 GGGGCTTGGAGACCAAGGAGTGTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTGGAGACCAAGGAGTGTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGGCTTGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGGCTTGG 360
QY 361 GGGAGCTAGATGACAGTGGTGGTGTGAGCCAGGAGTACAGTCCGTGGAGAAAGATCTG 420
DB 361 GGGAGCTAGATGACAGTGGTGGTGTGAGCCAGGAGTACAGTCCGTGGAGAAAGATCTG 420
QY 421 GAGAGCTCCACAGAGTGGTGGTGTGAGCCAGGAGTACAGTCCGTGGAGAAAGATCTG 480
DB 421 GAGAGCTCCACAGAGTGGTGGTGTGAGCCAGGAGTACAGTCCGTGGAGAAAGATCTG 480
QY 481 CTCAGGAGACAGTGAAGCAAGAGGAGACAAAGAGAGTGTCTATCATCTGGCC 540
DB 481 CTCAGGAGACAGTGAAGCAAGAGGAGACAAAGAGAGTGTCTATCATCTGGCC 540
QY 541 TCTGCCCAATGGAAATTCAGAAATGTAAGTAAATCTCTGCTGACAGAGATCTCAACTTAAT 600
DB 541 TCTGCCCAATGGAAATTCAGAAATGTAAGTAAATCTCTGCTGACAGAGATCTCAACTTAAT 600
QY 601 GTCCTTGACAAACAAAGAGAGAGTGTATGAAGGCGTGTACAAATCCAGAGAAAGATGAA 660
DB 601 GTCCTTGACAAACAAAGAGAGAGTGTATGAAGGCGTGTACAAATCCAGAGAAAGATGAA 660

QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAGTATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAGTATGGAAT 720
QY 721 ACCACTCTGCACTACCTATCTATTAATGAATTAATTAATGGCCAAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTACCTATCTATTAATGAATTAATTAATGGCCAAAGCACTGCTTA 780
QY 781 TATGTCCTATATTCAGATCAATCAAAAAACAGATGGCTCCACACAGTGTACTTGGTGA 840
DB 781 TATGTCCTATATTCAGATCAATCAAAAAACAGATGGCTCCACACAGTGTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTCTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAAGTCTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGTGTCTCATCTGCTGATAGTGTGATGAGCAAGTATA 960
DB 901 CTGATATGATATGGAAGAGTGTCTCATCTGCTGATAGTGTGATGAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATGATATCTTCAAGATCATCTGAGACAGCG 1020
DB 961 GTGAGCCTTCTACTTGAGCAAAATATGATATCTTCAAGATCATCTGAGACAGCG 1020
QY 1021 GCCAGAGATATGCTGTTCTTACTCATCATATGATTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTTACTCATCATATGATTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATATCTCTGAAAAACGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAATATCTCTGAAAAACGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTGCACAAAGTTCAAAAGGCAAGTAAATATGAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTGCACAAAGTTCAAAAGGCAAGTAAATATGAGCCAGAGAAA 1200
QY 1201 ATGCTTCAGAACACAGAAATTAATGAAGATGATGATGAGAGTGTGAAGAAATGAAG 1260
DB 1201 ATGCTTCAGAACACAGAAATTAATGAAGATGATGATGAGAGTGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTATATATGAGGATTAATGAAACCTGCTATGATGCTGCTGGC 1320
DB 1261 AAGCATGAAGTATATATGAGGATTAATGAAACCTGCTATGATGCTGCTGGC 1320
QY 1321 AATGCTATATGATTAATTTCTCAAAAGGAGAGCAAGACACTGAAATTCAGCAATTT 1380
DB 1321 AATGCTATATGATTAATTTCTCAAAAGGAGAGCAAGACACTGAAATTCAGCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGATATCACAGATTTGCGAATTAATTTGCTGACTACAAAGAA 1440
DB 1381 CTTGACACAGAAAGTGAAGATATCACAGATTTGCGAATTAATTTGCTGACTACAAAGAA 1440
QY 1441 AAGCAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGCAAGCACTTAAGGCTGACA 1500
DB 1441 AAGCAGATGCAAAATATCTTCTGAAAAACAGCAACCCAGCAAGCACTTAAGGCTGACA 1500
QY 1501 TCAGAGGAGAGTGCACAAAGCTTGAAGGCAAGTAAATGCGCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGGAGAGTGCACAAAGCTTGAAGGCAAGTAAATGCGCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATGAAGTGGTGAATGAGAGCTATCAAAATTTTATGGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATGAAGTGGTGAATGAGAGCTATCAAAATTTTATGGCTATCGAA 1620
QY 1621 GAATATGAAGAGCAGGAATTAATCAATGCTGGAATTCGCAAAACGATTAATGGGCGC 1680
DB 1621 GAATATGAAGAGCAGGAATTAATCAATGCTGGAATTCGCAAAACGATTAATGGGCGC 1680
QY 1681 ACTGCTGCAATGATGATGATTAATTCCTCAAGAGAGAGAGCAACCTGGAAGG 1740
DB 1681 ACTGCTGCAATGATGATGATTAATTCCTCAAGAGAGAGAGCAACCTGGAAGG 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTACAGCAACAAATGATCTCAG 1800

```
|||||
Db 1741 CAGCATTTTCTGACACTGAGATGAGATACAGATGACGACGACAAATGATCTACAG 1800
|||
Qy 1801 AAGCATTTTGTGAGAAAGACAACTGGAATTTACAGATGACATGTTGATCTATGAA 1860
|||
Db 1801 AAGCATTTTGTGAGAAAGACAACTGGAATTTACAGATGACATGTTGATCTATGAA 1860
|||
Qy 1861 GAAAGCAGATGAAAGTGTGAAAAAATGAATTTGACCTTCTCTTGAAGTAAAGAA 1920
|||
Db 1861 GAAAGCAGATGAAAGTGTGAAAAAATGAATTTGACCTTCTCTTGAAGTAAAGAA 1920
|||
Qy 1921 GAAAGACATCTTGACATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1980
|||
Db 1921 GAAAGACATCTTGACATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1980
|||
Qy 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTT 2040
|||
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTT 2040
|||

RESULT 19
US-09-685-166-375
; Sequence 375, Application US/09685166
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jilang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166-375

Query Match 100.0%; Score 2040; DB 27; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 241 GGCCTTCTGAGACACGACGACCTGCTATGAGACACTGAGAACAAAGATGGCAAG 300
|||
Db 241 GGCCTTCTGAGACACGACGACGACCTGCTATGAGACACTGAGAACAAAGATGGCAAG 300
|||
Qy 301 TGGTGTGCCACTGCTTCCCTGCTCAGGAGGAGGCGCAAGACAGAGTGGCGCTTGG 360
|||
Db 301 TGGTGTGCCACTGCTTCCCTGCTCAGGAGGAGGCGCAAGACAGAGTGGCGCTTGG 360
|||
Qy 361 GGAGACTAGCATGACAGTGGCTTCAATGAGAGCCAGGTACCAGTCCGTGGAGAAATCTG 420
|||
Db 361 GGAGACTAGCATGACAGTGGCTTCAATGAGAGCCAGGTACCAGTCCGTGGAGAAATCTG 420
|||
Qy 421 GACACCTCCACAGAGCTGCTGGGGGAAAGTCCCGAAGAAAGATCCTCATGCTGATG 480
|||
Db 421 GACACCTCCACAGAGCTGCTGGGGGAAAGTCCCGAAGAAAGATCCTCATGCTGATG 480
|||
Qy 481 CTCAGGAGACACTGACGTGAACAAGAGACAAAGCAAGAGAGACTGCTACATCTGGCC 540
|||
Db 481 CTCAGGAGACACTGACGTGAACAAGAGACAAAGCAAGAGAGACTGCTACATCTGGCC 540
|||
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACACAGACATGCTCAACTTAAT 600
|||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACACAGACATGCTCAACTTAAT 600
|||
Qy 601 GTCCCTTGACAAACAAAAGAGAGACGCTGATAAAGGCGCTACAAATGGCCAGAAATGAA 660
|||
Db 601 GTCCCTTGACAAACAAAAGAGAGACGCTGATAAAGGCGCTACAAATGGCCAGAAATGAA 660
|||
Qy 661 TGTGCTTAATGTTGTGTGAAACATGACGACATGATCAAAATATTCAGATGATGAAAT 720
|||
Db 661 TGTGCTTAATGTTGTGTGAAACATGACGACATGATCAAAATATTCAGATGATGAAAT 720
|||
Qy 721 ACCACTGTGACATGACGCTATCTAATGAAGATAAATTAATGGCCAAAGACTGCTCTTA 780
|||
Db 721 ACCACTGTGACATGACGCTATCTAATGAAGATAAATTAATGGCCAAAGACTGCTCTTA 780
|||
Qy 781 TATGGTGTGATATGAAATCAAAAACAGCATGGGCTCACACAGCTTACTTGGTAT 840
|||
Db 781 TATGGTGTGATATGAAATCAAAAACAGCATGGGCTCACACAGCTTACTTGGTAT 840
|||
Qy 841 CATGACCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
|||
Db 841 CATGACCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
|||
Qy 901 CTGATATGATATGAAAGAGACTGCTCATATCTGCTATGTTGTGATCAGCAAGTATA 960
|||
Db 901 CTGATATGATATGAAAGAGACTGCTCATATCTGCTATGTTGTGATCAGCAAGTATA 960
|||
Qy 961 GTGAGCTTCTACTTGAAGAAATATTTGATGATCTTCTCAAAATATCTGAGACAGAG 1020
|||
Db 961 GTGAGCTTCTACTTGAAGAAATATTTGATGATCTTCTCAAAATATCTGAGACAGAG 1020
|||
Qy 1021 GCCAGAGATATGCTTGTCTAGTCAATCATGATGATTTGGCAGTACTTCTGACTAC 1080
|||
Db 1021 GCCAGAGATATGCTTGTCTAGTCAATCATGATGATTTGGCAGTACTTCTGACTAC 1080
|||
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCAGAAACAGACTTAAG 1140
|||
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCAGAAACAGACTTAAG 1140
|||
Qy 1141 CTGACATCAGAGAAAGATCACAAGGTTCAAGAGCAAGTCAAAATATGAGCCAGAGAAA 1200
|||
Db 1141 CTGACATCAGAGAAAGATCACAAGGTTCAAGAGCAAGTCAAAATATGAGCCAGAGAAA 1200
|||
Qy 1201 ATGCTCAAGAACCAAAATTAATAGATGAGATGAGAGAGGTTGAAGAAAGAAAGAAAG 1260
|||
Db 1201 ATGCTCAAGAACCAAAATTAATAGATGAGATGAGAGAGGTTGAAGAAAGAAAGAAAG 1260
|||
Qy 1261 AAGCATGAAAGTAAATATGAGATTAAGAAACCTGATTAATGATGCTGCTGCTG 1320
|||
Db 1261 AAGCATGAAAGTAAATATGAGATTAAGAAACCTGATTAATGATGATGCTGCTGCTG 1320
|||
```


OY	901	CTGATATGATATGGAAGAGACTGCTCTCATATCTTGGTATGTTGGATCAGCAATATTA	960
Dp	901	CTGATATGATATGGAAGAGACTGCTCTCATATCTTGGTATGTTGGATCAGCAATATTA	960
OY	961	GTCAGCCTTACTTGAAGCAAAATATATGATATCTTCAAGATCTATTCGACAGACG	1020
Dp	961	GTCAGCCTTACTTGAAGCAAAATATATGATATCTTCAAGATCTATTCGACAGACG	1020
OY	1021	GCCAGAGATATGCTGTTCTTCTAGTCATCATATGTAATTTGCCAGTTACTTCTGACTAC	1080
Dp	1021	GCCAGAGATATGCTGTTCTTCTAGTCATCATATGTAATTTGCCAGTTACTTCTGACTAC	1080
OY	1081	AAAGAAAACAGATGCTAAAAATCTCTTGAAACACGAATCCAGAAACAGACTTAAG	1140
Dp	1081	AAAGAAAACAGATGCTAAAAATCTCTTGAAACACGAATCCAGAAACAGACTTAAG	1140
OY	1141	CTGACATCAGAGGAAAGATGCACAAAGTTCCAAAGCAGTGAATAATAGCAGCAGAGAAA	1200
Dp	1141	CTGACATCAGAGGAAAGATGCACAAAGTTCCAAAGCAGTGAATAATAGCAGCAGAGAAA	1200
OY	1201	ATGCTCTCAAGAACCCAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAATGAG	1260
Dp	1201	ATGCTCTCAAGAACCCAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAATGAG	1260
OY	1261	AAGCATGAAGTATATATGCGGATACATAGAAAACCTCATAATAGTGCACCTGCGC	1320
Dp	1261	AAGCATGAAGTATATATGCGGATACATAGAAAACCTCATAATAGTGCACCTGCGC	1320
OY	1321	AATGGTATTAATGGATTAAATCTCTCAAGGAAAGCAGAACCTGAAATATCAGCAATTT	1380
Dp	1321	AATGGTATTAATGGATTAAATCTCTCAAGGAAAGCAGAACCTGAAATATCAGCAATTT	1380
OY	1381	CCTGACACGAAAGTGAAGATATCACAATAATTTGGATTAGTTTGTTCTGACTACAAAGAA	1440
Dp	1381	CCTGACACGAAAGTGAAGATATCACAATAATTTGGATTAGTTTGTTCTGACTACAAAGAA	1440
OY	1441	AAACAGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA	1500
Dp	1441	AAACAGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA	1500
OY	1501	TCACAGAAAGATGCACAAAGCTTGAAGGCAATGCGCCAGCCAGAGAAAAGATCT	1560
Dp	1501	TCACAGAAAGATGCACAAAGCTTGAAGGCAATGCGCCAGCCAGAGAAAAGATCT	1560
OY	1561	CAGAACCCAGAAATTAATTAAGATGGTATAGAGACTTGAATAATTTATGGCTATCGAA	1620
Dp	1561	CAGAACCCAGAAATTAATTAAGATGGTATAGAGACTTGAATAATTTATGGCTATCGAA	1620
OY	1621	GAAATGAAGAGCAGGAACTACTCATATGCGATTTCCAGAAAACCTGAATATGTCGCC	1680
Dp	1621	GAAATGAAGAGCAGGAACTACTCATATGCGATTTCCAGAAAACCTGAATATGTCGCC	1680
OY	1681	ACTGCTGGCATGGTATGATGATTAATTTCCGCCAAGGAAGAGAGAAACCTGAAAGC	1740
Dp	1681	ACTGCTGGCATGGTATGATGATTAATTTCCGCCAAGGAAGAGAGAAACCTGAAAGC	1740
OY	1741	CAGCAATTTCTGCACTGGAATGAAGATACAGTACAGCAACAAATGATACTAG	1800
Dp	1741	CAGCAATTTCTGCACTGGAATGAAGATACAGTACAGCAACAAATGATACTAG	1800
OY	1801	AAGCAATTTCTGGAAGAACGAACTGGAATTTACAGATGAAGAAATCTGATTCATGAA	1860
Dp	1801	AAGCAATTTCTGGAAGAACGAACTGGAATTTACAGATGAAGAAATCTGATTCATGAA	1860
OY	1861	GAAAGCAGATAGAAAGTGTGAAAAAATTAATTCGACCTTCTCTTATGTTAGTAAAGAA	1920
Dp	1861	GAAAGCAGATAGAAAGTGTGAAAAAATTAATTCGACCTTCTCTTATGTTAGTAAAGAA	1920
OY	1921	GAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTCGATGCTAAGACTG	1980
Dp	1921	GAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTCGATGCTAAGACTG	1980

[illegible]

```

US-RESULT21
US-09-699-295-303
; Sequence 303, Application US/09699295
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Mishner, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; CURRENT FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-303

```

Query Match	100.0%	Score 2040;	DB 27;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 2.7e-264;		
Matches 2040; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATGGGCGTTGAGGATTGATTCATCCGCGGCTCCCTTCTGTGGAAAGACCAATTGGCTC	60
Dd	1	ATGGGTGTTGAGGTTGATTCATCCGCGGCTCCCTTCTGTGGAAAGACCAATTGGCTC	60
OY	61	AGGAGCAAGATGGCGAAGTGGTGGCTGGCTTGTCCCTGTCTGACGGGAGAGCGGCAG	120
Dd	61	AGGAGCAAGATGGCGAAGTGGTGGCTGGCTTGTCCCTGTCTGACGGGAGAGCGGCAG	120
OY	121	AGCAACGTGGGCACCTTCTGGAGACCACGAGCACTCTGTATGAAGACACTCAGAGCAAG	180
Dd	121	AGCAACGTGGGCACCTTCTGGAGACCACGAGCACTCTGTATGAAGACACTCAGAGCAAG	180
OY	181	ATGGCAGATGGTGGCGCCGCACTGCTTCCCTGCTGCAGGGGGAATGGCAAGACAGCTG	240
Dd	181	ATGGCAGATGGTGGCGCCGCACTGCTTCCCTGCTGCAGGGGGAATGGCAAGACAGCTG	240
OY	241	GCGCGTTCTGAGACCAACGACGACGACTGTCTATGAAGACACTCAGAACCAAGATGGCAAG	300
Dd	241	GCGCGTTCTGAGACCAACGACGACGACTGTCTATGAAGACACTCAGAACCAAGATGGCAAG	300
OY	301	TGGTCTCTCCACTGCTTCCCTGCTGCGAGGGGGGAGCGGCAAGCAAGATGGGGCGCTTGG	360
Dd	301	TGGTCTCTCCACTGCTTCCCTGCTGCGAGGGGGGAGCGGCAAGCAAGATGGGGCGCTTGG	360
OY	361	GGAGACTCGATGACAGTGGCTTTCATGGAGGCCACGACCACTGCTCGCTGGAGAAATCTG	420
Dd	361	GGAGACTCGATGACAGTGGCTTTCATGGAGGCCACGACCACTGCTCGCTGGAGAAATCTG	420
OY	421	GACAAAGCTCCACAGAGCTGCTGTGGGGTTAAAGTCCCCGAGAAAGATTCATCTGTATG	480
Dd	421	GACAAAGCTCCACAGAGCTGCTGTGGGGTTAAAGTCCCCGAGAAAGATTCATCTGTATG	480
OY	481	CTCAGGGCACTGACGTATACAAAGAGCAAGCAAGAAAAGAGACTGTCTACATCTGGCC	540
Dd	481	CTCAGGGCACTGACGTATACAAAGAGCAAGCAAGAAAAGAGACTGTCTACATCTGGCC	540
OY	541	TCCTGCAATGGGAATTCAAGAGTGTAAAACTCCTGCTGGACAGCAGATGTCAACTTAAT	600

Db 541 TCTGCCAATGGGAATTCAGAAAGTAATAAACTCTGCTGGACAGACGATGCAACTTAAT 600
 QY 601 GTCTTGACAAACAAAAGAGAGACGCTGTGATTAAGGCCGCTAGCAATCCAGAGATGAA 660
 Db 601 GTCTTGACAAACAAAAGAGAGACGCTGTGATTAAGGCCGCTAGCAATCCAGAGATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGSCATGTCCTCAAAATATTCAGATGAGTATGAAAT 720
 Db 661 TGTGCGTTAATGTTGCTGGAACATGSCATGTCCTCAAAATATTCAGATGAGTATGAAAT 720
 QY 721 ACCACCTGCACTACGCTATCTATTAATGAGATTAATTAATGSCCAAGCAGCTCTCTTA 780
 Db 721 ACCACCTGCACTACGCTATCTATTAATGAGATTAATTAATGSCCAAGCAGCTCTCTTA 780
 QY 781 TATGTCCTGATATCGAATCAAAAACAGCATGGCTCACACACCTGTTACTGTGTGA 840
 Db 781 TATGTCCTGATATCGAATCAAAAACAGCATGGCTCACACACCTGTTACTGTGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
 Db 841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGATGATGATGGAAGAGCTGCTCTCATCTGCTGATGTTGATGATCAGCAAGTATA 960
 Db 901 CTGATGATGATGGAAGAGCTGCTCTCATCTGCTGATGTTGATGATCAGCAAGTATA 960
 QY 961 GTCAGCCTTCTACTGTCGAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
 Db 961 GTCAGCCTTCTACTGTCGAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCANGTAATTTGCCAGTTACTTCTGACTAC 1080
 Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCANGTAATTTGCCAGTTACTTCTGACTAC 1080
 QY 1081 AAGGAAAAAGAGATGCTAAAAATCTCTGAAACAGCAATCCAGAAACAGATTTAAAG 1140
 Db 1081 AAGGAAAAAGAGATGCTAAAAATCTCTGAAACAGCAATCCAGAAACAGATTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGAGTACAAAGGTTCAAGAGCAGTGAATAATACCCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGAGTACAAAGGTTCAAGAGCAGTGAATAATACCCAGAGAAA 1200
 QY 1201 ATGCTCTAAGAACAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAAGAAATGAG 1260
 Db 1201 ATGCTCTAAGAACAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAAGAAATGAG 1260
 QY 1261 AAGCATGAAGTATATATGTTGGGATTTACTAGAAAACCTGATATGATGTCACGCTGGC 1320
 Db 1261 AAGCATGAAGTATATATGTTGGGATTTACTAGAAAACCTGATATGATGTCACGCTGGC 1320
 QY 1321 AATGCTGATATGATTAATTTCTCTCAAGAGAGAGAGACAGAACCTGAAATACACATTTT 1380
 Db 1321 AATGCTGATATGATTAATTTCTCTCAAGAGAGAGAGACAGAACCTGAAATACACATTTT 1380
 QY 1381 CTTGACACAGAAAGTGAAGATATCACAGAAATTTGCCAATTTAGTTTCTGACTACAAAGAA 1440
 Db 1381 CTTGACACAGAAAGTGAAGATATCACAGAAATTTGCCAATTTAGTTTCTGACTACAAAGAA 1440
 QY 1441 AAACAGATGCAAAATCTCTCTGAAACACAGAACCCAGAACCAAGCTTTAAACCTGACA 1500
 Db 1441 AAACAGATGCAAAATCTCTCTGAAACACAGAACCCAGAACCAAGCTTTAAACCTGACA 1500
 QY 1501 TCAGAGAGAAAGTACAAAGGCTTGAGGAGAGTGAATAATGGCCAGCCAGAGAAAGATCT 1560
 Db 1501 TCAGAGAGAAAGTACAAAGGCTTGAGGAGAGTGAATAATGGCCAGCCAGAGAAAGATCT 1560
 QY 1561 CAAGAAGCAAGAAATTAATAGAGTGTGATAGAGAGCTAGAAAAATTTTATGCTATGCAA 1620
 Db 1561 CAAGAAGCAAGAAATTAATAGAGTGTGATAGAGAGCTAGAAAAATTTTATGCTATGCAA 1620
 QY 1621 GAATGAAGAAAGCAGGAAAGTACTATGTGGATTTCCCAAGAAAACCTGACTAATGTGACC 1680
 Db 1621 GAATGAAGAAAGCAGGAAAGTACTATGTGGATTTCCCAAGAAAACCTGACTAATGTGACC 1680

QY 1681 ACTGCTGCAATGGTGTATGATGATTAATTCCTCAAGAGAGACAGAACCTGAAAGC 1740
 Db 1681 ACTGCTGCAATGGTGTATGATGATTAATTCCTCAAGAGAGACAGAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTGTGACACTGAGAAATGAAGAGATATACAGTACAGAAACAAATGATACCTAG 1800
 Db 1741 CAGCAATTTCTGTGACACTGAGAAATGAAGAGATATACAGTACAGAAACAAATGATACCTAG 1800
 QY 1801 AAGCAATTTGTGAAGAACAGAACACTGGAATTTATACAGATGATGATTCATGAA 1860
 Db 1801 AAGCAATTTGTGAAGAACAGAACACTGGAATTTATACAGATGATGATTCATGAA 1860
 QY 1861 GAAAGCAGATAGAAAGTGTGAAAAATGAAATTCAGCTTCTCTAGTTGTAAGAAA 1920
 Db 1861 GAAAGCAGATAGAAAGTGTGAAAAATGAAATTCAGCTTCTCTAGTTGTAAGAAA 1920
 QY 1921 GAAAAAGCATCTTGATGAAATATGTAACGTGGGAGAAATTTGCCATGCTAAGACTG 1980
 Db 1921 GAAAAAGCATCTTGATGAAATATGTAACGTGGGAGAAATTTGCCATGCTAAGACTG 1980
 QY 1981 GAGCTAGACCAATGAACATCAGAGCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040
 Db 1981 GAGCTAGACCAATGAACATCAGAGCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040

 RESULT 22
 US-09-709-729-375
 ; Sequence 375, Application us/09709729
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yugu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Wang, Aljun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C22
 ; CURRENT APPLICATION NUMBER: US/09/709,729
 ; CURRENT FILING DATE: 2000-11-09
 ; NUMBER OF SEQ ID NOS: 351
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 375
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-709-729-375

 Query Match 100.0%; Score 2040; DB 28; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 2,7e-264;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Db 181 ATGGGCAAGTGTGCCCCCATCTCCCTCGTCGAGGGGAGTGGCAAGACAAGCTG 240
QY 241 GGGCTTCTGGAGACCGAGACTGCTTGAAGACACTCAGAAACAATGGGCAAG 300
Db 241 GGGCTTCTGGAGACCGAGACTGCTTGAAGACACTCAGAAACAATGGGCAAG 300
QY 301 TGGTGTCCACTGCTCCCTGCTGCAAGGGGAGCGCAGAGCAAGAGTGGGCTTGG 360
Db 301 TGGTGTCCACTGCTCCCTGCTGCAAGGGGAGCGCAGAGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTACGTACAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGTACAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
QY 421 GACAAAGTCCACAGAGTGCCTGTTGGGGTAAATCCCAAAAAGATCTATGCTATG 480
Db 421 GACAAAGTCCACAGAGTGCCTGTTGGGGTAAATCCCAAAAAGATCTATGCTATG 480
QY 481 CTCAGGACACTGACGTGAACAGAGGACAAAGCAAAAGAGTGCCTACATCTGACC 540
Db 481 CTCAGGACACTGACGTGAACAGAGGACAAAGCAAAAGAGTGCCTACATCTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGTCAACTTAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGTCAACTTAT 600
QY 601 GTCCCTTACACAACAAAAGAGACAGCTCTGTAAAGCCGTCACATGGCAGGAAGATGAA 660
Db 601 GTCCCTTACACAACAAAAGAGACAGCTCTGTAAAGCCGTCACATGGCAGGAAGATGAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGACGACTGATCAAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTAAATGTTGCTGGAACATGACGACTGATCAAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTACGTATCTATTAATGAATGAATGAATGAATGAATGAATGAAT 780
Db 721 ACCACTGTGCACTACGTATCTATTAATGAATGAATGAATGAATGAATGAATGAAT 780
QY 781 TATGCTGTGATATGCAATCAAAAACAGATGGCCCTACACACACTTACTGTGTA 840
Db 781 TATGCTGTGATATGCAATCAAAAACAGATGGCCCTACACACACTTACTGTGTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
QY 901 CTGATAGATATGGAAGACTGCTCATACCTGCTATGTTGATGATGACAGCAATTA 960
Db 901 CTGATAGATATGGAAGACTGCTCATACCTGCTATGTTGATGATGACAGCAATTA 960
QY 961 GTGAGCCTTCTACTGAGCAAAAATATGATATCTTCAAGATCTATCTGAGACAG 1020
Db 961 GTGAGCCTTCTACTGAGCAAAAATATGATATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTCCAGTTACTTCTGACATAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTCCAGTTACTTCTGACATAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAGGCAAGTGAATAGCCAGACAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAGGCAAGTGAATAGCCAGACAGAGAA 1200
QY 1201 ATGTCTCAGAGACAGAAATTAATAGAGTGTGATAGAGAGTGAAGAAATAGAG 1260
Db 1201 ATGTCTCAGAGACAGAAATTAATAGAGTGTGATAGAGAGTGAAGAAATAGAG 1260
QY 1261 AAGCATGAAGTAAATATGTTGGAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
|||||

Db 1261 AAGCATGAAGTAAATATGTTGGAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
QY 1321 AATGGTAAATATGATTAATCTTCAAGAGAGACAGACCAACCTGAATAATGCAATTT 1380
Db 1321 AATGGTAAATATGATTAATCTTCAAGAGAGACAGACCAACCTGAATAATGCAATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGTATACAGAAATTTCCGAATTAAGTCTGACATCAAGAA 1440
Db 1381 CCTGACACAGAAAGTGAAGTATACAGAAATTTCCGAATTAAGTCTGACATCAAGAA 1440
QY 1441 AAACGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACAGACTTAAAGTACA 1500
Db 1441 AAACGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACAGACTTAAAGTACA 1500
QY 1501 TCAGAGAGAGTTCACAAAGCTTGAGGGCAGTGAATTTGGCCAGAGAGAAAGTCT 1560
Db 1501 TCAGAGAGAGTTCACAAAGCTTGAGGGCAGTGAATTTGGCCAGAGAGAAAGTCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGAGATGATAGACAGCTAGAAATTTATGCGTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATAGAGATGATAGACAGCTAGAAATTTATGCGTATCGAA 1620
QY 1621 GAATGAAGAAACAGCAGAGTATCTATGCGATTCAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAATGAAGAAACAGCAGAGTATCTATGCGATTCAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCCAAAGAGAGCAGAAACACTTAAAGC 1740
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCCAAAGAGAGCAGAAACACTTAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCACAGTGAAGCAAAATATGACTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCACAGTGAAGCAAAATATGACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTACAGATGAGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTCTGAGCTTCTTCTAGTTGTAAGAA 1920
Db 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTCTGAGCTTCTTCTAGTTGTAAGAA 1920
QY 1921 GAAAAGCAGATTTGCAATGAATATGATGCTGCGGAGAAATTTGCAATGCTAAGACTG 1980
Db 1921 GAAAAGCAGATTTGCAATGAATATGATGCTGCGGAGAAATTTGCAATGCTAAGACTG 1980
QY 1981 GAGCTAGACACATGAACATCAGAGCAGCTAAAAAAGAAAAAAGAAAAAAGAAAA 2040
Db 1981 GAGCTAGACACATGAACATCAGAGCAGCTAAAAAAGAAAAAAGAAAAAAGAAAA 2040

RESULT 23
US-09-759-143-375
Sequence 375, Application US/09759143
GENERAL INFORMATION:
APPLICANT: Xu, Jiangshun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jlang, Yungui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Rafter, Gary R.
APPLICANT: Rafter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, AlJun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 29; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAATGGGCAAGTGTGCTCCGTTGCCCTCCCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAATGGGCAAGTGTGCTCCGTTGCCCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGCGCGGCACTGCTCCGCTGCTGAGGAGGAGTGGCAAGACACGAG 240
DB 181 ATGGGCAATGGTGCGCGGCACTGCTCCGCTGCTGAGGAGGAGTGGCAAGACACGAG 240
QY 241 GCGGCTTCTGAGAGACGACGACGACTGTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGAGACGACGACGACTGTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGCTGCCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGCTGCCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGATGACGATGCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAAGTCTG 420
DB 361 GGAGACTAGATGACGATGCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAAGTCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATCTGTCAG 480
DB 421 GACAACTCCACAGAGCTGCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATCTGTCAG 480
QY 481 CTCAGGACACTGACGTGAACAAGAAAGACAAAGAGACTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAAAGAGCAAGCAAGAGACTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCACAAGTAGTAAGAACTCTGAGACAGAGATGCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCACAAGTAGTAAGAACTCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCTTTCAGACAAAGAGAGAGAGCTGTATGAAGCCGTACAAAGCCAGAGAGATGA 660
DB 601 GTCTTTCAGACAAAGAGAGAGAGCTGTATGAAGCCGTACAAAGCCAGAGAGATGA 660
QY 661 TGTGCTTAATGTGCTGGAACATGCGACTGATCCAAATATTCACATGATGTAAT 720
DB 661 TGTGCTTAATGTGCTGGAACATGCGACTGATCCAAATATTCACATGATGTAAT 720
QY 721 ACCAGCTGACACTAGCTTCTATATGAAGTAATTAATGAGCCAAAGACAGCTCTTA 780
DB 721 ACCAGCTGACACTAGCTTCTATATGAAGTAATTAATGAGCCAAAGACAGCTCTTA 780
QY 781 TATGCTGATATGATCAAAATCAAAAGCAAGATGCGCTCACACACATGTTACTTGGTGA 840
DB 781 TATGCTGATATGATCAAAATCAAAAGCAAGATGCGCTCACACACATGTTACTTGGTGA 840
QY 841 CATGACAAACAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900

DB 841 CATGACAAACAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGAGAGAGCTGCTCATACATGCTGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATAGATATGAGAGAGCTGCTCATACATGCTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTCAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATATCTGAGCAGAGC 1020
DB 961 GTCAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATATCTGAGCAGAGC 1020
QY 1021 GCCAGAGATATGCTTCTTCTACTCATCATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTTCTTCTACTCATCATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGACAAAGCTTAAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGGTTCAAAAGGAGTGAATAATAGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGATCACAAGGTTCAAAAGGAGTGAATAATAGCCAGCCAGAGAA 1200
QY 1201 ATGCTCAAGAACCAAAATTAATTAAGATGTTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACCAAAATTAATTAAGATGTTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATATGTTGGATTACTAGAAACCTGCTAATGTTGCTCACTGCTGGC 1320
DB 1261 AAGCATGAAGTAATATGTTGGATTACTAGAAACCTGCTAATGTTGCTCACTGCTGGC 1320
QY 1321 AATGTTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
DB 1321 AATGTTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGGCAATTTACTTCTACTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGGCAATTTACTTCTACTCAAGAA 1440
QY 1441 AAGCATGCAAAATATCTTCTGAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
DB 1441 AAGCATGCAAAATATCTTCTGAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCCAAAGGCTTGAAGGCGAGTGAATATGCTGATGCTG 1560
DB 1501 TCAGAGGAAGAGTCCAAAGGCTTGAAGGCGAGTGAATATGCTGATGCTG 1560
QY 1561 CAAGAACCGAATAATTAAGATGTTGATAGAGACTGAGAAATTTTATGGCTATCGAA 1620
DB 1561 CAAGAACCGAATAATTAAGATGTTGATAGAGACTGAGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAGCAGGAAGTACTCATGTCGATTTCCAGAAACCTGACTAATGCTG 1680
DB 1621 GAAATGAAGAGCAGGAAGTACTCATGTCGATTTCCAGAAACCTGACTAATGCTG 1680
QY 1681 ACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGTAAGC 1740
DB 1681 ACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGTAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGATTAACAAGTACAGAGCAAAATGATACTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAGATTAACAAGTACAGAGCAAAATGATACTGAG 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACCTGGAATTTTACAGATGAGATCTGATTCATGA 1860
DB 1801 AAGCAATTTTGTGAAGACAGAACCTGGAATTTTACAGATGAGATCTGATTCATGA 1860
QY 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAATTTCTGAGCTTCTTATGTTGAAGAA 1920
DB 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAATTTCTGAGCTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1980

Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Oy 1981 GAGCTAGACAAATGAATGAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACAAATGAATGAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 24
US-09-780-669-375
: Sequence 375, Application US/09780669
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skelky, Yastir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hurst, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C24
: CURRENT APPLICATION NUMBER: US/09/780, 669
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-780-669-375

Query Match 100.0%; Score 2040; DB 30; Length 2040;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;

Db 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGACACAGCTCCGTGAGAAATCTG 420
Oy 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
Oy 481 CTCAGGACACTGAGCTGAACAAAGAGCAAGCAAAAGAGACTGCTACATGTCGGCC 540
Db 481 CTCAGGACACTGAGCTGAACAAAGAGCAAGCAAAAGAGACTGCTACATGTCGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAACTAGTAAAACTCTGCTGGAGACAGAGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTAGTAAAACTCTGCTGGAGACAGAGATGTCACTTAAT 600
Oy 601 GTCTTTGACAAACAAAAGAGACAGCTCTGATTAAGGCGCTACATGCTCCAGAAATGAA 660
Db 601 GTCTTTGACAAACAAAAGAGACAGCTCTGATTAAGGCGCTACATGCTCCAGAAATGAA 660
Oy 661 TGTGGGTTAATGTTGCTGGACATGGCACTGATCCAAATATTCCAGATAGTATGGAAT 720
Db 661 TGTGGGTTAATGTTGCTGGACATGGCACTGATCCAAATATTCCAGATAGTATGGAAT 720
Oy 721 ACCACTCTGCACTAGCCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTTA 780
Db 721 ACCACTCTGCACTAGCCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTTA 780
Oy 781 TATGCTGCTGATATGCAATCAAAAACAGATGCGCTACACCACTGTTACTGTGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAACAGATGCGCTACACCACTGTTACTGTGTGA 840
Oy 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAAAAGCAATTAATTAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAAAAGCAATTAATTAATGA 900
Oy 901 CTGATATGATATGAAGAGCTGCTCATATCTGCTGATGTTGTTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAGAGCTGCTCATATCTGCTGATGTTGTTGATCAGCAAGTATA 960
Oy 961 GTACGCTTCTACTTGGACAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
Db 961 GTACGCTTCTACTTGGACAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
Oy 1021 GCCAGAGTATGCTGTTCTATGATCATCATGATTAATTTGCAAGTATCTTCTGCTAC 1080
Db 1021 GCCAGAGTATGCTGTTCTATGATCATCATGATTAATTTGCAAGTATCTTCTGCTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Oy 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCAAGGCAAGTGAATAATGACCAAGCAAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCAAGGCAAGTGAATAATGACCAAGCAAGAA 1200
Oy 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
Oy 1261 AAGCATGAAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Oy 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAAAATGCAATTT 1380
Db 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAAAATGCAATTT 1380
Oy 1381 CCTGACAAACGAAGTGAAGATGATCAAGAAATTTGGAATTTGTTCTGACACAAAGAA 1440
Db 1381 CCTGACAAACGAAGTGAAGATGATCAAGAAATTTGGAATTTGTTCTGACACAAAGAA 1440
Oy 1441 AAACAGATCCAAAATACTCTCTGAAAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1500
Db 1441 AAACAGATCCAAAATACTCTCTGAAAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1500

Db	1441	AAACAGATCCAAAAATCTTCTGTGAAAACAGAACCCAGAACACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGAGTCACAAAAGCGTTGAGGGCAGTGAATAATGCCAGCAGAGAAAGATCT	1560
Db	1501	TCAGAGGAAGAGTCACAAAAGCGTTGAGGGCAGTGAATAATGCCAGCAGAGAAAGATCT	1560
Qy	1561	CAGAAACCGAATATTAATGAAGTGGTATGATAGAGCTGAAAAATTTATGGCTATCGAA	1620
Db	1561	CAGAAACCGAATATTAATGAAGTGGTATGATAGAGCTGAAAAATTTATGGCTATCGAA	1620
Qy	1621	GAATGCAAGACACGAGGAAGTACTCATGTCGGATTGCCAGAAAAACCTGACTAATGGTGCC	1680
Db	1621	GAATGCAAGACACGAGGAAGTACTCATGTCGGATTGCCAGAAAAACCTGACTAATGGTGCC	1680
Qy	1681	ACTGCTGGCAATGGTGATGATGATTAATTTCTCCAGAGAAAGCAGAAACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGATGATGATTAATTTCTCCAGAGAAAGCAGAAACCTGAAAGC	1740
Qy	1741	CAGCAATTTCTCGACACTGAGATGAAGAGTATCACAGTGACAGCAAAAATGATCTACG	1800
Db	1741	CAGCAATTTCTCGACACTGAGATGAAGAGTATCACAGTGACAGCAAAAATGATCTACG	1800
Qy	1801	AAGCAATTTTGTGAAGACAGAAACACTGGAATATTACAGATGAGATTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGACAGAAACACTGGAATATTACAGATGAGATTCTGATTCATGAA	1860
Qy	1861	GAAGAAGACATGGAAGTGGTTGAAAAAATGAATTCGACCTTCTTGTGGTAAAGAA	1920
Db	1861	GAAGAAGACATGGAAGTGGTTGAAAAAATGAATTCGACCTTCTTGTGGTAAAGAA	1920
Qy	1921	GAAGAAAGACATCTTGATGATAAATAGTACGTTGCCGGAGAAATTCATGCTGAAGCTG	1980
Db	1921	GAAGAAAGACATCTTGATGATAAATAGTACGTTGCCGGAGAAATTCATGCTGAAGCTG	1980
Qy	1981	GAGCTGACACATGAAACATCAGAGCCAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTGACACATGAAACATCAGAGCCAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040

Query Match	100.0%;	Score 2040;	DB 31;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 2.7e-264;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 ATGCGGTTGAGGTTGATTCACAGCGGGCTGCTCTTGTAAGAAGCCATTGGTCTC 60
|||||
Db 1 ATGCGGTTGAGGTTGATTCACAGCGGGCTCTTCTGTGAAGAAGCCATTGGTCTC 60

QY	61	AGGACCAAGATGGGCAAGTGGTGGTGGCGTTGGTCCCGTCCGCTGCGAGGGAGGCGGGCAAG	120
Db	61	AGGACCAAGATGGGCAAGTGGTGGTGGCGTTGGTCCCGTCCGCTGCGAGGGAGGCGGGCAAG	120
QY	121	AGCAACGtGGGCACTTCTGGAGACCAAGAGACTCTGCTATGAAGCACTCTAGAGCAAG	180
Db	121	AGCAACGtGGGCACTTCTGGAGACCAAGAGACTCTGCTATGAAGCACTCTAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGGCCGCACTGGTTCCTGCTGCAGAGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCCGCACTGGTTCCTGCTGCAGAGGGAGTGGCAAGCAAGCTG	240
QY	241	GGCGCTTGTGGAGACCAAGAGACTCTGCTATGAAGCACTCGAAGCAAGATGGGCAAG	300
Db	241	GGCGCTTGTGGAGACCAAGAGACTCTGCTATGAAGCACTCGAAGCAAGATGGGCAAG	300
QY	301	TGGTGTCCCACTGGCTTCCTGCTGTCAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360
Db	301	TGGTGTCCCACTGGCTTCCTGCTGTCAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360
QY	361	GGAGACTAGATGACAGAGCGCTTCATGAGCCCGAGGACACAGCTCCGCTGGAACATCTG	420
Db	361	GGAGACTAGATGACAGAGCGCTTCATGAGCCCGAGGACACAGCTCCGCTGGAACATCTG	420
QY	421	GACAAAGCTCCAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATG	480
Db	421	GACAAAGCTCCAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATG	480
QY	481	CTCAGGGACACTGACGtGtAACAGAGACCAAGAAAGAGAGCTCTTACACTGGCC	540
Db	481	CTCAGGGACACTGACGtGtAACAGAGACCAAGAAAGAGAGCTCTTACACTGGCC	540
QY	541	TCTGCAATGGGAATTCAGAAATGTAATAACTCTGCTGAGACAGAGATGCACTTAAT	600
Db	541	TCTGCAATGGGAATTCAGAAATGTAATAACTCTGCTGAGACAGAGATGCACTTAAT	600
QY	601	GTCCTTGACACAAAAGAGACAGCTGCTATGAAGCGGTACAAATGCCAGGAACATGA	660
Db	601	GTCCTTGACACAAAAGAGAGACAGCTGCTATGAAGCGGTACAAATGCCAGGAACATGA	660
QY	661	TGTGCGTAAATGTTGCTGGAACAATGAGCACTGATCCAAATATTCAGATAGTGGAAAT	720
Db	661	TGTGCGTAAATGTTGCTGGAACAATGAGCACTGATCCAAATATTCAGATAGTGGAAAT	720
QY	721	ACCACTCTGCACTACGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTTGA	780
Db	721	ACCACTCTGCACTACGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTTGA	780
QY	781	TATGTCGTGATATCGAATCAAAAACAAACATGAGGCTCACACACTGTTACTTGGTGA	840
Db	781	TATGTCGTGATATCGAATCAAAAACAAACATGAGGCTCACACACTGTTACTTGGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTTTATCAAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTTTATCAAGAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGGAATAGATATGGAAGAGCTGCTCTCATCTTGCCTGATATGTTGGAGATCAGCAAGTATA	960
Db	901	CTGGAATAGATATGGAAGAGCTGCTCTCATCTTGCCTGATATGTTGGAGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGGAGCAAAATATTTGAATGATCTTCTCAAGATCTATCTGGACAGACG	1020
Db	961	GTCAGCCTTCTACTTGGAGCAAAATATTTGAATGATCTTCTCAAGATCTATCTGGACAGACG	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC	1080
QY	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAACAAAGAAATCCAGAACAAAGACTTAAG	1140
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAACAAAGAAATCCAGAACAAAGACTTAAG	1140

QY	1141	CTGCATCAGAGAGAAAGTCACAAAGGCTTCAAAGCCAGTGGAAATATAGCCAGCCAGAGAA	1200
Db	1141	CTGCATCAGAGAGAAAGTCACAAAGGCTTCAAAGCCAGTGGAAATATAGCCAGCCAGAGAA	1200
QY	1201	ATGCTCTAAAGACACAGAAATTAATTAAGATGGGATAGAGAGGTTGAAGAAAGAAATGAG	1260
Db	1201	ATGCTCTAAAGACACAGAAATTAATTAAGATGGGATAGAGAGGTTGAAGAAAGAAATGAG	1260
QY	1261	AAGCATGAAAGTAAATATGAGGATTACTAAGAAACCTGACTAAATGAGTGTCACTGCTGGC	1320
Db	1261	AAGCATGAAAGTAAATATGAGGATTACTAAGAAACCTGACTAAATGAGTGTCACTGCTGGC	1320
QY	1321	AATGGTATTAATGATTAATCTCTCAAAGGAGACAGAACCTGAAAAATCAGCAATTT	1380
Db	1321	AATGGTATTAATGATTAATCTCTCAAAGGAGACAGAACCTGAAAAATCAGCAATTT	1380
QY	1381	CTGTACACAGAAAGTGAAGATTCACAAATTTGGATTTAGTTTCTGACTACAAAGAA	1440
Db	1381	CTGTACACAGAAAGTGAAGATTCACAAATTTGGATTTAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGACAGACTTAAAGCTGACA	1500
QY	1501	TCACAGGAGAGAGTCACAAAGGCTTGAAGGCACTGAAAATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCACAGGAGAGAGTCACAAAGGCTTGAAGGCACTGAAAATGGCCAGCCAGAGAAAAGATCT	1560
QY	1561	CAGAACCCAAATTAATTAAGATGGTGTATAGAGAGCTTGAATTTTATGGCTATCGAA	1620
Db	1561	CAGAACCCAAATTAATTAAGATGGTGTATAGAGAGCTTGAATTTTATGGCTATCGAA	1620
QY	1621	GAATGAAAGACAGGAGAGTACTCATGTGCGATTTCCGAAACCTGACTAATGGTGGC	1680
Db	1621	GAATGAAAGACAGGAGAGTACTCATGTGCGATTTCCGAAACCTGACTAATGGTGGC	1680
QY	1681	ACTGCTGGCAATGATGATGATTAATTTCTCCAAAGGAGAGAGCAACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGATGATGATTAATTTCTCCAAAGGAGAGAGCAACCTGAAAGC	1740
QY	1741	CAGCAATTCCTGACACTGAGATGAAAGATTCACAGTACAGAACCAAAATGATTAAGTACG	1800
Db	1741	CAGCAATTCCTGACACTGAGATGAAAGATTCACAGTACAGAACCAAAATGATTAAGTACG	1800
QY	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTCCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTCCTGATTCATGAA	1860
QY	1861	GAAGACAGATAGAGTGGTTGAAAAAATGAATTCAGACTTCTTCACTAGTTGTAAAGAA	1920
Db	1861	GAAGACAGATAGAGTGGTTGAAAAAATGAATTCAGACTTCTTCACTAGTTGTAAAGAA	1920
QY	1921	GAAGAAACATCTTGCATGAAAATAGTACGTTGCGGGAGAAATTCAGCTAAGACTG	1980
Db	1921	GAAGAAACATCTTGCATGAAAATAGTACGTTGCGGGAGAAATTCAGCTAAGACTG	1980
QY	1981	GAGCTGACACATGAAACATCAGACCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAAA	2040
Db	1981	GAGCTGACACATGAAACATCAGACCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAAA	2040
RESULT 26			
US-09-822-827-375			
; Sequence 375, Application US/09822827			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121_534C1			
; CURRENT APPLICATION NUMBER: US/09/822,827			
; NUMBER OF SEQ ID NOS: 982			
; SOFTWARE: FastSeq for Windows Version 3.0			

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; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
us-09-822-827-375

Query Match      100.0%; Score 2040; DB 31; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGGTGTTGAGGTGATTCATCGCGGGTGGCTCTCTCTGTTGAAGAAGCAATTTGGTCTC 60
Db       1  ATGGGTGTTGAGGTGATTCATCGCGGGTGGCTCTCTCTGTTGAAGAAGCAATTTGGTCTC 60

QY      61  AGGAGCAAGATGGCGAAGTGTGCTGCCCTTCTCCCTGCTGCGAGGAGGACGGCAAG 120
Db       61  AGGAGCAAGATGGCGAAGTGTGCTGCCCTTCTCCCTGCTGCGAGGAGGACGGCAAG 120

QY      121  AGCAACGTGGGCACTTCTGAGACACGACGACTCTGCTATGAAGACACTGACGAGCAAG 180
Db       121  AGCAACGTGGGCACTTCTGAGACACGACGACTCTGCTATGAAGACACTGACGAGCAAG 180

QY      181  ATGGGCAATGGTGGCCGCCACCTGCTTCCCTGCTGAGGAGGAGTGGCAAGACACGTG 240
Db       181  ATGGGCAATGGTGGCCGCCACCTGCTTCCCTGCTGAGGAGGAGTGGCAAGACACGTG 240

QY      241  GGGCGCTTGTGAGACCAAGCAGCACTCTGCTATGAAGACACTGAGAAACAAGTGGCAAG 300
Db       241  GGGCGCTTGTGAGACCAAGCAGCACTCTGCTATGAAGACACTGAGAAACAAGTGGCAAG 300

QY      301  TGGTGTGCACTGCTTCCCTGCTGTCAGAGGGGGAGCGGCAAGACGAAGTGGCGCTTGG 360
Db       301  TGGTGTGCACTGCTTCCCTGCTGTCAGAGGGGGAGCGGCAAGACGAAGTGGCGCTTGG 360

QY      361  GGAGACTACGATGACAGTGCCTTCATGTGAGGCCAGGTACCAGTCCGTGGAAAGATCTG 420
Db       361  GGAGACTACGATGACAGTGCCTTCATGTGAGGCCAGGTACCAGTCCGTGGAAAGATCTG 420

QY      421  GACAAGCTCCACAGAGCTCCTGTTGGGGTAAAGTCCCGACAAGAGATCTCATCTGCATG 480
Db       421  GACAAGCTCCACAGAGCTCCTGTTGGGGTAAAGTCCCGACAAGAGATCTCATCTGCATG 480

QY      481  CTCAGGGACCTGACGTGGAACAAGAGCAACAAGAGAGACTGCTTACATCTGGCC 540
Db       481  CTCAGGGACCTGACGTGGAACAAGAGCAACAAGAGAGACTGCTTACATCTGGCC 540

QY      541  TCTGCCAATGGGAATTCACAAGTACGTAAACCTCTGCTGACAGACGATGTCACTTAAT 600
Db       541  TCTGCCAATGGGAATTCACAAGTACGTAAACCTCTGCTGACAGACGATGTCACTTAAT 600

QY      601  GTTCCTGACAAACAAAAAGGAGCAGTCTGATPAAAGCGGCTCAATGCCAGGAAGTGA 660
Db       601  GTTCCTGACAAACAAAAAGGAGCAGTCTGATPAAAGCGGCTCAATGCCAGGAAGTGA 660

QY      661  TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db       661  TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720

QY      721  ACCACTCTGACACTAGCTATCTATTAATGAAGTAAATTAATGAGCCAAACACTGCTT 780
Db       721  ACCACTCTGACACTAGCTATCTATTAATGAAGTAAATTAATGAGCCAAACACTGCTT 780

QY      781  TATGGTGTGATATGGAATCAAAAAACAAGATGGCTCAGACACCTGTTACTTGGTGA 840
Db       781  TATGGTGTGATATGGAATCAAAAAACAAGATGGCTCAGACACCTGTTACTTGGTGA 840

QY      841  CATGAGCAAAAAACGCAAGTCTGAAATTTTAAATCAGAAAAAGCGAATTTAAATGA 900
Db       841  CATGAGCAAAAAACGCAAGTCTGAAATTTTAAATCAGAAAAAGCGAATTTAAATGA 900

QY      901  CTGGATAGATATGGAAGACCTGCTCATACTGCTGTATGTGTTGGATCAGCAAGTATA 960
Db       901  CTGGATAGATATGGAAGACCTGCTCATACTGCTGTATGTGTTGGATCAGCAAGTATA 960

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|||||
Db 181 ATGGGAAAGTGTGCGCCGCTCTCCCTGCTGCAAGGGGAGTGGCAAGCAACGCTG 240
QY 241 GGGGCTTTGGAGACGACGACGACTGCTATGAAGACATCTCAGGAACAAGATGGGCAAG 300
Db 241 GGGGCTTTGGAGACGACGACGACTGCTATGAAGACATCTCAGGAACAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCTGAGGGGGAGGGGCAAGAGCAAGTGGGCGCTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCTGAGGGGGAGGGGCAAGAGTGGGCGCTGG 360
QY 361 GGAAGACTAGATGACAGTGGCTTCAATGAGCCAGGATCCAGCTCCGTGAGAAATCTG 420
Db 361 GGAAGACTAGATGACAGTGGCTTCAATGAGCCAGGATCCAGCTCCGTGAGAAATCTG 420
QY 421 GAAAGCTCCAGAGCTGCTGCTGGGGTAAAGTCCCGCAAGAAAGATCTCATGCTATG 480
Db 421 GAAAGCTCCAGAGCTGCTGCTGGGGTAAAGTCCCGCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGAGACACTGACGTGAAACAAGAGACAAAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGACGTGAAACAAGAGAGACAAAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCCTGCTGACAGACATGCTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCCTGCTGACAGACATGCTCAACTTAAT 600
QY 601 GTGCTTGACAAACAAAAGAGAGAGCTGATAAAGGCGCTACAAATCCGAGGAAGATGA 660
Db 601 GTGCTTGACAAACAAAAGAGAGAGCTGATAAAGGCGCTACAAATCCGAGGAAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGATGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGATGAAT 720
QY 721 ACCACTCTGCACATACCTATCTATTAATGAAGATTAATTAATGCGCAAGACATGCTT 780
Db 721 ACCACTCTGCACATACCTATCTATTAATGAAGATTAATTAATGCGCAAGACATGCTT 780
QY 781 TATGCTGCTGATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 840
Db 781 TATGCTGCTGATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGA 900
QY 901 CTGATATGATATGGAAGAGACTGCTCTCATCTTGTATGTTGTGATATGCAAGATATA 960
Db 901 CTGATATGATATGGAAGAGACTGCTCTCATCTTGTATGTTGTGATATGCAAGATATA 960
QY 961 GTGAGCCTTTACTGAGCAAAATATGATTAATCTCTCAAGATCATATCTGAGCAGAG 1020
Db 961 GTGAGCCTTTACTGAGCAAAATATGATTAATCTCTCTCAAGATCATATCTGAGCAGAG 1020
QY 1021 GCCAGAGAGATGCTGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGAGATGCTGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGACAAAGCTTAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGACAAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGGCGAGTAAATAGCCAGCAAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGGCGAGTAAATAGCCAGCAAGAGAA 1200
QY 1201 ATGCTTCAGAACACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTTCAGAACACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGTTGGATTAATGAGAAACCTGACTAATGTTGCTGCTGC 1320
|||||

Db 1261 AAGCATGAAGATTAATTAATGTTGGATTAATGAGAAACCTGACTAATGTTGCTGCTGC 1320
QY 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGAGAGACACCTGAAATATGCAATTT 1380
Db 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGAGAGACACCTGAAATATGCAATTT 1380
QY 1381 CTTGACAAACGAAAGTGAAGATATCAGAGATTTGCGAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAACGAAAGTGAAGATATCAGAGATTTGCGAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCGCAAAATTTCTTCTGAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCGCAAAATTTCTTCTGAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGTGCACAAAGGCTTGAAGGCGATGAAATTTGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGTGCACAAAGGCTTGAAGGCGATGAAATTTGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCCAGAAATTAATTAAGATGATGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACCCAGAAATTAATTAAGATGATGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
QY 1621 GAATGAAGAGACGAGAAATTTCTGAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1680
Db 1621 GAATGAAGAGACGAGAAATTTCTGAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1680
QY 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCAAGAGAGAGAGACACCTGGAAGC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCAAGAGAGAGAGACACCTGGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGGAATGAAGATATCACAGTACAGCAACAAATGATGATCGAG 1800
Db 1741 CAGCAATTTCTGACACTGGAATGAAGATATCACAGTACAGCAACAAATGATGATCGAG 1800
QY 1801 AAGCAATTTGTAAGAGACAGAACTGGAATTTACAGATGATGATGATGATGATGATG 1860
Db 1801 AAGCAATTTGTAAGAGACAGAACTGGAATTTACAGATGATGATGATGATGATGATG 1860
QY 1861 GAAAGAGAGATGAAGAGTGTGAAAAATGAAATTTGAGCTTCTGATGTTGAAGAA 1920
Db 1861 GAAAGAGAGATGAAGAGTGTGAAAAATGAAATTTGAGCTTCTGATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGCGGAGAGAAATGGCATGTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGCGGAGAGAAATGGCATGTAAGACTG 1980
QY 1981 GAGCTAGACACATGAAACCTGAGAGCCAGCTAATTAATTAATTAATTAATTAATTA 2040
Db 1981 GAGCTAGACACATGAAACCTGAGAGCCAGCTAATTAATTAATTAATTAATTAATTA 2040

RESULT 29
US-09-895-793-375
; Sequence 375, Application US/09895793
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguang
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-375

Query Match 100.0%; Score 2040; DB 33; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTGGTTGAGTGGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGTGCTC 60
DB 1 AAGGTGGTTGAGTGGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGTGCTC 60
QY 61 AAGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGAGGAGAGGAGGCAAG 120
DB 61 AAGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGAGGAGAGGAGGCAAG 120
QY 121 ACGAAGTGGGCACTTCTGGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAG 180
DB 121 ACGAAGTGGGCACTTCTGGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAG 180
QY 181 AAGGGCAATGGTCCCGCCACTGCTTCCCTGCTGAGGGGAGGTGGCAAGCAACGTG 240
DB 181 AAGGGCAATGGTCCCGCCACTGCTTCCCTGCTGAGGGGAGGTGGCAAGCAACGTG 240
QY 241 AAGGGCAATGGTCCCGCCACTGCTTCCCTGCTGAGGGGAGGTGGCAAGCAACGTG 240
DB 241 AAGGGCAATGGTCCCGCCACTGCTTCCCTGCTGAGGGGAGGTGGCAAGCAACGTG 240
QY 301 TGGTGGTGGCAAGTGTGCTCCCTGCTGAGGGGAGGCGGCAAGCAAGGTGGCGCTTG 360
DB 301 TGGTGGTGGCAAGTGTGCTCCCTGCTGAGGGGAGGCGGCAAGCAAGGTGGCGCTTG 360
QY 361 GAGAGCTAGATGACAGTGTGCTCCCTGCTGAGGGGAGGCGGCAAGCAAGGTGGCGCTTG 420
DB 361 GAGAGCTAGATGACAGTGTGCTCCCTGCTGAGGGGAGGCGGCAAGCAAGGTGGCGCTTG 420
QY 421 GAGAGCTAGATGACAGTGTGCTCCCTGCTGAGGGGAGGCGGCAAGCAAGGTGGCGCTTG 480
DB 421 GAGAGCTAGATGACAGTGTGCTCCCTGCTGAGGGGAGGCGGCAAGCAAGGTGGCGCTTG 480
QY 481 CTCAGGAGACACTGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGGAGACACTGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGGCAATGGGAATTCAGAACTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 TCTGGCAATGGGAATTCAGAACTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GTCCTTGACAAACAAAG 660
DB 601 GTCCTTGACAAACAAAG 660
QY 661 TGTGGTGAATGTGCTGAG 720
DB 661 TGTGGTGAATGTGCTGAG 720
QY 721 ACCACTCTGAGTACGCTATCTATATGAAGATTAATTAATGAGAGAGAGAGAGAGAG 780
DB 721 ACCACTCTGAGTACGCTATCTATATGAAGATTAATTAATGAGAGAGAGAGAGAGAG 780

QY 781 TATGCTGTGATATGCAATCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGCTGTGATATGCAATCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATGACCAAAAAAG 900
DB 841 CATGACCAAAAAAG 900
QY 901 CTGGATAGATATGGAAG 960
DB 901 CTGGATAGATATGGAAG 960
QY 961 GTCAGCCTTCTACTTACGAG 1020
DB 961 GTCAGCCTTCTACTTACGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTATCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTATCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATTCACAAAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATTCACAAAGACTTAAG 1140
QY 1141 CTGACATCAG 1200
DB 1141 CTGACATCAG 1200
QY 1201 ATGCTCAAGAACAG 1260
DB 1201 ATGCTCAAGAACAG 1260
QY 1261 AAGCATGAAGAGATTAATGTGGATTAATGTGGATTAATGTGGATTAATGTGGATTA 1320
DB 1261 AAGCATGAAGAGATTAATGTGGATTAATGTGGATTAATGTGGATTAATGTGGATTA 1320
QY 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCGTGAACAG 1440
DB 1381 CCGTGAACAG 1440
QY 1441 AAGCAATGCAAAATATCTTCTGAAAAACAGCAATTCAGAACTTAAGAGTGA 1500
DB 1441 AAGCAATGCAAAATATCTTCTGAAAAACAGCAATTCAGAACTTAAGAGTGA 1500
QY 1501 TCAG 1560
DB 1501 TCAG 1560
QY 1561 CAAGAACAG 1620
DB 1561 CAAGAACAG 1620
QY 1621 GAAATGAAG 1680
DB 1621 GAAATGAAG 1680
QY 1681 ACTGCTGGCAATGATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ACTGCTGGCAATGATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAG 1800
QY 1801 AAGCAATTTTGTGAG 1860
DB 1801 AAGCAATTTTGTGAG 1860
QY 1861 GAAAGCAGATGAATGATGATTAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920

|||||
Db 1861 GAAAGACGATAGAGGTGAAAAATGAATCTGAGCTTCTTACTGTGAAGAAA 1920
QY 1921 GAAAAACATCTTGCATGTAATAGTACGTGGGAGAGAAATTCGCACTGTAAGCTG 1980
Db 1921 GAAAAACATCTTGCATGTAATAGTACGTGGGAGAGAAATTCGCACTGTAAGCTG 1980
QY 1981 GAGCTAGACACAATGAAACATCAGAGCCAGCTAAAAA 2040
Db 1981 GAGCTAGACACAATGAAACATCAGAGCCAGCTAAAAA 2040

RESULT 30
US-09-895-814-375
; Sequence 375, Application us/09895814
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-895-814-375

Query Match 100.0%; Score 2040; DB 33; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e+264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 GGGCTTCTGAGACACAGACGACTGTGTATGAGACACTCAGAGCAAAAGATGGCGAAG 300
QY 301 TGGTGTCCACTGCTTCCCTCTCGCAGGGGAGCGGCAAGACAGATGGCGCTGG 360
Db 301 TGGTGTCCACTGCTTCCCTCTCGCAGGGGAGCGGCAAGACAGATGGCGCTGG 360
QY 361 GGAGACTAGCATGACAGTGCCTTCATGAGCCCAAGGTACACGCTCCGTGGAGAAAGTCTG 420
Db 361 GGAGACTAGCATGACAGTGCCTTCATGAGCCCAAGGTACACGCTCCGTGGAGAAAGTCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCATGCTCATG 480
Db 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCATGCTCATG 480
QY 481 CTCAGGACACTGACGTGACAAAGAGACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGACACTGACGTGACAAAGAGAGACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCCTGCTGACAGAGAGATGCAATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCCTGCTGACAGAGAGATGCAATTAAT 600
QY 601 GTCTTACACAAACAAAAGAGAGACAGCTGTATAAAGCCGTACAAATGCCAGGAAGTAA 660
Db 601 GTCTTACACAAACAAAAGAGAGACAGCTGTATAAAGCCGTACAAATGCCAGGAAGTAA 660
QY 661 TGTGCGTTAATGTTGCTGTAACATGCGCATGATCCAAATATTCAGATGATGTAAT 720
Db 661 TGTGCGTTAATGTTGCTGTAACATGCGCATGATCCAAATATTCAGATGATGTAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAAGATTAATTAATGGCAAGACAGCTGCTT 780
Db 721 ACCACTGCACTACGCTATCTATATGAAGATTAATTAATGGCAAGACAGCTGCTT 780
QY 781 TATGCTGCTATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
Db 781 TATGCTGCTATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
QY 841 CATGAGCAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGAGAGAGAGCTGCTCATACCTGCTATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAGAGAGAGCTGCTCATACCTGCTATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTGTGAGCAAAATATGATGATATCTCAAGATCATCTGAGCAGACG 1020
Db 961 GTGAGCCTTCTACTGTGAGCAAAATATGATGATATCTCAAGATCATCTGAGCAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGTAATAATCTCTTCTGAAAAACGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGTAATAATCTCTTCTGAAAAACGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAGGGCAGTGAATATACCGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAGGGCAGTGAATATACCGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATTAATGAGGATTAATGAGAAACCTGACTAATGCTGCTGCTG 1320
Db 1261 AAGCATGAAAGTAAATTAATGAGGATTAATGAGAAACCTGACTAATGCTGCTGCTGCTG 1320
QY 1321 AATGATATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGATATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

Oy	1381	CTGTGACACGAAGAAAGTGAAGAGTATCACAATAATTTGGCAATTAGTTTGTGACTACCAAGAA	1440
Db	1381	CTGTGACACGAAGAAAGTGAAGAGTATCACAATAATTTGGCAATTAGTTTGTGACTACCAAGAA	1440
Oy	1441	AACAGATGCCAAATAATCTTTCTTGAAAACACGAACCCGAAACAGACTTAAGCTGACA	1500
Db	1441	AACAGATGCCAAATAATCTTTCTTGAAAACACGAACCCGAAACAGACTTAAGCTGACA	1500
Oy	1501	TCAGAGGAAGAGTCCACAAAGGCTTGGAGGCACTGAAATATGGCCACGAGAAAAAGATCT	1560
Db	1501	TCAGAGGAAGAGTCCACAAAGGCTTGGAGGCACTGAAATATGGCCACGAGAAAAAGATCT	1560
Oy	1561	CAAAACCAACAAATTAATTAAGATAGTGTATACAGAGCTTGAATAATTTATGCTATCGAA	1620
Db	1561	CAAAACCAACAAATTAATTAAGATAGTGTATACAGAGCTTGAATAATTTATGCTATCGAA	1620
Oy	1621	GAATGGAAGAAGCAGGAAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGTTGCC	1680
Db	1621	GAATGGAAGAAGCAGGAAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGTTGCC	1680
Oy	1681	ACTGCTGGCAATGGTGTATGTGATTAATTTCTCCAAAGAGAGACGAACACCTGAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGTGATTAATTTCTCCAAAGAGAGACGAACACCTGAAGC	1740
Oy	1741	CAGCAATTCCTGACACTGTGAATGAAGATACACAGTACGACAAACAAATGATATCTAG	1800
Db	1741	CAGCAATTCCTGACACTGTGAATGAAGATACACAGTACGACAAACAAATGATATCTAG	1800
Oy	1801	AAGCAATTTTGTGAAAGAACGAACACTGGAAATATTACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAAGAACGAACACTGGAAATATTACAGATGAGATTTCTGATTCATGAA	1860
Oy	1861	GAAGAAGCAGATAGAAAGTGTGAAAAAATGAATTCCTGACCTTTCTTAGTTGAAGAA	1920
Db	1861	GAAGAAGCAGATAGAAAGTGTGAAAAAATGAATTCCTGACCTTTCTTAGTTGAAGAA	1920
Oy	1921	GAAAAAACACATCTTGATGTAATAATACTAGCTTGGGGAAGAAATGGCATGCTAAGACTG	1980
Db	1921	GAAAAAACACATCTTGATGTAATAATACTAGCTTGGGGAAGAAATGGCATGCTAAGACTG	1980
Oy	1981	GAGCTAGACACAATGAAACATCGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACAATGAAACATCGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040

US-09-924-400-303			
Query Match	100.0%	Score 2040;	DB 34; Length 2040;
Best Local Similarity	100.0%;	Pred. No. 2,76-264;	
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
OY	1	ATGGTGTTGAGGTGTGATTCATGCCGGGTGGCTCTTCTGTGAAGAAGCCATTTGGTCTC	60
DB	1	ATGGTGTTGAGGTGTGATTCATGCCGGGTGGCTCTTCTGTGAAGAAGCCATTTGGTCTC	60
OY	61	AGGAGCAAGATGGGCAAGTGTGTGCCCTGTCCCTCGTCGAGGGAGAGCGGCAG	120
DB	61	AGGAGCAAGATGGGCAAGTGTGTGCCCTGTCCCTCGTCGAGGGAGAGCGGCAG	120
OY	121	ACCAACGTGGGCACTTCTTGAGACCAGCAGACTCTGTATGAAGACACTCAGAGCAAG	180
DB	121	ACCAACGTGGGCACTTCTTGAGACCAGCAGACTCTGTATGAAGACACTCAGAGCAAG	180
OY	181	ATGGGCAMGTGTGCCGCCACTGCTTCCCTCTGTGAGGGGAGTGGCAAGACGTG	240
DB	181	ATGGGCAMGTGTGTGCCGCCACTGCTTCCCTCTGTGAGGGGAGTGGCAAGACGTG	240
OY	241	GGCGCTTCGAGAGACCAGACAGACTGCTATGAAGACACTGAGAAACAAGATGGGCAAG	300
DB	241	GGCGCTTCGAGAGACCAGACAGACTGCTATGAAGACACTGAGAAACAAGATGGGCAAG	300
OY	301	TGGTCTGCCACTGCTTCCCTGTGTCAGAGGGGAGCGGCAAGACAAAGTGGGCGCTTG	360
DB	301	TGGTCTGCCACTGCTTCCCTGTGTCAGAGGGGAGCGGCAAGACAAAGTGGGCGCTTG	360
OY	361	GGAGACTAGATGAGAGAGTGCCTCATGAGACCCAGGTACACAGTCCGTGGAGAAAGTCTG	420
DB	361	GGAGACTAGATGAGAGAGTGCCTCATGAGACCCAGGTACACAGTCCGTGGAGAAAGTCTG	420
OY	421	GACAAAGCTCCACAGAGCTCCCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG	480
DB	421	GACAAAGCTCCACAGAGCTCCCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG	480
OY	481	CTCAGGAGACCTGCAGCTGTGAACAAGAAAGCAAGCAAAAGAGCTCTCTACATCTGGGC	540
DB	481	CTCAGGAGACCTGCAGCTGTGAACAAGAAAGCAAGCAAAAGAGCTCTCTACATCTGGGC	540
OY	541	TCCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGAGACAGATGTCAACTTAAT	600
DB	541	TCCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGAGACAGATGTCAACTTAAT	600
OY	601	GTCTCTTGACACAAAAAGAGACAGCTCTGTATTAAGGCCGTACATGCCAGAAATGAA	660
DB	601	GTCTCTTGACACAAAAAGAGACAGCTCTGTATTAAGGCCGTACATGCCAGAAATGAA	660
OY	661	TTGTGGTTAATGTGCTGTGAACATGGCACTGTATCCAAATTAATTCAGATGATGGAAAT	720
DB	661	TTGTGGTTAATGTGCTGTGAACATGGCACTGTATCCAAATTAATTCAGATGATGGAAAT	720
OY	721	ACCACTGTGCACACTAGCTATCTATATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
DB	721	ACCACTGTGCACACTAGCTATCTATATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
OY	781	TATGTGCTGTATGTGAATCAAAAAACAAGCATGGCTCTACACACACTGTACTTGGTGTGA	840
DB	781	TATGTGCTGTATGTGAATCAAAAAACAAGCATGGCTCTACACACACTGTACTTGGTGTGA	840
OY	841	CATGAGCAAAAAACCAAGTGTGGAATTTTAATCAAAAAAAGCGAATTTAAATGGA	900
DB	841	CATGAGCAAAAAACCAAGTGTGGAATTTTAATCAAAAAAAGCGAATTTAAATGGA	900
OY	901	CTGAGATAGATATGAAGAGACTGCTGTATGCTACTTGTGCTATGTGTGGAGACAGATATA	960
DB	901	CTGAGATAGATATGAAGAGACTGCTGTATGCTACTTGTGCTATGTGTGGAGACAGATATA	960
OY	961	GTACAGCTTCTACTTGAGCAAAAAATATGATGTATCTTCAAGATCTATCTGGACAGACG	1020
DB	961	GTACAGCTTCTACTTGAGCAAAAAATATGATGTATCTTCAAGATCTATCTGGACAGACG	1020

QY	1021	GCACAGAGATGCTGTTCTTCAGACATCATCATGTAATTTGGCAGTACTTTCTGACATAC	1080
QY	1021	GCACAGAGATGCTGTTCTTCAGACATCATCATGTAATTTGGCAGTACTTTCTGACATAC	1080
Db	1021	GCCAGAGATGCTGTTCTTCTAGCTCATCATCATGTAATTTGGCAGTACTTTCTGACATAC	1080
QY	1081	AAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACACTTAAG	1140
Db	1081	AAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACACTTAAG	1140
QY	1141	CTGACATCAGAGGAAGGTCTCCAAAGGCTCAAAAGGAGTGAATATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGGTCTCCAAAGGCTCAAAAGGAGTGAATATAGCCAGCCAGAGAA	1200
QY	1201	ATGTCTCAAGAACACAGAAATTAATTAAGATGCTGATAGAGAGTGTGAAGAACAAATGAAG	1260
Db	1201	ATGTCTCAAGAACACAGAAATTAATTAAGATGCTGATAGAGAGTGTGAAGAACAAATGAAG	1260
QY	1261	AAGCATGAAAGTAATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGGC	1320
QY	1321	AATGGTGTATATGATTAATTTCTCCAAAGGAGAGACAGAACCTGAAATTCAGCAATTT	1380
Db	1321	AATGGTGTATATGATTAATTTCTCCAAAGGAGAGACAGAACCTGAAATTCAGCAATTT	1380
QY	1381	CCTGCACAAGAAAGTGAAGATATCACAGATTTGGCAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGCACAAGAAAGTGAAGATATCACAGATTTGGCAATTAAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA	1500
QY	1501	TCAGAGGAAGAGTACACAAAGCTTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGGAAGAGTACACAAAGCTTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAGATCT	1560
QY	1561	CAAGACCAGAAATTAATTAAGATGTGTGATAGAGACTGAAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGACCAGAAATTAATTAAGATGTGTGATAGAGACTGAAAAATTTTATGGCTATCGAA	1620
QY	1621	GAATGGAAGAAAGCAACGGAACTACTCATGTCCGATTTCCAGAAAACCTGACTAATGTGTCC	1680
Db	1621	GAATGGAAGAAAGCAACGGAACTACTCATGTCCGATTTCCAGAAAACCTGACTAATGTGTCC	1680
QY	1681	ACTGCTGGCATGTGTGATGATTAATTTCCCAAGGAGAGAGAGAAACCTGAAAGC	1740
Db	1681	ACTGCTGGCATGTGTGATGATTAATTTCCCAAGGAGAGAGAGAGAAACCTGAAAGC	1740
QY	1741	CAGCAATTTCTGCACTGAGAAATGGAAGATATCACAGTGACGAACAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGCACTGAGAAATGGAAGATATCACAGTGACGAACAAATGATACTCAG	1800
QY	1801	AAGCAATTTTGTGAAGAACAGAACTGGAATTAACAGATGAAGAAATTTCTGATTCAGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACTGGAATTAACAGATGAAGAAATTTCTGATTCAGAA	1860
QY	1861	GAAGAAGCAGATAGAAAGTGTGTGAATAAATGAATTTCTGACCTTTCTTATGTTGTAAGAA	1920
Db	1861	GAAGAAGCAGATAGAAAGTGTGTGAATAAATGAATTTCTGACCTTTCTTATGTTGTAAGAA	1920
QY	1921	GAAGAAAGCATCTTGCATGAATAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGCTG	1980
Db	1921	GAAGAAAGCATCTTGCATGAATAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGCTG	1980
QY	1981	GAGCTAGACACATGAAGAACTCTGAGCCAGCTGAAAAATTTTAAAAATTTTAAAAATTTT	2040
Db	1981	GAGCTAGACACATGAAGAACTCTGAGCCAGCTGAAAAATTTTAAAAATTTTAAAAATTTT	2040

RESULT 32
US-10-006-920-375
; Sequence 375, Application US/10006920

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: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Wantanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/006.920
: CURRENT FILING DATE: 2001-12-07
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-006-920-375

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Query Match	Similarity	100.0%	Score 2040;	DB 38;	Length 2040;
Best Local	Similarity	100.0%	Pred. No. 2,7e-264;		
Matches 2040;	Conservative	0;	Mismatches	0;	Indels
					Gaps
QY	1	ATGTGTTGAGTGTGATTCATGCGCGCTGCTCTTCTGTGAGAGACCATTTGGCTTC	60		
Db	1	ATGTGTTGAGTGTGATTCATGCGCGCTGCTCTTCTGTGAGAGACCATTTGGCTTC	60		
OY	61	AGGACCAAGATGGGGAAGTGTGCGCGTTCCTCCCTGCTGGAGGGAGCGGCAG	120		
Db	61	AGGACCAAGATGGGGAAGTGTGCGCGTTCCTCCCTGCTGGAGGGAGCGGCAG	120		
OY	121	AGCAACGTGGGCACTTCTGGAGACCAGCAGCACTCTGCTATGAAGACACTCGAGGACAG	180		
Db	121	AGCAACGTGGGCACTTCTGGAGACCAGCAGCACTCTGCTATGAAGACACTCGAGGACAG	180		
OY	181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTGCTGCACAGGGGAGTGGGCAAGGACAAAGCG	240		
Db	181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTGCTGCACAGGGGAGTGGGCAAGGACAAAGCG	240		
OY	241	GGCGCTTCTGGAGACACGACGACTCTGCTATGAAGACACTGAGAACAAATGGGCAAG	300		
Db	241	GGCGCTTCTGGAGACACGACGACTCTGCTATGAAGACACTGAGAACAAATGGGCAAG	300		
OY	301	TGTGTCTCCCACTGTTCCCTGCTGTCAGGGGGAGCGGCACAGCAAGTGGGCCCTTGG	360		
Db	301	TGTGTCTCCCACTGTTCCCTGCTGTCAGGGGGAGCGGCACAGCAAGTGGGCCCTTGG	360		
OY	361	GGAGACTAGATGAGACAGTGCCTTCATGTGAGAGCCAGCAAGTACCAAGTCCGTGGAGAAATCTG	420		
Db	361	GGAGACTAGATGAGACAGTGCCTTCATGTGAGAGCCAGCAAGTACCAAGTCCGTGGAGAAATCTG	420		
OY	421	GACAAAGTCCACAGAGCTGCTGGTGGGGTAAGTCCCAAGAAAGATCTCATTCGTCAAG	480		
Db	421	GACAAAGTCCACAGAGCTGCTGGTGGGGTAAGTCCCAAGAAAGATCTCATTCGTCAAG	480		

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Qy 481 CTCAGGACACTGACGTGTAACAGAGACAAAGAGAGACTGCTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGTAACAGAGACAAAGAGAGACTGCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAGTCTGCTGAGACAGATGTCACCTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAGTCTGCTGAGACAGATGTCACCTTAAT 600
Qy 601 GTCTTGACAAACAAAGAGACAGCTGTATTAAGGCGGTCATATGCGCAGAGAGATGAA 660
Db 601 GTCTTGACAAACAAAGAGACAGCTGTATTAAGGCGGTCATATGCGCAGAGAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACTGACACTGATCCAAATATTTCCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACTGACACTGATCCAAATATTTCCAGATGATGGAAT 720
Qy 721 ACCACTGTCACACTACGCTATCTATTAAGTAAGTAATTAATGCGCAAGCACTGCTTA 780
Db 721 ACCACTGTCACACTACGCTATCTATTAAGTAAGTAATTAATGCGCAAGCACTGCTTA 780
Qy 781 TATGTTGCTGATATCGATCAAAAAACAAGATGGCTCACAACACTGTTACTGCTGTA 840
Db 781 TATGTTGCTGATATCGATCAAAAAACAAGATGGCTCACAACACTGTTACTGCTGTA 840
Qy 841 CATGAGCAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGACTGCTCTACTACTGCTGATGTTGCTGATCAGCAATATA 960
Db 901 CTGATAGATATGGAAGAGACTGCTCTACTACTGCTGATGTTGCTGATCAGCAATATA 960
Qy 961 GTCAGCCCTTCTACTGAGCAAAATTTGATATCTCTCAAGATCTATCTGAGACAGC 1020
Db 961 GTCAGCCCTTCTACTGAGCAAAATTTGATATCTCTCTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTCCAGATGTTCTTCTGATAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTCCAGATGTTCTTCTGATAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGAGCTCAAAAGTTCAAAAGGCACTGAAATAGCCACAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGCTCAAAAGTTCAAAAGGCACTGAAATAGCCACAGAGAAA 1200
Qy 1201 ATGTCACAGAACAGAAATTAATTAAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCACAGAACAGAAATTAATTAAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAATTAATTAATGTTGAGATTAAGTAAACCTGACTAATGTTGCTGCTGGC 1320
Db 1261 AAGCATGAAATTAATTAATGTTGAGATTAAGTAAACCTGACTAATGTTGCTGCTGGC 1320
Qy 1321 AATGTTATATGATTAATTAATCTCAAGAGAGACAGAACTGAAATTCAGCAATTT 1380
Db 1321 AATGTTATATGATTAATTAATCTCAAGAGAGACAGAACTGAAATTCAGCAATTT 1380
Qy 1381 CCTGACAAACAGAAATGAGATATCACAGAAATTTGCAATAGTTTCTGATACAAAAGA 1440
Db 1381 CCTGACAAACAGAAATGAGATATCACAGAAATTTGCAATAGTTTCTGATACAAAAGA 1440
Qy 1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAGGCTGAGGAGAGTGAAGATGAGCCAGAGAGAGAGAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAAAAGGCTGAGGAGAGTGAAGATGAGCCAGAGAGAGAGAGATCT 1560

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Qy 1561 CAAGAACAGAAATTAATTAAGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGACAGAAATGATGATGCTGATGCTGATGCTGATGCTGATGCTG 1680
Db 1621 GAAATGAAGAGACAGAAATGATGATGCTGATGCTGATGCTGATGCTGATGCTG 1680
Qy 1681 ACTGCTGCAATGCTGATGATGATGATTAATTCCTCCAAAGAGAGAGAAACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGCTGATGATGATGATTAATTCCTCCAAAGAGAGAGAAACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATGATGATGATGATGATGATGATGATGATG 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
Qy 1861 GAAAAGCAGATGAAGTGTGTAAGAAATGAATTTGACCTTCTTCTAGTTGTAAGAA 1920
Db 1861 GAAAAGCAGATGAAGTGTGTAAGAAATGAATTTGACCTTCTTCTAGTTGTAAGAA 1920
Qy 1921 GAAAAGCAGATGCTGATGAAGAAATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 GAAAAGCAGATGCTGATGAAGAAATGATGATGATGATGATGATGATGATGATGATG 1980
Qy 1981 GAGCTAGACACATGAAACATTCAGAGCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 GAGCTAGACACATGAAACATTCAGAGCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 2040

RESULT 33
US-10-010-940-375
: Sequence 375, Application US/10010940
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David
: APPLICANT: Mitchell, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yuqi
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retter, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427D3
: CURRENT APPLICATION NUMBER: US/10/010, 940
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
: US-10-010-940-375

Query Match 100.0%; Score 2040; DB 38; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTTGTTGAGTTGATTCATGCGCGCTGCTTCTGTAAGAACCAATTTGCTGTC 60
Db 1 ATGTTGTTGAGTTGATTCATGCGCGCTGCTTCTGTAAGAACCAATTTGCTGTC 60
Qy 61 AGGAGCAAGATGGGCAATGTTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAATGTTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

```

QY 121 AGCAAGTGGGACCTTCTGGAGACGACGACTGCTATGAAAGCACTCAGAGCAAG 180
 |||||
 Db 121 AGCAAGTGGGACCTTCTGGAGACGACGACTGCTATGAAAGCACTCAGAGCAAG 180
 QY 181 ATGGGAATGTCGCGCCACTGCTTCCCTGCTGAGAGGGGAGTGGCAAGACCAACGTC 240
 |||||
 Db 181 ATGGGAATGTCGCGCCACTGCTTCCCTGCTGAGAGGGGAGTGGCAAGACCAACGTC 240
 QY 241 GGGGCTTTCGAGAGACGACGACTGCTGATGAAACACTCAGAAACAAGATGGGCAAG 300
 |||||
 Db 241 GGGGCTTTCGAGAGACGACGACTGCTGATGAAACACTCAGAAACAAGATGGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGCAAGGTGGCGCTGG 360
 |||||
 Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGCAAGGTGGCGCTGG 360
 QY 361 GGAGATAGATGACAGTGTGCTTCATGAGCCGACAGTACCAGTCCGCTGGAAGAAGTCTG 420
 |||||
 Db 361 GGAGATAGATGACAGTGTGCTTCATGAGCCGACAGTACCAGTCCGCTGGAAGAAGTCTG 420
 QY 421 GACAACTCCACAGAGCTGCTGGGGGTAAGTCCCGCAAAAGATCTCATGTCATG 480
 |||||
 Db 421 GACAACTCCACAGAGCTGCTGGGGGTAAGTCCCGCAAAAGATCTCATGTCATG 480
 QY 481 CTCAGGACACTGACGTGAACAAGAGACAAAGCAAAAGAGACTGCTTACATCTGGCC 540
 |||||
 Db 481 CTCAGGACACTGACGTGAACAAGAGACAAAGCAAAAGAGACTGCTTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGACAGAGATGTCACCTTAAT 600
 |||||
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGACAGAGATGTCACCTTAAT 600
 QY 601 GTCTTGAACAACAAAAGAGAGACGCTGATTAAGGCCCTACATGCGCAGAAAGATGAA 660
 |||||
 Db 601 GTCTTGAACAACAAAAGAGAGACGCTGATTAAGGCCCTACATGCGCAGAAAGATGAA 660
 QY 661 TGTGCGTAAATGTTGCTGGAACATGSCACTGATCCAAATATTCAGATGATGGAAT 720
 |||||
 Db 661 TGTGCGTAAATGTTGCTGGAACATGSCACTGATCCAAATATTCAGATGATGGAAT 720
 QY 721 ACCACTCTGCACACTACGCTATCTTAATGAAGATTAATTAATGSCAAAGACAGCTCTTA 780
 |||||
 Db 721 ACCACTCTGCACACTACGCTATCTTAATGAAGATTAATTAATGSCAAAGACAGCTCTTA 780
 QY 781 TATGTCGTGATATCGAATCAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGA 840
 |||||
 Db 781 TATGTCGTGATATCGAATCAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGA 840
 QY 841 CATGACCAAAAACAGCAAGTCTGAAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
 |||||
 Db 841 CATGACCAAAAACAGCAAGTCTGAAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGGATAGCAAGTATA 960
 |||||
 Db 901 CTGGATAGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGGATAGCAAGTATA 960
 QY 961 GTGAGCTTCTACTTACGCAAAAATATGATGATTTCTTCAAGATCTATCTGAGCAGAG 1020
 |||||
 Db 961 GTGAGCTTCTACTTACGCAAAAATATGATGATTTCTTCAAGATCTATCTGAGCAGAG 1020
 QY 1021 GCCAGAGATATGCTTTCTACTCATCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
 |||||
 Db 1021 GCCAGAGATATGCTTTCTACTCATCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTTAAAAATCTCTCTGAAAAACAGCAATCAAGCAAGCTTAAAG 1140
 |||||
 Db 1081 AAAGAAAAACAGATGCTTAAAAATCTCTCTGAAAAACAGCAATCAAGCAAGCTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTACAAAGTTCAAGGCAAGTGAATATGCCAGCCAGAGAAA 1200
 |||||
 Db 1141 CTGACATCAGAGAGAGTACAAAGTTCAAGGCAAGTGAATATGCCAGCCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACCAAAAATTAATGAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260

Db 1201 ATGTCTCAAGAACCAAAAATTAATGAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
 QY 1261 AACATGAAGATATATGTCGGATTAATAGAAAACCTGACTAATGTCGACTGTCG 1320
 |||||
 Db 1261 AACATGAAGATATATGTCGGATTAATAGAAAACCTGACTAATGTCGACTGTCG 1320
 QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGCAAGAACCTGATAATGCAATTT 1380
 |||||
 Db 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGCAAGAACCTGATAATGCAATTT 1380
 QY 1381 CTTGACAAAGAAAGTAAAGATATCACAGAAATTTGGGAATTAATTTCTGACTCAAGAA 1440
 |||||
 Db 1381 CTTGACAAAGAAAGTAAAGATATCACAGAAATTTGGGAATTAATTTCTGACTCAAGAA 1440
 QY 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGCAAGAACTTAAAGTGA 1500
 |||||
 Db 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGCAAGAACTTAAAGTGA 1500
 QY 1501 TCAGAGGAAGAGTTCACAAAGGCTTGAAGGCGAGTGAATGGCCAGCAGAGAAAGATCT 1560
 |||||
 Db 1501 TCAGAGGAAGAGTTCACAAAGGCTTGAAGGCGAGTGAATGGCCAGCAGAGAAAGATCT 1560
 QY 1561 CAAGAACCAAGAAATTAATTAAGATGATAGAGCTGAGAAATTTTATGGCTATCGAA 1620
 |||||
 Db 1561 CAAGAACCAAGAAATTAATTAAGATGATAGAGCTGAGAAATTTTATGGCTATCGAA 1620
 QY 1621 GAAATGAAGAGACAGGAAGTACTCATGTCGATGTCGCAAAACCTGACTAATGGTGC 1680
 |||||
 Db 1621 GAAATGAAGAGACAGGAAGTACTCATGTCGATGTCGCAAAACCTGACTAATGGTGC 1680
 QY 1681 ACTGTGCGCAATGATGATGATTAATTTCTCAAGAGAGAGCAAGCAACCTGAAAGC 1740
 |||||
 Db 1681 ACTGTGCGCAATGATGATGATTAATTTCTCAAGAGAGAGCAAGCAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTCTACACTGGAATGAAGATATCACAGTACAGCAACAAATGATCTCAG 1800
 |||||
 Db 1741 CAGCAATTTCTCTACACTGGAATGAAGATATCACAGTACAGCAACAAATGATCTCAG 1800
 QY 1801 AAGCAATTTTGTGAAGAGCAAGCACTGGAATTTACAGATGATGATGATGAA 1860
 |||||
 Db 1801 AAGCAATTTTGTGAAGAGCAAGCACTGGAATTTACAGATGATGATGATGAA 1860
 QY 1861 GAAAGCAGATAGAAAGGTTGAAAAAATGAAATTTCTGAGCTTCTCTAGTTGAAGAA 1920
 |||||
 Db 1861 GAAAGCAGATAGAAAGGTTGAAAAAATGAAATTTCTGAGCTTCTCTAGTTGAAGAA 1920
 QY 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGCGGAGAGAAATTTGCCATGTAAGCTG 1980
 |||||
 Db 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGCGGAGAGAAATTTGCCATGTAAGCTG 1980
 QY 1981 GAGCTAGACCAATGAAACATCGAGCGCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
 |||||
 Db 1981 GAGCTAGACCAATGAAACATCGAGCGCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 34
 US-10-012-896-375

; Sequence 375, Application US/10012896
 ; GENERAL INFORMATION:

; APPLICANT: Xu, JIANGCHUN
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun

Db 1741 CAGCAATTCCTGACACTGAGAAATGAAAGACTATCACAGTACGACAGCAAAATGATACTCAG 1800
QY 1801 AACCAATTTGTGAGAGACAGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
Db 1801 AACCAATTTGTGAGAGACAGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGAAAAAATGAAATTCGAGCTTCTCTTACTTGTAGAAA 1920
Db 1861 GAAAGCAGATAGAGTGTGAAAAAATGAAATTCGAGCTTCTCTTACTTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGCACTGAAAAATAGTACGTTCGCGGAGAGAAATTCGCAATGTAAGCTG 1980
Db 1921 GAAAAAGACATCTTGCACTGAAAAATAGTACGTTCGCGGAGAGAAATTCGCAATGTAAGCTG 1980
QY 1981 GAGCTAGACACATGAAACATGACGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAAACATGACGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040

RESULT 35
US-10-079-137B-303
: Sequence 303, Application US/10079137B
: GENERAL INFORMATION:
: APPLICANT: Fridakis, Tony N.
: APPLICANT: Reed, Steven G.
: APPLICANT: Smith, John M.
: APPLICANT: Misher, Lynda E.
: APPLICANT: Dillon, David C.
: APPLICANT: Retter, Marc W.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A. W.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Day, Craig H.
: APPLICANT: Li, Samuel X.
: APPLICANT: Deng, Ts
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.419C13
: CURRENT APPLICATION NUMBER: US/10/079,137B
: CURRENT FILING DATE: 2002-02-20
: NUMBER OF SEQ ID NOS: 428
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 303
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-079-137B-303

Query Match 100.0%; Score 2040; DB 39; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGTGATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCGCTGTCAGAGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCGCTGTCAGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACGAGACTGTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACGAGACTGTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGCTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGCTG 240
QY 241 GGGCTTTCTGAGACACGAGCACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCTTTCTGAGACACGAGCACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCGCACACTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360

Db 301 TGGTGTGCGCACACTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GGAGACTACAGATACAGTGTCTTCATGAGACCCAGGATACAGCTCCGTGGAGAAAGATCTG 420
Db 361 GGAGACTACAGATACAGTGTCTTCATGAGACCCAGGATACAGCTCCGTGGAGAAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGGGTAAGATGCCAGAAAGATCTCATCTGCATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGGGTAAGATGCCAGAAAGATCTCATCTGCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGACAAAGAGACTGCTTACATCTGCGC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGACAAAGAGACTGCTTACATCTGCGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCCTGTGACAGAGCATCTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCCTGTGACAGAGCATCTCAACTTAAT 600
QY 601 GTCCCTTGACACAAAAAGAGAGAGCTGTATAAAGCCGTACAAATGCCAGAAAGATGAA 660
Db 601 GTCCCTTGACACAAAAAGAGAGAGCTGTATAAAGCCGTACAAATGCCAGAAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAAATATCCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAAATATCCAGATGATGAAAT 720
QY 721 ACCACTGTGACATACCTATCTAATGAATGAATTAATGGCCAAAGACATGCTCTTA 780
Db 721 ACCACTGTGACATACCTATCTAATGAATGAATTAATGGCCAAAGACATGCTCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAAACAAAGCATGGCCTCACACACTGTACTTGGTGA 840
Db 781 TATGCTGCTGATATCGAATCAAAAAACAAAGCATGGCCTCACACACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGTGTCTCATCTGCTGATGCTGTATGTTGATGATGAGATGA 960
Db 901 CTGATATGATATGGAAGAGTGTCTCATCTGCTGATGCTGTATGTTGATGATGAGATGA 960
QY 961 GTGAGCTTCTACTTGGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTGAGCTTCTACTTGGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCAAGGCAAGTGAATATAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCAAGGCAAGTGAATATAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAAAAATTAAGATGATGATGAGAGGTTGAAGAAATGAG 1260
Db 1201 ATGTCTCAAGAACCAAAAAATTAAGATGATGATGAGAGGTTGAAGAAATGAG 1260
QY 1261 AACCATGAAAGTAATATGATGAGATTAATGAAGAACTGCTAATGGTGTCACTGCTGC 1320
Db 1261 AACCATGAAAGTAATATGATGAGATTAATGAAGAACTGCTAATGGTGTCACTGCTGC 1320
QY 1321 AATGATGATTAATGATTAATCTCAAGAGAGAGAGCAACCTGAAAAATTCAGCAATTT 1380
Db 1321 AATGATGATTAATGATTAATCTCAAGAGAGAGAGCAACCTGAAAAATTCAGCAATTT 1380
QY 1381 CTTGACAAAGAAATGAAGATATCAGAAATTTGGCAATTTCTGACTCAAGAA 1440
Db 1381 CTTGACAAAGAAATGAAGATATCAGAAATTTGGCAATTTCTGACTCAAGAA 1440

Db 1381 COTGACAAAGAAAGTGAAGAGTATCATAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440
Qy 1441 AAACGATGCGCAAAATCTCTCTGAAAACAGAACCCAGAACAGACTTAAGCTGANA 1500
Db 1441 AAACGATGCGCAAAATCTCTCTGAAAACAGAACCCAGAACAGACTTAAGCTGANA 1500
Qy 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCACTGAAAATGCGCAGCAGAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCACTGAAAATGCGCAGCAGAGAGAAAGATCT 1560
Qy 1561 CAGAGACAGAAATTAATTAAGAGTGTGATAGAGACTTGAATAATTTATGCTATCGAA 1620
Db 1561 CAGAGACAGAAATTAATTAAGAGTGTGATAGAGACTTGAATAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAAGCAGGGAAGTCTCATGTCGATCCCGAAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAAGCAGGGAAGTCTCATGTCGATCCCGAAGAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCCAGAGAGCAGAACACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCCAGAGAGCAGAACACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAACCAAAATGATACTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAACCAAAATGATACTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTTACAGAGATGATCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTTACAGAGATGATCTGATTCATGAA 1860
Qy 1861 GAAAGACAGATGAGTGTGTAAGAAATGAATTCGACCTTCTTCTTGTGTAAGAA 1920
Db 1861 GAAAGACAGATGAGTGTGTAAGAAATGAATTCGACCTTCTTCTTGTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTTCATGAAATAGTACGTTGCGGGAAGAAATTCGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTCATGAAATAGTACGTTGCGGGAAGAAATTCGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAATCATAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
Db 1981 GAGCTAGACACATGAATCATAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 36
US-10-144-678A-375
; Sequence 375, Application US/10144678A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Renger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ya
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-375

Query Match 100.0%; Score 2040; DB 40; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTGCTGCGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCCGACCTGCTCCCTGCTGAGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCCGACCTGCTCCCTGCTGAGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGGCTTGTGAGACACAGACGACTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGGCTTGTGAGACACAGACGACTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Qy 301 TGTGTGCTGACACTGCTCCCTGCTGCTGAGGGAGCGGCAAGCAAGTGGGCGCTTG 360
Db 301 TGTGTGCTGACACTGCTCCCTGCTGCTGAGGGAGCGGCAAGCAAGTGGGCGCTTG 360
Qy 361 GAGACTACAGTACAGTGTGCTGCTGCTGAGAGCCAGTACCGTCCGTGAGAGATCTG 420
Db 361 GAGACTACAGTACAGTGTGCTGCTGCTGAGAGCCAGTACCGTCCGTGAGAGATCTG 420
Qy 421 GACAACTCCACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAACTCCACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CTCAGGACACTGACGTGTAAGAAAGAGCAAGCAAGAGAGCAAGTCTCTACATCGGCC 540
Db 481 CTCAGGACACTGACGTGTAAGAAAGAGCAAGCAAGAGAGCAAGTCTCTACATCGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACAGAGATGCACTTAAT 600
Qy 601 GTCTTGACAAACAAAAGAGGACGCTGTGATTAAGGCGGTACAAATGCCAGAGATGAA 660
Db 601 GTCTTGACAAACAAAAGAGGACGCTGTGATTAAGGCGGTACAAATGCCAGAGATGAA 660
Qy 661 TGTGCTTAATGTTGCTGGAACATGACATGCAATTAATTCAGATGATGATGAAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGACATGCAATTAATTCAGATGATGATGAAAT 720
Qy 721 ACCACTCTGACACTACGCTATCTAATAATGAAGATTAATTAATGACCAAGCACTGCTTA 780
Db 721 ACCACTCTGACACTACGCTATCTAATAATGAAGATTAATTAATGACCAAGCACTGCTTA 780
Qy 781 TATGTGCTGATATGCAATCAAAAGCAAGCATGGCTCAGACACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAGCAAGCATGGCTCAGACACTGTTACTTGGTGA 840
Qy 841 CATGACAAAAGCAAGCAAGTGTGAAATTTTAATCAAGAAAAGCAATTTAAATGA 900
Db 841 CATGACAAAAGCAAGCAAGTGTGAAATTTTAATCAAGAAAAGCAATTTAAATGA 900

D	841	CAIAGAGCAAAAAACGCAAGTCGTGAAATTTTAAATCAAGAAAAAACCGAATTTAAATGCA	900
Q	901	CTGGATAGATATVGGAAAGACTGCTCTCATACCTTGCTGTATGTTGGATCAGCAAGTATA	960
D	901	CTGGATAGATATVGGAAAGACTGCTCTCATACCTTGCTGTATGTTGGATCAGCAAGTATA	960
Q	961	GTACGCTTCTACTTGGACAAATATTTGAGGTATCTTTCMAAGTCTATCTGGACAGACG	1020
D	961	GTACGCTTCTACTTGGACAAATATTTGAGGTATCTTTCMAAGTCTATCTGGACAGACG	1020
Q	1021	GCCAGAGAGATVGGCTGTTTCTAGCATCATCATGTAAATTTGGCAGTACTTCTGACATC	1080
D	1021	GCCAGAGAGATVGGCTGTTTCTAGCATCATCATGTAAATTTGGCAGTACTTCTGACATC	1080
Q	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAACAGCAATCCAGAACMACACTTAAAG	1140
D	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAACAGCAATCCAGAACMACACTTAAAG	1140
Q	1141	CTGACATCAGAGGAAGAGTCACAAAGTTCTAAAGGACGTGAAAATATGCCAGCCAGAGAA	1200
D	1141	CTGACATCAGAGGAAGAGTCACAAAGTTCTAAAGGACGTGAAAATATGCCAGCCAGAGAA	1200
Q	1201	ATGTCTCAAGAACACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAACAAATTAAG	1260
D	1201	ATGTCTCAAGAACACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAACAAATTAAG	1260
Q	1261	AAGCATGAAGATTAATATGTGGATTACTAGAAAAACCTGACTAATAGTGTCACTGCTGC	1320
D	1261	AAGCATGAAGATTAATATGTGGATTACTAGAAAAACCTGACTAATAGTGTCACTGCTGC	1320
Q	1321	AATGCTGATTAATGATTAATTTCTCTCAAGGAAGACAGAACACCTGAAAATATGCAATTT	1380
D	1321	AATGCTGATTAATGATTAATTTCTCTCAAGGAAGACAGAACACCTGAAAATATGCAATTT	1380
Q	1381	CCTGCACAACGAATATGAAGATATCACAGAAATTTGGCAATTTAGTTCTGACTACAGAA	1440
D	1381	CCTGCACAACGAATATGAAGATATCACAGAAATTTGGCAATTTAGTTCTGACTACAGAA	1440
Q	1441	AAACGATGCCAAATATCTCTTGAAAAACAGCAACCCAGAACACAGACTTAAAGCTGACA	1500
D	1441	AAACGATGCCAAATATCTCTTGAAAAACAGCAACCCAGAACACAGACTTAAAGCTGACA	1500
Q	1501	TCAGAGGAAGAGTCCAAAGGCTTGAGGGACGTGAAAATATGGCCAGCCAGAGAAAAGATCT	1560
D	1501	TCAGAGGAAGAGTCCAAAGGCTTGAGGGACGTGAAAATATGGCCAGCCAGAGAAAAGATCT	1560
Q	1561	CAAGACACAGAAATTAATTAAGATGAGTATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
D	1561	CAAGACACAGAAATTAATTAAGATGAGTATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Q	1621	GAATTAAGAAAGCACGGAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC	1680
D	1621	GAATTAAGAAAGCACGGAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC	1680
Q	1681	ACTGCTGGCAATGCTGATGATGATTAATTTCCCTCCAAGGAAGCAGAACACTTAAGC	1740
D	1681	ACTGCTGGCAATGCTGATGATGATTAATTTCCCTCCAAGGAAGCAGAACACTTAAGC	1740
Q	1741	CAGCAATTTCTCTGACACTGTAGATGAAGATATCACAGTACGAGCAACAAAATATATCTAG	1800
D	1741	CAGCAATTTCTCTGACACTGTAGATGAAGATATCACAGTACGAGCAACAAAATATATCTAG	1800
Q	1801	AAGCAATTTTGTGAAGAACAGAACACTGCAATTTATCACAGATGAGATTTCTGATTCATGAA	1860
D	1801	AAGCAATTTTGTGAAGAACAGAACACTGCAATTTATCACAGATGAGATTTCTGATTCATGAA	1860
Q	1861	GAAGAAAGCATAGAGATGAGTGTGAAAAATATGATTTCTGACCTTCTTATGTTAAGAAA	1920
D	1861	GAAGAAAGCATAGAGATGAGTGTGAAAAATATGATTTCTGACCTTCTTATGTTAAGAAA	1920
Q	1921	GAAGAAAGCATCTTGGATGAAATATCTAGCTTCCGGGAGAAATTTGCCATGCTAAGACTG	1980
D	1921	GAAGAAAGCATCTTGGATGAAATATCTAGCTTCCGGGAGAAATTTGCCATGCTAAGACTG	1980

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QY      1981 GAGCTAGACACATGAAACATCATGAGCCGCTTAAAAAAAAAAAAAAAAAAAAA 2040
        |||||||
Db       1981 GAGCTAGACACATGAAACATCATGAGCCGCTTAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 37
US-10-212-679-303
; Sequence 303, Application US/10212679
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-303

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Query Match	100.0%	Score 2040;	DB 42;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 2,7e-264;		
Matches 2040;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;
OY	1	ATGGGTGTGAGGTGTGATTCATATGCCGGGTGGCTCTTCTGTGAAGAAGCCATTGGTCTC	60	
Db	1	ATGGGTGTGAGGTGTGATTCATATGCCGGGTGGCTCTTCTGTGAAGAAGCCATTGGTCTC	60	
OY	61	ACGACCAAGATGGCGAAGTGTGTGTCGCCGTTCCTTCCCCTGCTGCAGGAGAGCGGCAG	120	
Db	61	ACGACCAAGATGGCGAAGTGTGTGTCGCCGTTCCTTCCCCTGCTGCAGGAGAGCGGCAG	120	
OY	121	ACCAACGAGGGGACATCTTGAGACCAACGACACTCTGCTATGAACACACTCAGAGCAAG	180	
Db	121	ACCAACGAGGGGACATCTTGAGACCAACGACACTCTGCTATGAACACACTCAGAGCAAG	180	
OY	181	ATGGGCAAGTGTGTGCCGCCACTGCTTCCCCTCTCTCAGAGGGAGTGGCAAGACAACTG	240	
Db	181	ATGGGCAAGTGTGTGCCGCCACTGCTTCCCCTCTCTCAGAGGGAGTGGCAAGACAACTG	240	
OY	241	GGCGCTTCTTGAGACACAGACACACTCTGTAAGAAGACACTCAGGAACAAGTGGGCAAG	300	
Db	241	GGCGCTTCTTGAGACACAGACACACTCTGTAAGAAGACACTCAGGAACAAGTGGGCAAG	300	
OY	301	TGGTCTGGCAATGCTTCCCCTCTCTGCAAGGGGAGCGGCAAGGCAAGTGGGCCCTTGG	360	
Db	301	TGGTCTGGCAATGCTTCCCCTCTCTGCAAGGGGAGCGGCAAGGCAAGTGGGCCCTTGG	360	
OY	361	GGAGACTACGATGACAGAGTGCCTTCAATGGAAGCCAGTACACGTCCCTGGAGAAATCTG	420	
Db	361	GGAGACTACGATGACAGAGTGCCTTCAATGGAAGCCAGTACACGTCCCTGGAGAAATCTG	420	
OY	421	GACAGACTCCACAGAGTGCCTGAGGGGTAAAGTCCACAGAAAGATCTCATCTGCTCATG	480	
Db	421	GACAGACTCCACAGAGTGCCTGAGGGGTAAAGTCCACAGAAAGATCTCATCTGCTCATG	480	
OY	481	CTCAGGGAACACTGACGTGTAACAAGGCAAGCAAAAGAGAGACTCTTACATCTGGCC	540	
Db	481	CTCAGGGAACACTGACGTGTAACAAGGCAAGCAAAAGAGAGACTCTTACATCTGGCC	540	
OY	541	TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGTGACACAGCATGTCACTTAAT	600	
Db	541	TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGTGACACAGCATGTCACTTAAT	600	

QY	601	GTGTTTGACAAACAAAAGAGGAGACGCTGATTAAGAGGCGCTATGCAATGGCCAGAGAATGAA	660
Db	601	GTGCTTGACACACAAAAGAGAGACGCTGATTAAGAGGCGCTATGCAATGGCCAGAGAATGAA	660
QY	661	TGTCGCTTAATCTTGCTGGAACTGGCACTGATCCCAAAATATCTCCAGATATATGATAAT	720
Db	661	TGTCGCTTAATCTTGCTGGAACTGGAACATGGCACTGATCCCAAAATATCTCCAGATATATGATAAT	720
QY	721	ACCACTCTGCACCTACGCTATCTATATGAAGTAAATTTAATGATGCGCAAAAGCACTGCTCTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTATATGAAGTAAATTTAATGATGCGCAAAAGCACTGCTCTTA	780
QY	781	TATGTCGTGATTTGCAATCAACAAAAACAAGCATGGGCGTCACACCGCACTTACTTGCGTGA	840
Db	781	TATGTCGTGATTTGCAATCAACAAAAACAAGCATGGGCGTCACACCGCACTTACTTGCGTGA	840
QY	841	CATGAGCAAAAACAGCAAGCTGCGTAATTTTAAATCAAGAAAAAGCGAATTTAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGCTGCGTAATTTTAAATCAAGAAAAAGCGAATTTAATGCA	900
QY	901	CTGGATTTGATTTGAGAGAGACTGCTCCATACCTTGCTGATATGTTGCGATTCAGCAAGTATA	960
Db	901	CTGGATTTGATTTGAGAGAGACTGCTCCATACCTTGCTGATATGTTGCGATTCAGCAAGTATA	960
QY	961	GTCAGCCTTTACTTATGAGCAAAATATTTGATGATCTTTCACAAAGATCTATTCGACAGACG	1020
Db	961	GTCAGCCTTTACTTATGAGCAAAATATTTGATGATATCTTTCACAAAGATCTATTCGACAGACG	1020
QY	1021	GCCAGAGATATCTGTTTCTTAAGTATCATATGTAATTTGCCAGTATCTTCTGACTAC	1080
Db	1021	GCCAGAGATATCTGTTTCTTAAGTATCATATGTAATTTGCCAGTATCTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAAATCTCTTGTAAGACAGAAATCCGAGAACAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAAATCTCTTGTAAGACAGAAATCCGAGAACAGACTTAAG	1140
QY	1141	CTGACATCAGAGAGAGAGACAGTCCAAAGGTTCAAAAGCAGTGAATAATAGCCAGACAGAGAA	1200
Db	1141	CTGACATCAGAGAGAGAGACAGTCCAAAGGTTCAAAAGCAGTGAATAATAGCCAGACAGAGAA	1200
QY	1201	ATGTCCTCAAAACCACAAAATTAATTAAGATTTGGTGATTAAGAGAGTTGAAAGAAATGAG	1260
Db	1201	ATGTCCTCAAAACCACAAAATTAATTAAGATTTGGTGATTAAGAGAGAGTTGAAAGAAATGAG	1260
QY	1261	AAGCATGAAGTATATATGTTGGGATATCTAGAGAAACCTGACTATATGTTGCTACATGCTGGC	1320
Db	1261	AAGCATGAAGTATATATGTTGGGATATCTAGAGAAACCTGACTATATGTTGCTACATGCTGGC	1320
QY	1321	AATGTCATTAATGATTAATTTCTCTCAAGAGAGAGAGCAACCTGAAATCAGCAATTT	1380
Db	1321	AATGTCATTAATGATTAATTTCTCTCAAGAGAGAGAGCAACCTGAAATCAGCAATTT	1380
QY	1381	CCTGACCAAGAAAGTGAAGTATTCACAAATTTGCGAATTTGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACCAAGAAAGTGAAGTATTCACAAATTTGCGAATTTGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATTAATCTTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATTAATCTTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA	1500
QY	1501	TCGAGAGAAAGTACCAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
Db	1501	TCGAGAGAAAGTACCAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
QY	1561	CAGGAACCAAGAAATTAATTAAGATTTGTTGATAGAGCTTGAAGAAATTTTATGCTATGCA	1620
Db	1561	CAGGAACCAAGAAATTAATTAAGATTTGTTGATAGAGCTTGAAGAAATTTTATGCTATGCA	1620
QY	1621	GAATTAAGAGACAGGAAGTACTCATGTCGATTTCCAGAAAACCTGACTATATGCTGCC	1680
Db	1621	GAATTAAGAGACAGGAAGTACTCATGTCGATTTCCAGAAAACCTGACTATATGCTGCC	1680

Qy	1681	ACCTCGGCAATGGTGTATGATGAATTAAATTCCTCCCAAGGAAGAAGCAACCTGAAAGC	1740
Db	1681	ACTCTCTGGCAATGGTGATGTATGATTAATTTCTCCCAAGGAAGAAGCAACCTGAAAGC	1740
Qy	1741	CAGCAATTTCTGTGCACCTGTGATGAAGAGTATCACAGTAGACAACAAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGTGCACCTGTGATGAAGAGTATCACAGTAGACAACAAAATGATACTCAG	1800
Qy	1801	AAGCAATTTTGTGTAAGAACGAAACACTGTGAATATTACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGTAAGAACGAAACACTGTGAATATTACAGATGAGATTTCTGATTCATGAA	1860
Qy	1861	GAAAPAGCAGATAGAGTGTGTGAAAAAATGAATTCTGACCTTTCCTTAGTTGTAAGAA	1920
Db	1861	GAAAPAGCAGATAGAGTGTGTGAAAAAATGAATTCTGACCTTTCCTTAGTTGTAAGAA	1920
Qy	1921	GAAAAAGACATCTTGCATGAAAAATAGTAGCTTGGGGAAGAAATTGCCATGCTAAGACTG	1980
Db	1921	GAAAAAGACATCTTGCATGAAAAATAGTAGCTTGGGGAAGAAATTGCCATGCTAAGACTG	1980
Qy	1981	GAGCTAACAACAATGAACACTGACGCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTAACAACAATGAACACTGACGCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040

DB	241	GGCGCTTCGTGAGACACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG	300
OY	241	GGCGCTTCGTGAGACACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG	300
DB	181	ATGGGCAAGTGGTGGCCGACACTGCTTCCCTCTCTCAGAGGGGAGTGGCAAGAGCAACTGTG	240
OY	181	ATGGGCAAGTGGTGGCCGACACTGCTTCCCTCTCTCAGAGGGGAGTGGCAAGAGCAACTGTG	240
DB	161	ATGGGCAAGTGGTGGCCGACACTGCTTCCCTCTCTCAGAGGGGAGTGGCAAGAGCAACTGTG	240
OY	161	ATGGGCAAGTGGTGGCCGACACTGCTTCCCTCTCTCAGAGGGGAGTGGCAAGAGCAACTGTG	240
DB	121	AGCAACGTGGGACACTTCTGGAGACCAACGACGACTGCTATGAAGACACTCAGGAGCAAG	180
OY	121	AGCAACGTGGGACACTTCTGGAGACCAACGACGACTGCTATGAAGACACTCAGGAGCAAG	180
DB	61	AGGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTCTCTGCGAGGAGAGCGGCAAG	120
OY	61	AGGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTCTCTGCGAGGAGAGCGGCAAG	120
DB	1	ATGGTGGTTGAGAGTTGATTCATGCGCGGCTGCTTCTGTGAGAGAACCATTTGGTCTC	60
OY	1	ATGGTGGTTGAGAGTTGATTCATGCGCGGCTGCTTCTGTGAGAGAACCATTTGGTCTC	60
DB	1	ATGGTGGTTGAGAGTTGATTCATGCGCGGCTGCTTCTGTGAGAGAACCATTTGGTCTC	60
OY	1	ATGGTGGTTGAGAGTTGATTCATGCGCGGCTGCTTCTGTGAGAGAACCATTTGGTCTC	60
Query Match			
		76.0%;	Score 1551; DB 1; Length 2000;
		Best Local Similarity	100.0%; Pred. No. 5e-199;
		Matches 1551; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
PCT-US02-24917-302			
PCT-US02-24917			
SEQUENCE 302. APPLICATION PCT/US0224917			
GENERAL INFORMATION:			
APPLICANT: Corixa Corporation			
APPLICANT: Fanger, Gary R.			
APPLICANT: Hirst, Shannon Kathleen			
APPLICANT: Dillon, Davin C.			
APPLICANT: Foy, Teresa M.			
APPLICANT: Houghton, Raymond L.			
APPLICANT: Persing, David H.			
APPLICANT: Kalos, Michael D.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER			
FILE REFERENCE: 210121.41931PC			
CURRENT APPLICATION NUMBER: PCT/US02/24917			
CURRENT FILING DATE: 2002-08-05			
NUMBER OF SEQ ID NOS: 428			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 302			
LENGTH: 2000			
TYPE: DNA			
ORGANISM: Homo sapiens			
PCT-US02-24917-302			

OY	301	TGAGCTCCACACTGCTCCCTCGCTGAGGGGAGGGCAAGGCAAGGTGGGGCTTGG	360
OY	301	TGAGCTCCACACTGCTCCCTCGCTGAGGGGAGGGCAAGGCAAGGTGGGGCTTGG	360
Db	301	TGAGCTCCACACTGCTCCCTCGCTGAGGGGAGGGCAAGGCAAGGTGGGGCTTGG	360
OY	361	GGAGACTACGATGACAGTGGCTTCATGAGAGCCAGGTACCACGTCCTGAGAGATGTG	420
Db	361	GGAGACTACGATGACAGTGGCTTCATGAGAGCCAGGTACCACGTCCTGAGAGATGTG	420
OY	421	GACAAAGCTCCACAGAGTGGCTGGGGTAAAGTCCCAAGAAAGATTCATCTGATG	480
Db	421	GACAAAGCTCCACAGAGTGGCTGGGGTAAAGTCCCAAGAAAGATTCATCTGATG	480
OY	481	CTCAGGGACACTGACGTGAACAAAGAAAGACAACAAAGAGACTGCTTACATGTGGCC	540
Db	481	CTCAGGGACACTGACGTGAACAAAGAAAGACAACAAAGAGACTGCTTACATGTGGCC	540
OY	541	TCCTGCATGGGAATTCAGAAATGTAACCTCCTGCTGACAGACGATGTCACCTAAT	600
Db	541	TCCTGCATGGGAATTCAGAAATGTAACCTCCTGCTGACAGACGATGTCACCTAAT	600
OY	601	GTCCTTGACAACAAAGAGAGACAGCTCTGATTAAGAGCGGTACAAATGCCAGAAATGAA	660
Db	601	GTCCTTGACAACAAAGAGAGACAGCTCTGATTAAGAGCGGTACAAATGCCAGAAATGAA	660
OY	661	TGTGCGTTAATGTTGCTGGAAATGGCACTGATCCAAATATTCACAGATGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAAATGGCACTGATCCAAATATTCACAGATGATGGAAT	720
OY	721	ACCACTGCGACCTAGCTATCTAATGAAGATTAATTAAGCCAAACCACTGCTCTA	780
Db	721	ACCACTGCGACCTAGCTATCTAATGAAGATTAATTAAGCCAAACCACTGCTCTA	780
OY	781	TATGATGCTGATATCGAATCAACAAAACACAGCATGGCTCACACACTGTACTTGSTTA	840
Db	781	TATGATGCTGATATCGAATCAACAAAACACAGCATGGCTCACACACTGTACTTGSTTA	840
OY	841	CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
OY	901	CTGGAATGATATGGAAGAGACTGCTCATACTGCTGATGTTGTTGAGATCAGCAAGTATA	960
Db	901	CTGGAATGATATGGAAGAGACTGCTCATACTGCTGATGTTGTTGAGATCAGCAAGTATA	960
OY	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGTATCTTCAAGATCATCTGAGACAGG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGTATCTTCAAGATCATCTGAGACAGG	1020
OY	1021	GCCAGAGATGCTGCTTTCTAGCAATCAATGTATTTGCGAGTACTTCTGACATAC	1080
Db	1021	GCCAGAGATGCTGCTTTCTAGCAATCAATGTATTTGCGAGTACTTCTGACATAC	1080
OY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACACAGCAATCCAGAACANACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACACAGCAATCCAGAACANACTTAAG	1140
OY	1141	CTGACATCAGAGGAAGAGTCAACAAGGTTCAAAAGGACAGTGAAGAAATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGAGTCAACAAGGTTCAAAAGGACAGTGAAGAAATAGCCAGCCAGAGAA	1200
OY	1201	ATGCTCTAAGAACACAGAAATTAATTAAGATGGTGATAGAGAGTTGAAGAACAAATGAG	1260
Db	1201	ATGCTCTAAGAACACAGAAATTAATTAAGATGGTGATAGAGAGTTGAAGAACAAATGAG	1260
OY	1261	AAGCATTAAGATAATTAATGTTGGATTAAGAAAACCTGACTAATGGTGCTACTCTGGC	1320
Db	1261	AAGCATTAAGATAATTAATGTTGGATTAAGAAAACCTGACTAATGGTGCTACTCTGGC	1320
OY	1321	AATGTGTATTAATGATTAATTTCTTCAAGAGAGACAGCAACCTGAAAATCAGCAATTT	1380
Db	1321	AATGTGTATTAATGATTAATTTCTTCAAGAGAGACAGCAACCTGAAAATCAGCAATTT	1380

QY	1381	CCTGCAACGAAAGTGAAGATATACAGAAATTGGCAATTGTTCTGTACTACAAAGAA	1440
Db	1381	CCTGCAACGAAAGTGAAGATATACAGAAATTGGCAATTGTTCTGTACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGTGCAC	1500
Db	1441	AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGTGCAC	1500
QY	1501	TCAGAGGAAGATCCAAAGGCTTGAAGGCGACTGAAAAATGGCCACCAGAG	1551
Db	1501	TCAGAGGAAGATCCAAAGGCTTGAAGGCGACTGAAAAATGGCCACCAGAG	1551
RESULT 39			
US-09-288-946-374			
Sequence 374, Application US/09288946			
GENERAL INFORMATION:			
APPLICANT: Xu, Jianshun			
APPLICANT: Dillon, Davin C.			
TITLE OF INVENTION: Compounds for immunotherapy and diagnosis			
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE			
FILE REFERENCE: 210121.427C7			
CURRENT APPLICATION NUMBER: US/09/288,946			
CURRENT FILING DATE: 1999-04-09			
NUMBER OF SEQ ID NOS: 381			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 374			
LENGTH: 2000			
TYPE: DNA			
ORGANISM: Homo sapien			
US-09-288-946-374			
Query Match			
Best Local Similarity 76.0%; Score 1551; DB 16; Length 2000;			
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGTGTTTGAAGTTGATTCATGCCGGCTGCTCTGTGTAAGAGCATTGTGCTC	60
Db	1	ATGGTGTTTGAAGTTGATTCATGCCGGCTGCTCTGTGTAAGAGCATTGTGCTC	60
QY	61	AGGAGCAAGATGGGCAAGTGCTGCTGCGGTGCTTCCCTGCTGAGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGCTGCTGCGGTGCTTCCCTGCTGAGGAGAGCGGCAAG	120
QY	121	AGCAACGTTGGGCACTTCTTGAGAGACCAGACACTCTGCTATGAAACACTCAGAGCAAG	180
Db	121	AGCAACGTTGGGCACTTCTTGAGAGACCAGACACTCTGCTATGAAACACTCAGAGCAAG	180
QY	181	ATGGCAGTGGTGGCGGCACAGTCCCTGCTGACAGGGGAGTGGGAAGAGCAAGCTG	240
Db	181	ATGGCAGTGGTGGCGGCACAGTCCCTGCTGACAGGGGAGTGGGAAGAGCAAGCTG	240
QY	241	GGCGTTTGGAGACAGACGACTCTGCTATGAAGACTCAGGAACAAGTGGGCAAG	300
Db	241	GGCGTTTGGAGACAGACGACTCTGCTATGAAGACTCAGGAACAAGTGGGCAAG	300
QY	301	TGGTCTCCCACTGCTTCCCTGCTGTCAGAGGGGAGACGGCAGAGCAAGTGGGCTTGG	360
Db	301	TGGTCTCCCACTGCTTCCCTGCTGTCAGAGGGGAGACGGCAGAGCAAGTGGGCTTGG	360
QY	361	GGAGACTCGATGAGAGTGCCTTCATGGAAGCCAGAGTACCAAGTCCGTTGAGAAATGTG	420
Db	361	GGAGACTCGATGAGAGTGCCTTCATGGAAGCCAGAGTACCAAGTCCGTTGAGAAATGTG	420
QY	421	GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCCAGAAAAGATCTCATCTCATG	480
Db	421	GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCCAGAAAAGATCTCATCTCATG	480
QY	481	CTCAGGGCACTGACGTATAACAAGAAGCAAGCAAAAAGAGAGCTGCTTACATCTGGCC	540
Db	481	CTCAGGGCACTGACGTATAACAAGAAGCAAGCAAAAAGAGAGCTGCTTACATCTGGCC	540

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Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGATGTCACATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGATGTCACATTAAT 600
Qy 601 GTCTTGCACAAACAAAAGAGAGACGCTGTGATTAAGGCCGTCACATGCGCAGAGATGAA 660
Db 601 GTCTTGCACAAACAAAAGAGAGACGCTGTGATTAAGGCCGTCACATGCGCAGAGATGAA 660
Qy 661 TGTGGTAAATGTGCTGAGACATGAGCCTGATCCAAATATATCCAGATGATGTAAT 720
Db 661 TGTGGTAAATGTGCTGAGACATGAGCCTGATCCAAATATATCCAGATGATGTAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAGATTAATTAATGAGCAAGCACTGCTCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAGATTAATTAATGAGCAAGCACTGCTCTTA 780
Qy 781 TATGCTGTGATTCGAAATCAAAAAACAGATGCGCTCACACCCTGTTACTGTGTGA 840
Db 781 TATGCTGTGATTCGAAATCAAAAAACAGATGCGCTCACACCCTGTTACTGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAATGCTGAATTTTAAATCAAGAAAAAGCAATTTAATGCA 900
Db 841 CATGAGCAAAAACAGCAATGCTGAATTTTAAATCAAGAAAAAGCAATTTAATGCA 900
Qy 901 CTGATAGATATGAGAGAGCTGCTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATAGATATGAGAGAGCTGCTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
Qy 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGACAGAG 1020
Db 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGACAGAG 1020
Qy 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATGTAATTTGCGCACTTCTTCTACATAC 1080
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATGTAATTTGCGCACTTCTTCTACATAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGACTCACAAGGTTCAAGGAGTGAATAATGAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGACTCACAAGGTTCAAGGAGTGAATAATGAGCCAGCAGAGAA 1200
Qy 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAGAG 1260
Db 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAGAG 1260
Qy 1261 AAGCATGAAATTAATATGAGGATTAATAGAAAACTGACTAATGATGCTGCTGAGC 1320
Db 1261 AAGCATGAAATTAATATGAGGATTAATAGAAAACTGACTAATGATGCTGCTGAGC 1320
Qy 1321 AATGCTGTAATGATTAATCTCTCAAGAGAGACAGACCTGAAATCAGCAATTT 1380
Db 1321 AATGCTGTAATGATTAATCTCTCAAGAGAGACAGACCTGAAATCAGCAATTT 1380
Qy 1381 CCTGACAAGAGAGAGATGATCAGAGATTTGCGAATTAATGTTCTGACATCAAAAAGAA 1440
Db 1381 CCTGACAAGAGAGAGATGATCAGAGATTTGCGAATTAATGTTCTGACATCAAAAAGAA 1440
Qy 1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAAGCTTGAGGAGTGAATAATGCGCAGCAGAG 1551
Db 1501 TCAGAGAGAGAGTCAAAAAGCTTGAGGAGTGAATAATGCGCAGCAGAG 1551
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RESULT 40
US-09-289-198-302
; Sequence 302, Application US/09289198
; GENERAL INFORMATION:

```
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-302

Query Match          76.0%; Score 1551; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 601 GTCTTGACACAAAAAGAGACAGCTCTGATTAAGCCCTACAAATGCCAGGAGATGAA 660
    |||||||
Db 601 GTCTTGACACAAAAAGAGACAGCTCTGATTAAGCCCTACAAATGCCAGGAGATGAA 660
QY 661 TGTGCGTTAATGTTGGTGGAAACATGGACATGACCAAAATTTCCAGATGATGATGAAT 720
    |||||||
Db 661 TGTGCGTTAATGTTGGTGGAAACATGGACATGACCAAAATTTCCAGATGATGATGAAT 720
QY 721 ACCACTCTGCACATACGCTATCTAATTAAGATAAATTAATGAGCAAGACACTGCTCTTA 780
    |||||||
Db 721 ACCACTCTGCACATACGCTATCTAATTAAGATAAATTAATGAGCAAGACACTGCTCTTA 780
QY 781 TATGTCCTGATATCCAAATAAAAACAGACATGGCTCCACACCTGTTACTTGCTGA 840
    |||||||
Db 781 TATGTCCTGATATCCAAATAAAAACAGACATGGCTCCACACCTGTTACTTGCTGA 840
QY 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGATTTAAATGCA 900
    |||||||
Db 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGACTGCTCATACTGCTGATGTTGGATCAGCAAGTATA 960
    |||||||
Db 901 CTGGATAGATATGGAAGAGACTGCTCATACTGCTGATGTTGGATCAGCAAGTATA 960
QY 961 GTACGCTTCTACTTGACAAAAATTTGATGTAATCTTCAAGATCTATCTGACAGAG 1020
    |||||||
Db 961 GTACGCTTCTACTTGACAAAAATTTGATGTAATCTTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTACTCATCATGATTAATTTGSCAGTACTTCTGACTAC 1080
    |||||||
Db 1021 GCCAGAGATATGCTGTTTCTACTCATCATGATTAATTTGSCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTTAAATAATCTCTTGAAGAACAGCAATCCAGAACAGATTAAAG 1140
    |||||||
Db 1081 AAGAAAAACAGATGCTTAAATAATCTCTTGAAGAACAGCAATCCAGAACAGATTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGCAAGTAAATAGCCAGCAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGCAAGTAAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCCAGAAATTAATAGATGATAGAGGTTGAAGAAAGAAATGAAG 1260
    |||||||
Db 1201 ATGTCTCAAGAACCCAGAAATTAATAGATGATAGAGGTTGAAGAAAGAAATGAAG 1260
QY 1261 AAGCATGAAGAATTAATATGATGAGATTACTAGAAACCTGACTAATGCTGCTGCGC 1320
    |||||||
Db 1261 AAGCATGAAGAATTAATATGATGAGATTACTAGAAACCTGACTAATGCTGCTGCGC 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACCTGAATAATGCAATTTT 1380
    |||||||
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACCTGAATAATGCAATTTT 1380
QY 1381 CCTGACACAGAAAGTGAAGAGTATCAGAAATTTGGAAATTAATTTCTGCTCAAAAGAA 1440
    |||||||
Db 1381 CCTGACACAGAAAGTGAAGAGTATCAGAAATTTGGAAATTAATTTCTGCTCAAAAGAA 1440
QY 1441 AAGCATGACCAAAATTAATCTCTTGAAGAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||||||
Db 1441 AAGCATGACCAAAATTAATCTCTTGAAGAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAAGAAATGGCCAGCCAGAG 1551
    |||||||
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAAGAAATGGCCAGCCAGAG 1551

```

RESULT 41
US-09-429-755-302
; Sequence 302, Application US/09429755A

; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match      76.0%; Score 1551; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGGAAGAGCCATTGGTCTC 60
    |||||||
Db 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGGAAGAGCCATTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGACGGCAG 120
    |||||||
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGACGGCAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTGTGAAGACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTGTGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
    |||||||
Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
QY 241 GGGCTTCTGGAACACACGACTGCTGATTAAGACACTCAGGAACAAGATGGCAG 300
    |||||||
Db 241 GGGCTTCTGGAACACACGACTGCTGATTAAGACACTCAGGAACAAGATGGCAG 300
QY 301 TGGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGGCGCTTG 360
    |||||||
Db 301 TGGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGATACACGCTCCGTGAGAGAATCTG 420
    |||||||
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGATACACGCTCCGTGAGAGAATCTG 420
QY 421 GACAAAGTCCACAGAGCTGCTGTTGAGGATTAAGTCCCAAGAAAGATCTCATGCTATG 480
    |||||||
Db 421 GACAAAGTCCACAGAGCTGCTGTTGAGGATTAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGCTGAAGCAAGAGAGACCAAGAGAGAGCTGCTACATCTGGCC 540
    |||||||
Db 481 CTCAGGGACACTGACGCTGAAGCAAGAGAGAGACCAAGAGAGAGCTGCTACATCTGGCC 540
QY 541 TCTGCAATGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGAGATGCAACTTAAT 600
    |||||||
Db 541 TCTGCAATGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGACACAAAAAGAGAGAGCTGATTAAGCCGTACAAATGCCAGGAAGATGAA 660
    |||||||
Db 601 GTCTTGACACAAAAAGAGAGAGCTGATTAAGCCGTACAAATGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGGTGGAAACATGGACATGACCAAAATTTCCAGATGATGATGAAT 720
    |||||||
Db 661 TGTGCGTTAATGTTGGTGGAAACATGGACATGACCAAAATTTCCAGATGATGATGAAT 720
QY 721 ACCACTCTGCACATACGCTATCTAATTAAGATAAATTAATGAGCAAGACACTGCTCTTA 780
    |||||||
Db 721 ACCACTCTGCACATACGCTATCTAATTAAGATAAATTAATGAGCAAGACACTGCTCTTA 780
QY 781 TATGTCCTGATATCCAAATAAAAACAGATGGCTCCACACCTGTTACTTGCTGA 840
    |||||||

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Db 781 TATGTCGTGATATTCGAATCAAAAAACAGATGGCTTCACACCACTGTACTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
Qy 961 GTCAGCCTTCTACTTGACCAAAATTTGATGATATCTTCAAGATCTATCTGGACAGAG 1020
Db 961 GTCAGCCTTCTACTTGACCAAAATTTGATGATATCTTCAAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCAGTTCTTCTGACATC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCAGTTCTTCTGACATC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGGAAGAGTCCACAAAGTTCAAGGCACTGAAATATGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGGAAGAGTCCACAAAGTTCAAGGCACTGAAATATGCCAGCAGAGAAA 1200
Qy 1201 ATGCTCAAGAACGAAATTAATTAAGATGGTGTATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACGAAATTAATTAAGATGGTGTATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAATTAATGTTGGGATTTACTAGAAAACTGACTAATGTTCTGCTGCTG 1320
Db 1261 AAGCATGAAGTAATTAATGTTGGGATTTACTAGAAAACTGACTAATGTTCTGCTGCTG 1320
Qy 1321 AATGTTGATTAATGATTAATTCCTCAAGGAAGACAGAACCTGAAATATGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATTCCTCAAGGAAGACAGAACCTGAAATATGCAATTT 1380
Qy 1381 CCTGACACGAAGAGAGATCAGAGAAATTTGGAATTTCTGACTACACAAAGAA 1440
Db 1381 CCTGACACGAAGAGAGATCAGAGAAATTTGGAATTTCTGACTACACAAAGAA 1440
Qy 1441 AAACGATGCCAAAATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAAATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 42
US-09-443-686-374
; Sequence 374, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang Yungui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solik, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443.686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-374

Query Match 76.0%; Score 1551; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTGTTGAGTGTGATTCATGCCGGCTGCTTCTTGTGTAAGAACGCAATTGGTCTC 60
Db 1 ATGTTGTTGAGTGTGATTCATGCCGGCTGCTTCTTGTGTAAGAACGCAATTGGTCTC 60
Qy 61 AGGACCAAGATGGCAAGGGTGGTGGCTTCCCTGCTGAGGAGGAGGGGCAAG 120
Db 61 AGGACCAAGATGGCAAGGGTGGTGGCTTCCCTGCTGAGGAGGAGGGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGCTGTATGAAACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGCTGTATGAAACACTCAGAGCAAG 180
Qy 181 ATGGCAAGTGGTCCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACTG 240
Db 181 ATGGCAAGTGGTCCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACTG 240
Qy 241 GGGCTTCTGAGACACGAGACTCTGCTATGAAGACCTCAGAACAAAGATGGGCAAG 300
Db 241 GGGCTTCTGAGACACGAGACTCTGCTATGAAGACCTCAGAACAAAGATGGGCAAG 300
Qy 301 TGGTCTGCACTGCTCCCTGCTGACAGGGGAGCGCAAGAGAGTGGGCTTGG 360
Db 301 TGGTCTGCACTGCTCCCTGCTGACAGGGGAGCGCAAGAGAGTGGGCTTGG 360
Qy 361 GGAGACTACAGATGACAGTCCCTTCAATGAGCCAGGACCACTGCTGGAAGATCTG 420
Db 361 GGAGACTACAGATGACAGTCCCTTCAATGAGCCAGGACCACTGCTGGAAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCAGAAAGATCTCATGCTGAG 480
Db 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCAGAAAGATCTCATGCTGAG 480
Qy 481 CTCAGGAGACTGAGTGAACAGAGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
Db 481 CTCAGGAGACTGAGTGAACAGAGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
Qy 601 GTCCTTGAACAAAAAGAGACAGCTCTGATAAAGCCGCTCAATGCCAGAAATGAA 660
Db 601 GTCCTTGAACAAAAAGAGACAGCTCTGATAAAGCCGCTCAATGCCAGAAATGAA 660
Qy 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
Db 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Qy 781 TATGTTGCTGATATGAATCAAAAAAAGCAATGGCTTCACACCACTGTACTGTGTGA 840
Db 781 TATGTTGCTGATATGAATCAAAAAAAGCAATGGCTTCACACCACTGTACTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960

|||||
Db 1021 GCCAAGAGTATGCTGTTCTAGTCATCATGTAAATTTGCCAGTACTTCTGACTAC 1080
Oy 1081 AAAGAAAACAGATGCTAAAAATCTCTCTGAAACACCAATCCCAACACTTAAAG 1140
Db 1081 AAAGAAAACAGATGCTAAAAATCTCTCTGAAACACCAATCCCAACACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Oy 1201 ATGTCCTCAAGAACAGAAATAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCCTCAAGAACAGAAATAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGATTAATGTTGGGATTAAGTAAACCTGACTAAATGCTGCTGCTGCG 1320
Db 1261 AAGCATGAAGATTAATGTTGGGATTAAGTAAACCTGACTAAATGCTGCTGCTGCG 1320
Oy 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGCAGAACACCTGAAATCAGCAATT 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGCAGAACACCTGAAATCAGCAATT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTAAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTAAGTTCTGACTACAAAGAA 1440
Oy 1441 AAACGATGCCAAATTAATCTCTCTCAAAAGAGCAGAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATTAATCTCTCTCAAAAGAGCAGAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGTGAATAATGGCCAGCCAGAG 1551

RESULT 44

US-09-534-825A-302
; Sequence 302, Application US/09534825A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Reiter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C7
; CURRENT APPLICATION NUMBER: US/09/534.825A
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 317
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-534-825A-302

Query Match 76.0%; Score 1551; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGCTGCTTGAAGTTCATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGTGCTC 60
Db 1 ATGCTGCTTGAAGTTCATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGTGCTC 60
Oy 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTTCCCTGCTGAGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTTCCCTGCTGAGAGAGCGGCAAG 120
Oy 121 AGCAAGCTGGGCACTTCTGAGACAGAGCACTGCTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACAGAGCACTGCTATGAAGACACTGAGAGCAAG 180

Db 121 AGCAAGCTGGGCACTTCTGAGACAGAGCACTGCTATGAAGACACTGAGAGCAAG 180
Oy 181 ATGGGCAAGTGGTGGCGCCACAGTCCCTCCCTGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGCCACAGTCCCTCCCTGAGGGGAGTGGCAAGCAAGCTG 240
Oy 241 GCGCTTCTGAGAGACAGACAGTCTGCTATGAAGACACTGAGAACAAAGTGGGCAAG 300
Db 241 GCGCTTCTGAGAGACAGACAGTCTGCTATGAAGACACTGAGAACAAAGTGGGCAAG 300
Oy 301 TGTGCTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGGCTTGG 360
Db 301 TGTGCTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGGCTTGG 360
Oy 361 GGAGACTACGATGACAGTCCCTTCAATGAGGCCAGGTACACGTCCGTGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCAATGAGGCCAGGTACACGTCCGTGAGAAATCTG 420
Oy 421 GACAAAGCTCCACAGAGCTGCTGAGGGGTTAAAGTCCCGAAAGAGATCTCATGCTATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGAGGGGTTAAAGTCCCGAAAGAGATCTCATGCTATG 480
Oy 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAGAGAGACTGCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGACAGAGATGCTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGACAGAGATGCTCACTTAAT 600
Oy 601 GTCTTTGACAAACAAAAGAGAGAGTCTGATTAAGAGCGCTGCAATGCCAGAAATGAA 660
Db 601 GTCTTTGACAAACAAAAGAGAGAGTCTGATTAAGAGCGCTGCAATGCCAGAAATGAA 660
Oy 661 TGTGCTTAATGTGTGCTGAGACATGGACATGATCCAAATATTTCCAGATGATGGAAT 720
Db 661 TGTGCTTAATGTGTGCTGAGACATGGACATGATCCAAATATTTCCAGATGATGGAAT 720
Oy 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGGCCAAACACTGCTCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGGCCAAACACTGCTCTTA 780
Oy 781 TATGCTGCTGATATGATCAACAAAACAGCATGGGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGATCAACAAAACAGCATGGGCTCACACACTGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAATCAGAAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAATCAGAAAAAAGCGAATTTAATGCA 900
Oy 901 CTGAGATGATATGAAGAGACTGCTCATACTTGTGCTGATGTTGGATCAGCAAGTAA 960
Db 901 CTGAGATGATATGAAGAGACTGCTCATACTTGTGCTGATGTTGGATCAGCAAGTAA 960
Oy 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCCAGAGATCTATCTGGACAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCCAGAGATCTATCTGGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAAATTTGCCAGTACTTCTGACTAC 1080
Oy 1081 AAAGAAAACAGATGCTAAAAATCTCTCTGAAACACCAATCCCAACACTTAAAG 1140
Db 1081 AAAGAAAACAGATGCTAAAAATCTCTCTGAAACACCAATCCCAACACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Oy 1201 ATGTCCTCAAGAACAGAAATAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCCTCAAGAACAGAAATAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAACCTGACTAATGTGTCTACTGTGGC 1320
DB 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAACCTGACTAATGTGTCTACTGTGGC 1320
QY 1321 AATGTGATATATGATTAATTTCTCTCAAGAGACAGACAACTGATAATTCAGCAATTT 1380
DB 1321 AATGTGATATATGATTAATTTCTCTCAAGAGACAGACAACTGATAATTCAGCAATTT 1380
QY 1381 CCTGATACGAAGTGAAGATATCAAGATTTGGCAATTTCTGACTGACAAAGAA 1440
DB 1381 CCTGATACGAAGTGAAGATATCAAGATTTGGCAATTTCTGACTGACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGACAAAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGACAAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATGACAAAGGCTTGAGGAGCATGAAAATGAGCCAGCCAGAG 1551
DB 1501 TCAGAGGAAGATGACAAAGGCTTGAGGAGCATGAAAATGAGCCAGCCAGAG 1551

RESULT 45

US-09-536-857-374
Sequence 374, Application US/09536857
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536,857
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 592
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-374

Query Match 76.0%; Score 1551; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTTGATTCATGCGGCTGCTTTCTGTGAAGAAAGCCATTTGCTTC 60
DB 1 ATGTGTTGAGTTGATTCATGCGGCTGCTTTCTGTGAAGAAAGCCATTTGCTTC 60
QY 61 AGGAGAAAGTGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCGGAG 120
DB 61 AGGAGAAAGTGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCGGAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACTGTGCTATGAAGACATCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACTGTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCGGAG 240
DB 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCGGAG 240
QY 241 GGGGCTTGTGAGACACAGACTGTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTGTGAGACACAGACTGTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300

QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGACAGAGTGGCGCTTGG 360
DB 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGACAGAGTGGCGCTTGG 360
QY 361 GAGACTACATATACAGTGGCTTCTATGAGACCCAGAGTACACAGTCCGTGGAGAAAGTCTG 420
DB 361 GAGACTACATATACAGTGGCTTCTATGAGACCCAGAGTACACAGTCCGTGGAGAAAGTCTG 420
QY 421 GACAGCTCCACAGAGTGGCTGCTGGGCTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
DB 421 GACAGCTCCACAGAGTGGCTGCTGGGCTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGACAAAGAGAGAGTGTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAGAGACAAAGAGAGAGTGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGACATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGACATGTCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCGCTAGCAATGCCAGAAAGATGA 660
DB 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCGCTAGCAATGCCAGAAAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACATACGTATCTATATGAAGATTAATTAATGGCCAAAGACAGCTCTTGA 780
DB 721 ACCACTGTGACATACGTATCTATATGAAGATTAATTAATGGCCAAAGACAGCTCTTGA 780
QY 781 TATGTCCTGATATGCAATCAAAAACAGCATGCGCTCACACACAGTACTTGTGCTGA 840
DB 781 TATGTCCTGATATGCAATCAAAAACAGCATGCGCTCACACACAGTACTTGTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATATGAGAGAGTGTCTCATATCTGCTATGTTGTGATGACAGCAATATA 960
DB 901 CTGATGATATATGAGAGAGTGTCTCATATCTGCTGATGTTGTGATGACAGCAATATA 960
QY 961 GTGAGCCTTACTTGTGAGCAAAATATGATGATATCTCTCAAGATCTATCTGAGACAGC 1020
DB 961 GTGAGCCTTACTTGTGAGCAAAATATGATGATATCTCTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCGAGTTACTTGTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCGAGTTACTTGTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAGACGCAATCCAGAAAGCAAGCTTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAGACGCAATCCAGAAAGCAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGTGCACAAAGGTTCAAGGCGCTGAAATATAGCCAGAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGTGCACAAAGGTTCAAGGCGCTGAAATATAGCCAGAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAATATGTTGGGATTAATGAAAACTGTACTAATGTGTCTACTGTGGC 1320
DB 1261 AAGCATGAAAGTAATATGTTGGGATTAATGAAAACTGTACTAATGTGTCTACTGTGGC 1320
QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGCAAGACCTGAAATTCAGCAATTT 1380
DB 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGCAAGACCTGAAATTCAGCAATTT 1380

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Oy 1381 CCTGACAAAGAGTGAAGATATCAGAAATTTGCAATTAGTTCTGACTACAAAGNA 1440
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Db 1381 CCTGACAAAGAGTGAAGATATCAGAAATTTGCAATTAGTTCTGACTACAAAGNA 1440
    |||
Oy 1441 AACGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||
Db 1441 AACGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||
Oy 1501 TCAGAGAAAGATCACAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
    |||
Db 1501 TCAGAGAAAGATCACAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
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 Job time : 4035.93 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 09:20:29 : Search time 61.604 Seconds
(without alignments)
5201.412 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgttgatgttgc.....aaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 205966 seqs, 78536166 residues

Word size : 15

Total number of hits satisfying chosen parameters: 10880

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.5	298	5 US-09-513-999C-3605	Sequence 3605, Ap
2	32	1.6	2331	6 US-10-125-923A-59	Sequence 58, Appl
3	31	1.5	114	6 US-10-240-425-582	Sequence 59, App
4	31	1.5	931	6 US-10-264-237-1316	Sequence 1316, Ap
5	31	1.5	1522	6 US-10-258-105-12	Sequence 12, Appl
6	31	1.5	1996	6 US-10-264-237-1274	Sequence 1274, Ap
7	31	1.5	8238	6 US-10-240-454-43	Sequence 43, Appl
8	31	1.5	11735	6 US-10-240-453-42	Sequence 42, Appl
9	30	1.5	330	5 US-09-728-552-24	Sequence 24, Appl
10	30	1.5	452	6 US-10-240-425-442	Sequence 442, App
11	30	1.5	563	6 US-10-266-829-12	Sequence 12, Appl
12	30	1.5	776	6 US-10-266-829-26	Sequence 26, Appl
13	30	1.5	876	6 US-10-264-237-1227	Sequence 1227, Ap
14	30	1.5	983	6 US-10-230-437-47	Sequence 47, Appl
15	30	1.5	1018	5 US-09-699-266A-1	Sequence 1, Appl
16	30	1.5	1081	6 US-10-264-237-1295	Sequence 1295, Ap
17	30	1.5	1228	6 US-10-240-425-1474	Sequence 1474, Ap
18	30	1.5	1275	6 US-10-264-237-1171	Sequence 1171, Ap
19	30	1.5	1292	6 US-10-264-237-234	Sequence 234, App
20	30	1.5	1380	5 US-09-543-293C-21	Sequence 21, Appl
21	30	1.5	1459	6 US-10-264-237-744	Sequence 744, App
22	30	1.5	1726	5 US-09-674-988A-9	Sequence 9, Appl
23	30	1.5	1968	6 US-10-131-813A-163	Sequence 163, App
24	30	1.5	1968	6 US-10-131-819A-163	Sequence 163, App
25	30	1.5	1968	6 US-10-131-823A-163	Sequence 163, App
26	30	1.5	1968	6 US-10-131-824A-163	Sequence 163, App

27	30	1.5	1968	6 US-10-131-826A-163	Sequence 163, App
28	30	1.5	1968	6 US-10-131-829A-163	Sequence 163, App
29	30	1.5	1968	6 US-10-125-976A-163	Sequence 163, App
30	30	1.5	1968	6 US-10-127-829A-163	Sequence 163, App
31	30	1.5	1968	6 US-10-127-831A-163	Sequence 163, App
32	30	1.5	1968	6 US-10-127-835A-163	Sequence 163, App
33	30	1.5	1968	6 US-10-127-837A-163	Sequence 163, App
34	30	1.5	1968	6 US-10-127-842A-163	Sequence 163, App
35	30	1.5	1968	6 US-10-127-850A-163	Sequence 163, App
36	30	1.5	1968	6 US-10-127-901A-163	Sequence 163, App
37	30	1.5	1968	6 US-10-128-689A-163	Sequence 163, App
38	30	1.5	1968	6 US-10-131-830A-163	Sequence 163, App
39	30	1.5	1968	6 US-10-131-833A-163	Sequence 163, App
40	30	1.5	1968	6 US-10-131-837A-163	Sequence 163, App
41	30	1.5	1968	6 US-10-125-930A-163	Sequence 163, App
42	30	1.5	1968	6 US-10-127-825A-163	Sequence 163, App
43	30	1.5	1968	6 US-10-127-838B-163	Sequence 163, App
44	30	1.5	1968	6 US-10-127-843A-163	Sequence 163, App
45	30	1.5	1968	6 US-10-127-849A-163	Sequence 163, App

ALIGNMENTS

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RESULT 1
US-09-513-999C-3605
Sequence 3605, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3605
LENGTH: 298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 77..298
US-09-513-999C-3605

Query Match          2.5%: Score 50; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      811 CATGCCCTCACACACACTGTTACTGTGCTACATGACAAAACAGCAAGT 860
DB      83 CATGCCCTCACACACACTGTTACTGTGCTACATGACAAAACAGCAAGT 132

RESULT 2
US-10-125-923A-59
Sequence 59, Application US/10125923A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 59
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-923A-59

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Query Match
Best Local Similarity 100.0%; Score 32; DB 6; Length 2331;
Pred. No. 1.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
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Db 2273 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2304

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RESULT 3
; Sequence 582, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI349119
US-10-240-425-582

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Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 114;
Pred. No. 5e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
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Db 70 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 100

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RESULT 4
US-10-264-237-1316
; Sequence 1316, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1316
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1316

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Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 931;
Pred. No. 4.8e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
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Db 876 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 906

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RESULT 5
US-10-258-105-12
; Sequence 12, Application US/10258105
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: Novel Collectin
; FILE REFERENCE: 19036/38785
; CURRENT APPLICATION NUMBER: US/10/258,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 12
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(969)
US-10-258-105-12

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Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 1522;
Pred. No. 4.7e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db 1454 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1484

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RESULT 6
US-10-264-237-1274
; Sequence 1274, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.

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1 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
2 FILE REFERENCE: P4131P1
3 CURRENT APPLICATION NUMBER: US/10/264,237
4 CURRENT FILING DATE: 2002-10-04
5 PRIOR APPLICATION NUMBER: PCT/US01/16450
6 PRIOR FILING DATE: 2001-05-18
7 PRIOR APPLICATION NUMBER: US 60/205,515
8 PRIOR FILING DATE: 2000-05-19
9 NUMBER OF SEQ ID NOS: 2876
10 SOFTWARE: PatentIn Ver. 3.1
11 SEQ ID NO 1274
12 LENGTH: 1996
13 TYPE: DNA
14 ORGANISM: Homo sapiens
15 FEATURE:
16 NAME/KEY: misc_feature
17 LOCATION: (1975)..(1975)
18 OTHER INFORMATION: n equals a,t,g, or c
19 FEATURE:
20 NAME/KEY: misc_feature
21 LOCATION: (1980)..(1980)
22 OTHER INFORMATION: n equals a,t,g, or c
23 US-10-264-237-1274

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Qy	2010	GCTAAAAAAAAAAAAAAAAAAAAA	2040
Db	1917	GCTAAAAAAAAAAAAAAAAAAAAA	1947

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RESULT 7
US-10-240-454-43/c
: Sequence 43, Application US/10240454
: GENERAL INFORMATION:
: APPLICANT: OLEK, Alexander
: APPLICANT: PIEPENBROCK, Christian
: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
: FILE REFERENCE: 5013.1010
: CURRENT APPLICATION NUMBER: US/10/240.454
: CURRENT FILING DATE: 2002-10-02
: PRIOR APPLICATION NUMBER: PCV/EP01/04016
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: DE 10019058.8
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: DE 10019173.8
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: DE 10032529.7
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DE 10043826.1
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 68
: SEQ ID NO 43
: LENGTH: 8238
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: US-10-240-454-43

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Qy	2010	GCTAAAAAAAAAAAAAAAAAAAAA	2040
Db	2119	GCTAAAAAAAAAAAAAAAAAAAAA	2089

RESULT 8

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US-10-240-453.2/c
: Sequence 42, Application US/10240453
: GENERAL INFORMATION:
: APPLICANT: OLEK, Alexander
: APPLICANT: PIEPENBROCK, Christian
: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
: TITLE OF INVENTION: Transcription
: TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
: TITLE OF INVENTION: With DNA Transcription
: FILE REFERENCE: 5013.1009
: CURRENT APPLICATION NUMBER: US/10/240.453
: CURRENT FILING DATE: 2002-10-02
: PRIOR APPLICATION NUMBER: PCT/EP01/03973
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: DE 10019058.8
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: DE 10019173.8
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: DE 10032529.7
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DE 10043826.1
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 350
: SEQ ID NO 42
: LENGTH: 11735
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-42

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Qy	2010	GCTAAAAAAAAAAAAAAAAAAAAA	2040
Db	6782	GCTAAAAAAAAAAAAAAAAAAAAA	6752

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RESULT 9
US-09-728-552-24
: Sequence 24, Application US/09728552
:
: GENERAL INFORMATION:
: APPLICANT: Choo, Kong-Hong Andy
: APPLICANT: Du Sart, Desiree
: APPLICANT: Cancilla, Michael R.
: TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
: FILE REFERENCE: Davies Col
: CURRENT APPLICATION NUMBER: US/09/728,552
: CURRENT FILING DATE: 2000-12-02
: PRIOR APPLICATION NUMBER: 09/078,294
: PRIOR FILING DATE: 1998-05-13
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 24
: LENGTH: 330
: TYPE: DNA
: ORGANISM: BAC-F2 contlg 47 fragment 4
US-09-728-552-24

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QY	2011	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	144	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA	173

RESULT 10
US-10-240-425-442/c

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; Sequence 442, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 442
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI052543
US-10-240-425-442
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Query Match 1.5%; Score 30; DB 6; Length 452;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 31 CTAACAAAAAAAAAAAAAAAAAAAAA 2
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RESULT 11
US-10-266-829-12
; Sequence 12, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-12
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Query Match 1.5%; Score 30; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 514 CTAACAAAAAAAAAAAAAAAAAAAAA 543
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RESULT 12
US-10-266-829-26
; Sequence 26, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-26
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Query Match 1.5%; Score 30; DB 6; Length 776;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 744 CTAACAAAAAAAAAAAAAAAAAAAAA 773
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RESULT 13
US-10-264-237-1227/C
; Sequence 1227, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1227
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1227
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Query Match 1.5%; Score 30; DB 6; Length 876;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 30 CTAACAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 14
US-10-230-437-47
; Sequence 47, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC94
; CURRENT APPLICATION NUMBER: US/10/230,437
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 47
; LENGTH: 983
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-47

```

```

Query Match          1.5%; Score 30; DB 6; Length 983;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 940 CTAACAAAAAAAAAAAAAAAAAAAAA 969

```

```

RESULT 15
US-09-699-266A-1
; Sequence 1, Application US/09699266A
; GENERAL INFORMATION:
; APPLICANT: Ma, Hongchang
; APPLICANT: Morakinyo, Layo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Orozco Jr., Emil M.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: TRANSCRIPTION AND GENE EXPRESSION REGULATORS
; FILE REFERENCE: B1164 US NA
; CURRENT APPLICATION NUMBER: US/09/699,266A
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/US99/08385
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/083,212
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1018
; TYPE: DNA
; ORGANISM: Zea mays
US-09-699-266A-1

```

```

Query Match          1.5%; Score 30; DB 5; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 972 CTAACAAAAAAAAAAAAAAAAAAAAA 1001

```

```

RESULT 16
US-10-264-237-1295
; Sequence 1295, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1331P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1295
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1076)..(1076)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1078)..(1078)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1295

```

```

Query Match          1.5%; Score 30; DB 6; Length 1081;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1023 CTAACAAAAAAAAAAAAAAAAAAAAA 1052

```

```

RESULT 17
US-10-240-425-1474
; Sequence 1474, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1474
; LENGTH: 1228
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U92315
US-10-240-425-1474

```

```

Query Match          1.5%; Score 30; DB 6; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2011 CTAACAAAAA 2040
Db 1198 CTAACAAAAA 1227

RESULT 18
US-10-264-237-1171/c
; Sequence 1171, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Blrse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patentln Ver. 3.1
; SEQ ID NO 1171
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1171

Query Match 1.5%; Score 30; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAA 2040
Db 39 CTAACAAAAA 10

RESULT 19
US-10-264-237-234
; Sequence 234, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Blrse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patentln Ver. 3.1
; SEQ ID NO 234
; LENGTH: 1292
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (507)..(507)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-234

Query Match 1.5%; Score 30; DB 6; Length 1292;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAA 2040
Db 1262 CTAACAAAAA 1291

RESULT 20
US-09-543-293C-21
; Sequence 21, Application US/09543293C
; GENERAL INFORMATION:

; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Meyer, David J.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Tingey, Scott V.
; TITLE OF INVENTION: Secretory Pathway Proteins
; FILE REFERENCE: B1351 US NA
; CURRENT APPLICATION NUMBER: US/09/543,293C
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,191
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1370)
; OTHER INFORMATION: n = a, c, g or t
US-09-543-293C-21

Query Match 1.5%; Score 30; DB 5; Length 1380;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAA 2040
Db 1285 CTAACAAAAA 1314

RESULT 21
US-10-264-237-744
; Sequence 744, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Blrse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patentln Ver. 3.1
; SEQ ID NO 744
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-744

Query Match 1.5%; Score 30; DB 6; Length 1459;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAA 2040
Db 1394 CTAACAAAAA 1423

RESULT 22
US-09-674-988A-9
; Sequence 9, Application US/09674988A
; GENERAL INFORMATION:
; APPLICANT: McEliver, John A.
; APPLICANT: Zhao, Suling
; APPLICANT: Bowen, Benjamin A.

```
; TITLE OF INVENTION: Zea Mays Phosphate Transporter Genes
; FILE REFERENCE: 0859-PCT-US
; CURRENT APPLICATION NUMBER: US/09/674,988A
; CURRENT FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/085,292
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-674-988A-9

Query Match          1.5%: Score 30; DB 5; Length 1726;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db  1687 CTACAAAAAAAAAAAAAAAAAAAAA 1716

RESULT 23
US-10-131-813A-163
; Sequence 163, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
```

```
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-131-813A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db  1923 CTACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 24
US-10-131-819A-163
; Sequence 163, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C134
; CURRENT APPLICATION NUMBER: US/10/131,819A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-131-819A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
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```
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 25
US-10-131-823A-163
; Sequence 163, Application US/10131823A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C143
; CURRENT APPLICATION NUMBER: US/10/131, 823A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-823A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C126
; CURRENT APPLICATION NUMBER: US/10/131, 824A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-824A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 27
US-10-131-826A-163
; Sequence 163, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
```

```

: APPLICANT: Tumas,Daniel
: APPLICANT: Matanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C128
: CURRENT APPLICATION NUMBER: US/10/131,826A
: CURRENT FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-131-826A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 28
: Sequence 163, Application US/10131829A
: GENERAL INFORMATION:
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini,Maureen
: APPLICANT: Deforge,Laura
: APPLICANT: Desnoyers,Luc
: APPLICANT: Filvaroff,Ellen
: APPLICANT: Gao,Wei-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Audrey
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Matanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,829A
: CURRENT FILING DATE: 2002-04-27
: PRIOR APPLICATION NUMBER: 60/049911
```

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: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-131-829A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 29
: Sequence 163, Application US/10125926A
: GENERAL INFORMATION:
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini,Maureen
: APPLICANT: Deforge,Laura
: APPLICANT: Desnoyers,Luc
: APPLICANT: Filvaroff,Ellen
: APPLICANT: Gao,Wei-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Audrey
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Matanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C80
: CURRENT APPLICATION NUMBER: US/10/125,926A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
```



```
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-926A-163

Query Match
Best Local Similarity 1.5%; Score 30; DB 6; Length 1968;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 30
US-10-127-829A-163
; Sequence 163, Application US/10127829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
; CURRENT APPLICATION NUMBER: US/10/127, 829A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829A-163

Query Match
Best Local Similarity 1.5%; Score 30; DB 6; Length 1968;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 31
US-10-127-831A-163
; Sequence 163, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C107
; CURRENT APPLICATION NUMBER: US/10/127, 831A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-831A-163

Query Match
Best Local Similarity 1.5%; Score 30; DB 6; Length 1968;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
| | | | | | | | | | | | | | | | | | | |
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 32
US-10-127-835A-163
: Sequence 163, Application US/10127835A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Collin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C102
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-835A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Collin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C96
: CURRENT FILING DATE: 2002-10-17
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-837A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
| | | | | | | | | | | | | | | | | | | |
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 34
US-10-127-842A-163
: Sequence 163, Application US/10127842A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
```

```

: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C100
: CURRENT APPLICATION NUMBER: US/10/127,842A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO: 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-127-842A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 35
US-10-127-850A-163
: Sequence 163, Application US/10127850A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Zhang, Zemin
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C110
: CURRENT APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
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: CURRENT APPLICATION NUMBER: US/10/127,850A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO: 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-127-850A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 36
US-10-127-901A-163
: Sequence 163, Application US/10127901A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C86
: CURRENT APPLICATION NUMBER: US/10/127,901A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
```

```
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-901A-163
```

```
Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952
```

```
RESULT 37
US-10-128-689A-163
; Sequence 163, Application US/10128689A
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C117
; CURRENT APPLICATION NUMBER: US/10/128, 689A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
```

```
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-689A-163
```

```
Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952
```

```
RESULT 38
US-10-131-830A-163
; Sequence 163, Application US/10131830A
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C137
; CURRENT APPLICATION NUMBER: US/10/131, 830A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-830A-163
```

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
DB 1923 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 39

US-10-131-833A-163
; Sequence 163, Application US/10131833A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C142
; CURRENT APPLICATION NUMBER: US/10/131,833A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-833A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
DB 1923 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 40

US-10-131-837A-163
; Sequence 163, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C131
; CURRENT APPLICATION NUMBER: US/10/131,837A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-837A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
DB 1923 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 41

US-10-125-930A-163
; Sequence 163, Application US/10125930A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

```
APPLICANT: Goddard,Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C78
CURRENT APPLICATION NUMBER: US/10/125, 930A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-125-930A-163

Query Match      1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952
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```
RESULT 42
US-10-127-825A-163
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```
Sequence 163, Application US/10127825A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Laureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
```

```
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C84
CURRENT APPLICATION NUMBER: US/10/127, 825A
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-825A-163
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```
Query Match      1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952
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```
RESULT 43
US-10-127-838B-163
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```
Sequence 163, Application US/10127838B
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Laureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C98
CURRENT APPLICATION NUMBER: US/10/127, 838B
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
```

```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-838B-163
```

```
Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2011 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db 1923 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952
```

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RESULT 44
US-10-127-843A-163
; Sequence 163, Application US/10127843A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C09
; CURRENT APPLICATION NUMBER: US/10/127,843A
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
```

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-843A-163
```

```
Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2011 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db 1923 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952
```

```

RESULT 45
US-10-127-849A-163
; Sequence 163, Application US/10127849A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C103
; CURRENT APPLICATION NUMBER: US/10/127,849A
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
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; ORGANISM: Homo Sapien
US-10-127-849A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2011 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||
Db 1923 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

Search completed: November 8, 2002, 15:51:31
Job time : 117.604 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 09:20:29 ; Search time 60.396 Seconds
(without alignments)
5201.412 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atgtgtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaaa 2000

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 205966 seqs, 78536166 residues

Word size : 15

Total number of hits satisfying chosen parameters: 10881

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCF_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.5	298	US-09-513-999C-3605	Sequence 3605, App
2	37	1.8	2331	US-10-125-923A-59	Sequence 59, App
3	36	1.8	931	US-10-264-237-1316	Sequence 1316, App
4	36	1.8	1522	US-10-258-105-12	Sequence 12, App
5	36	1.8	1996	US-10-264-237-1274	Sequence 1274, App
6	36	1.8	8238	US-10-240-454-43	Sequence 43, App
7	35	1.8	114	US-10-240-425-582	Sequence 582, App
8	35	1.8	563	US-10-266-829-12	Sequence 12, App
9	35	1.8	983	US-10-230-437-47	Sequence 47, App
10	35	1.8	1018	US-09-699-266A-1	Sequence 1, App
11	35	1.8	1081	US-10-264-237-1295	Sequence 1295, App
12	35	1.8	180	US-09-543-293C-21	Sequence 21, App
13	35	1.8	1459	US-10-264-237-744	Sequence 744, App
14	35	1.8	1726	US-09-674-988A-9	Sequence 9, App
15	35	1.8	1968	US-10-131-813A-163	Sequence 163, App
16	35	1.8	1968	US-10-131-819A-163	Sequence 163, App
17	35	1.8	1968	US-10-131-823A-163	Sequence 163, App
18	35	1.8	1968	US-10-131-824A-163	Sequence 163, App
19	35	1.8	1968	US-10-131-826A-163	Sequence 163, App
20	35	1.8	1968	US-10-131-829A-163	Sequence 163, App
21	35	1.8	1968	US-10-125-926A-163	Sequence 163, App
22	35	1.8	1968	US-10-127-829A-163	Sequence 163, App
23	35	1.8	1968	US-10-127-831A-163	Sequence 163, App
24	35	1.8	1968	US-10-127-835A-163	Sequence 163, App
25	35	1.8	1968	US-10-127-837A-163	Sequence 163, App
26	35	1.8	1968	US-10-127-842A-163	Sequence 163, App

27	35	1.8	1968	US-10-127-850A-163	Sequence 163, App
28	35	1.8	1968	US-10-127-901A-163	Sequence 163, App
29	35	1.8	1968	US-10-128-689A-163	Sequence 163, App
30	35	1.8	1968	US-10-131-830A-163	Sequence 163, App
31	35	1.8	1968	US-10-131-833A-163	Sequence 163, App
32	35	1.8	1968	US-10-131-837A-163	Sequence 163, App
33	35	1.8	1968	US-10-125-930A-163	Sequence 163, App
34	35	1.8	1968	US-10-127-825A-163	Sequence 163, App
35	35	1.8	1968	US-10-127-838A-163	Sequence 163, App
36	35	1.8	1968	US-10-127-843A-163	Sequence 163, App
37	35	1.8	1968	US-10-127-849A-163	Sequence 163, App
38	35	1.8	1968	US-10-128-684A-163	Sequence 163, App
39	35	1.8	1968	US-10-128-685A-163	Sequence 163, App
40	35	1.8	1968	US-10-128-686A-163	Sequence 163, App
41	35	1.8	1968	US-10-128-690A-163	Sequence 163, App
42	35	1.8	1968	US-10-128-693A-163	Sequence 163, App
43	35	1.8	1968	US-10-131-821A-163	Sequence 163, App
44	35	1.8	1968	US-10-131-836A-163	Sequence 163, App
45	35	1.8	1968	US-10-137-872A-163	Sequence 163, App

ALIGNMENTS

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RESULT 1
US-09-513-999C-3605
; Sequence 3605, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122, 487
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3605
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77..298
US-09-513-999C-3605

Query Match      2.5%; Score 50; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.9e+13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      811 CATGGCCCTCACACACTGTCTGTGTACATGAGCAAAACAGCAAGT 860
        |||||||
Db       83 CATGGCCCTCACACACTGTCTGTGTACATGAGCAAAACAGCAAGT 132

RESULT 2
US-10-125-923A-59
; Sequence 59, Application US/10125923A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 59
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-923A-59
```

```
Query Match          1.8%; Score 37; DB 6; Length 2331;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1964 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 2273 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2309
```

```
RESULT 3
US-10-264-237-1316
; Sequence 1316, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1316
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1316
```

```
Query Match          1.8%; Score 36; DB 6; Length 931;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1965 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 876 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 911
```

```
RESULT 4
US-10-258-105-12
```

```
; Sequence 12, Application US/10258105
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: Novel Collectin
; FILE REFERENCE: 19036/38785
; CURRENT APPLICATION NUMBER: US/10/258,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 12
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(969)
US-10-258-105-12
```

```
Query Match          1.8%; Score 36; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1965 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1454 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1489
```

```
RESULT 5
US-10-264-237-1274
; Sequence 1274, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1274
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1975)..(1975)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1980)..(1980)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1274
```

```
Query Match          1.8%; Score 36; DB 6; Length 1996;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1965 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1917 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952
```

```
RESULT 6
US-10-240-454-43/C
; Sequence 43, Application US/10240454
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
```

```

; APPLICANT: PIEPERBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
; FILE REFERENCE: 5013.1010
; CURRENT APPLICATION NUMBER: US/10/240.454
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/04016
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 43
; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-454-43
Query Match
Best Local Similarity 1.8%; Score 36; DB 6; Length 8238;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1965 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 2119 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2084

RESULT 7
US-10-240-425-582
; Sequence 582, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginaid V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193.446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF349119
US-10-240-425-582
Query Match
Best Local Similarity 1.8%; Score 35; DB 6; Length 114;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1965 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1999
DB 70 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 104

RESULT 8
```

```

US-10-266-829-12
; Sequence 12, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266.829
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756.168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145.220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-12
Query Match
Best Local Similarity 1.8%; Score 35; DB 6; Length 563;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 514 CTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 548

RESULT 9
US-10-230-437-47
; Sequence 47, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C94
; CURRENT APPLICATION NUMBER: US/10/230.437
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119.480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
```

```

; SEQ ID NO 47
; LENGTH: 983
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-47

```

Query Match	1.8%;	Score 35;	DB 6;	Length 983;
Best Local Similarity	100.0%;	Pred. No. 9.3e-07;		
Matches 35;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1966	CTAAAAAAAAAAAAAAAAAAAAAAAAA	2000
Db	940	CTAAAAAAAAAAAAAAAAAAAAAAAAA	974

RESULT 10
US-09-699-266A-1
; Sequence 1, Application US/09699266A
GENERAL INFORMATION:

```

? APPLICANT: Orozco Jr., EmilM.
? APPLICANT: Rafalski, J. Antoni
? TITLE OR INVENTION: TRANSCRIPTION AND GENE EXPRESSION REGULATORS
? FILE REFERENCE: BB1164 US NA
? CURRENT APPLICATION NUMBER: US/09/699,266A
? CURRENT FILING DATE: 2000-10-27
? PRIOR APPLICATION NUMBER: PCT/US99/08385
? PRIOR FILING DATE: 1999-04-16
? PRIOR APPLICATION NUMBER: 60/083,212
? PRIOR FILING DATE: 1998-04-27
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: Microsoft Office 97
? SEQ ID NO: 1
? LENGTH: 1018
? TYPE: DNA
? ORGANISM: Zea mays
? US-09-699-266A-1

```

Query Match	1.8%;	Score 35;	DB 5;	Length 1018;
Best Local Similarity	100.0%;	Pred. No. 9.3e-07;		
Matches 35; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Qy	1966	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2000
Db	972	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1006

```

RESULT 11
US-10-264-237-1295
Sequence 1295, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birst et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1295
LENGTH: 1081
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1076)..(1076)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

```

```

; NAME/KEY: misc_feature
; LOCATION: (1078)..(1078)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1295

```

```

query Match      1.8%; Score 35; DB 6; Length 1081;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Qy	1966	CTAATAAAAAAAAAAAAAAAAAAAAAA	2000
Db	1023	CTAATAAAAAAAAAAAAAAAAAAAAAA	1057

RESULT 12
US-09-543-293C-21
; Sequence 21, Application US/09543293C
; GENERAL INFORMATION.

```

1 TITLE OF INVENTION: Secretary Pathway Proteins
2
3 FILE REFERENCE: BR1351 US NA
4
5 CURRENT APPLICATION NUMBER: 05/09/543,293C
6
7 CURRENT FILING DATE: 2000-04-06
8
9 PRIOR APPLICATION NUMBER: 60/128,191
10
11 PRIOR FILING DATE: 1999-04-07
12
13 NUMBER OF SEQ ID NOS: 39
14
15 SOFTWARE: Microsoft Office 97
16
17 SEQ ID NO 21
18
19 LENGTH: 1380
20
21 TYPE: DNA
22
23 ORGANISM: glycine max
24
25 FEATURE:
26
27 NAME/KEY: unsure
28
29 LOCATION: (1370)
30
31 OTHER INFORMATION: n = a, c, g or t
32
33 US-09-543-293C-21

```

Query Match	1.8%;	Score 35;	DB 5;	Length 1380;
Best Local Similarity	100.0%;	Pred. No. 9.2e-07;		
Matches 35; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1966	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2000
Db	1285	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1315

```

RESULT 13
US-10-264-237-744
Sequence 744, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birst et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 744
LENGTH: 1459
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (25)..(25)
OTHER INFORMATION: n equals a,t,g, or c

```



```

; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-819A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 17
US-10-131-823A-163
; Sequence 163, Application US/10131823A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C143
; CURRENT APPLICATION NUMBER: US/10/131.823A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
```

```

US-10-131-823A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 18
US-10-131-824A-163
; Sequence 163, Application US/10131824A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C126
; CURRENT APPLICATION NUMBER: US/10/131.824A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-824A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```

RESULT 19
US-10-131-826A-163
; Sequence 163, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCETIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-163

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
      |||
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 20
US-10-131-829A-163
; Sequence 163, Application US/10131829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

```

```

1  APPLICANT: Gao,Wei-Qiang
2  APPLICANT: Gerritsen,Mary E.
3  APPLICANT: Goddard,Audrey J.
4  APPLICANT: Godowski,Paul J.
5  APPLICANT: Gurney,Austin L.
6  APPLICANT: Sherwood,Steven
7  APPLICANT: Smith,Victoria
8  APPLICANT: Stewart,Timothy A.
9  APPLICANT: Tumas,Daniel
10 APPLICANT: Watanabe,Colin K
11 APPLICANT: Wood,William
12 APPLICANT: Zhang,Zemin
13 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
14 FILE REFERENCE: P3330R1C138
15 CURRENT APPLICATION NUMBER: US/10/131.829A
16 PRIOR FILING DATE: 2002-04-27
17 PRIOR APPLICATION NUMBER: 60/049911
18 PRIOR FILING DATE: 1997-06-18
19 PRIOR APPLICATION NUMBER: 60/056974
20 PRIOR FILING DATE: 1997-08-26
21 PRIOR APPLICATION NUMBER: 60/059113
22 PRIOR FILING DATE: 1997-09-17
23 PRIOR APPLICATION NUMBER: 60/059115
24 PRIOR FILING DATE: 1997-09-17
25 PRIOR APPLICATION NUMBER: 60/059117
26 PRIOR FILING DATE: 1997-09-17
27 PRIOR APPLICATION NUMBER: 60/059122
28 PRIOR FILING DATE: 1997-09-17
29 PRIOR APPLICATION NUMBER: 60/059184
30 PRIOR FILING DATE: 1997-09-17
31 PRIOR APPLICATION NUMBER: 60/059263
32 PRIOR FILING DATE: 1997-09-18
33 PRIOR APPLICATION NUMBER: 60/059352
34 PRIOR FILING DATE: 1997-09-19
35 PRIOR APPLICATION NUMBER: 60/059588
36 PRIOR FILING DATE: 1997-09-19
37 Remaining Prior Application data removed - See File Wrapper or PALM.
38 / NUMBER OF SEQ ID NOS: 550
39 / SEQ ID NO 163
40 / LENGTH: 1968
41 / TYPE: DNA
42 / ORGANISM: Homo Sapien
43 US-10-131-829A-163
44
45 Query Match 1.8%; Score 35; DB 6; Length 1968;
46 Best Local Similarity 100.0%; Pred. No. 9.1e-07;
47 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0
48
49 QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
50 |||
51 Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
52
53 RESULT 21
54 US-10-125-926A-163
55 / Sequence 163, Application US/10125926A
56 / GENERAL INFORMATION:
57 / APPLICANT: Baker, Kevin P.
58 / APPLICANT: Bereshni, Maureen
59 / APPLICANT: DeForge, Laura
60 / APPLICANT: Desnoyers, Luc
61 / APPLICANT: Filvaroff, Ellen
62 / APPLICANT: Gao, Wei-Qiang
63 / APPLICANT: Gerritsen, Mary E.
64 / APPLICANT: Goddard, Audrey
65 / APPLICANT: Godowski, Paul J.
66 / APPLICANT: Gurney, Austin L.
67 / APPLICANT: Sherwood, Steven
68 / APPLICANT: Smith, Victoria
69 / APPLICANT: Stewart, Timothy A.
70 / APPLICANT: Tumas, Daniel
71 / APPLICANT: Watanabe, Colin K
72 / APPLICANT: Zhang, Zemin

```

```
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C80
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-125-926A-163
```

```
Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```
RESULT 22
US-10-127-829A-163
Sequence 163, Application US/10127829A
GENERAL INFORMATION:
```

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C85
CURRENT APPLICATION NUMBER: US/10/127,829A
PRIOR FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
```

```
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-829A-163
```

```
Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```
RESULT 23
US-10-127-831A-163
Sequence 163, Application US/10127831A
GENERAL INFORMATION:
```

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C107
CURRENT APPLICATION NUMBER: US/10/127,831A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
```

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-831A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 24
US-10-127-835A-163
; Sequence 163, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumasz, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C102
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
```

```

; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-835A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 25
US-10-127-837A-163
; Sequence 163, Application US/10127837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumasz, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C96
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-837A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
```

Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 26
US-10-127-842A-163

Sequence 163, Application US/10127842A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C100
CURRENT APPLICATION NUMBER: US/10/127, 842A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-842A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 27
US-10-127-850A-163
Sequence 163, Application US/10127850A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C110
CURRENT APPLICATION NUMBER: US/10/127, 850A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-850A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 28
US-10-127-901A-163

Sequence 163, Application US/10127901A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria

```

; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC86
; CURRENT APPLICATION NUMBER: US/10/127,901A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-901A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 29
US-10-128-689A-163
; Sequence 163, Application US/10128689A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wel-Qiang
; APPLICANT: Gerltsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC117
; CURRENT APPLICATION NUMBER: US/10/128,689A
; CURRENT FILING DATE: 2002-10-15
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; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-689A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 30
US-10-131-830A-163
; Sequence 163, Application US/10131830A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wel-Qiang
; APPLICANT: Gerltsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC137
; CURRENT APPLICATION NUMBER: US/10/131,830A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-830A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 31
US-10-131-833A-163
; Sequence 163, Application US/10131833A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C142
; CURRENT APPLICATION NUMBER: US/10/131,833A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-833A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 32
US-10-131-837A-163
; Sequence 163, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C131
; CURRENT APPLICATION NUMBER: US/10/131,837A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-837A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-833A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 32
US-10-131-837A-163
; Sequence 163, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C131
; CURRENT APPLICATION NUMBER: US/10/131,837A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-837A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C98
; CURRENT APPLICATION NUMBER: US/10/127,838B
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-838B-163
```

```

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 36
US-10-127-843A-163
; Sequence 163, Application US/10127843A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C98
```

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; FILE REFERENCE: P3330R1C98
; CURRENT APPLICATION NUMBER: US/10/127,843A
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-843A-163
```

```

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 37
US-10-127-849A-163
; Sequence 163, Application US/10127849A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C103
; CURRENT APPLICATION NUMBER: US/10/127,849A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
```

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-849A-163

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 38
US-10-128-684A-163
; Sequence 163, Application US/10128684A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C118
; CURRENT APPLICATION NUMBER: US/10/128,684A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-684A-163
```

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; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-684A-163

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 39
US-10-128-685A-163
; Sequence 163, Application US/10128685A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C116
; CURRENT APPLICATION NUMBER: US/10/128,685A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-685A-163
```

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 40
US-10-128-686A-163

; Sequence 163, Application US/10128686A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey E.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P330R1C119

; CURRENT APPLICATION NUMBER: US/10/128,686A

; CURRENT FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 163

; LENGTH: 1968

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-10-128-686A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 41
US-10-128-690A-163

; Sequence 163, Application US/10128690A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey E.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P330R1C122

; CURRENT APPLICATION NUMBER: US/10/128,690A

; CURRENT FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 163

; LENGTH: 1968

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-10-128-690A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 42
US-10-128-693A-163

; Sequence 163, Application US/10128693A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

```
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C120
; CURRENT APPLICATION NUMBER: US/10/128, 693A
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-128-693A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9,1e-07; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 43
US-10-131-821A-163
; Sequence 163, Application US/10131821A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
```

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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C138
; CURRENT APPLICATION NUMBER: US/10/131, 831A
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-131-821A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9,1e-07; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 44
US-10-131-836A-163
; Sequence 163, Application US/10131836A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C135
; CURRENT APPLICATION NUMBER: US/10/131, 836A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-872A-163
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Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
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RESULT 45
US-10-137-872A-163

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; Sequence 163, Application US/10137872A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desjardis, Laura
; APPLICANT: Flivaioff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C150
; CURRENT APPLICATION NUMBER: US/10/137, 872A
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-872A-163
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Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
|||||
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
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Search completed: November 8, 2002, 15:50:35
Job time : 94.396 secs

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Db 241 GGGCTTCTGGAGACACAGACGACCTGCTATGAAGACACTCAGAAACAGATGGGCAAG 300
Qy 301 TGTGTCTCCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGTGTCTCCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
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Qy 541 TCTGCAATGGGAATTCGAAGTAGTAAACCTCGTGGAGACAGATGCTCACTTAT 600
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Db 1081 AAAGAAAAACAGATGTAAAAATCTTCTGAAACAGCAATCCAGAAACAGATTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
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Db 1201 ATGCTCTCAAG 1260
Qy 1261 AAGCATGAAGATTAATGTGGATTAATGTGGATTAATGTGGATTAATGTGGATTAAT 1320
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Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATGAGCCAGAGAGAGAGAGAG 1560
Qy 1561 TTTATGCTATCGAAG 1620
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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-759-143-374
Sequence 374, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Panger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGGTTGAGGTGATTCATGCCGGCTCTCTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATGCCGGCTCTCTCTGTGAAGAAGCCATTGGTCTC 60
OY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCCTGCTCCCTGCTGCGAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCCTGCTCCCTGCTGCGAGGAGCGGCAAG 120
OY 121 AGCAACGTGGGCACTTCTTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
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DB 181 ATGGGCAAGTGTGCCCGCCACATGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGTGG 240
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DB 241 GGGGCTCTGGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
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DB 301 TGGTGGTGGCACTGCTTCCCTGCTGCGAGGAGCGGCAAGCAAGTGGGCGCTTGG 360
OY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGTCCGCTGAGAGAGTCTG 420
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OY 661 TGTGCGTAAATGTCTGGAACATGAGCAATATTCAGATGATGATGAAT 720
DB 661 TGTGCGTAAATGTCTGGAACATGAGCAATATTCAGATGATGATGAAT 720
OY 721 ACCACTCTGACCTACGCTATCTAATGAAGATAATTAATGAGCAAGCAAGCACTGCTTA 780
DB 721 ACCACTCTGACCTACGCTATCTAATGAAGATAATTAATGAGCAAGCAAGCACTGCTTA 780
OY 781 TATGGGCTGATATGCAATCAAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 840
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OY 1141 CTGACATCAGAGAGAGTCACAAAAGCTTCAAAAGCAGTGAATAAGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAAAGCTTCAAAAGCAGTGAATAAGCCAGCAGAGAA 1200
OY 1201 ATGCTCAAGAACCAAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACCAAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
OY 1261 AAGCATGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 AAGCATGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
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DB 1321 AATGATATATGATATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 1380
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DB 1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGCAATTTAGTTCTGACTCAAAAGAA 1440
OY 1441 AAGCAATGCAAAATATCTTCTGAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
DB 1441 AAGCAATGCAAAATATCTTCTGAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
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DB 1501 TCAGAGAGAGTCAACAAAGCTTGAAGGAGTGAAGAAATGGCCAGCAGAGTGAAGAAAT 1560
OY 1561 TTTATGCTATCGAAGAAATGAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1620
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DB 1681 AGAAGCACTGAAGAGCAAGCAATTTCTGACACTGAGAGATGAAGATGATGATGATGATGAT 1740
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OY 1921 GCCATGCTAAGAGTGAAGTGAAGCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1980

Db 1921 GCCATGCTAGACTGAGCTAGACACAAATGAAATCATCAGACCCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-780-669-374
; Sequence 374, Application US/09780669
; Patent No. US20020051977A1

GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGTGGTGGAGTTGATTCATGCGCGCTGCTCTCTGTGAAGAACCATTTGCTCTC 60
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Db 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
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Db 121 AGCAAGCTGGGCACTTGTGAGACCAAGAGACTCTGTATGAAGACACTCAGAGAGAG 180
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Qy 361 GGAGACTACGATGACAGTGGCTTCATGAGCCGAGTACGACGCTCCGTGGAGAGATCTG 420
Db 361 GGAGACTACGATGACAGTGGCTTCATGAGCCGAGTACGACGCTCCGTGGAGAGATCTG 420
Qy 421 GACAGCTCCAGAGAGCTGGCTGGTAAAGTCCCGGAGAGAGATCTCATCTGATG 480
Db 421 GACAGCTCCAGAGAGCTGGCTGGTAAAGTCCCGGAGAGAGATCTCATCTGATG 480
Qy 481 CTCAGGACACTGACGTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Qy 901 CTGATAGATATGAG 960
Db 901 CTGATAGATATGAG 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCATCTGAGAGAG 1020
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Qy 1021 GCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
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Db 1141 CTGACATCAG 1200
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Db 1201 ATGTCCTAAG 1260
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Db 1381 CCTGACACAG 1440
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Db 1561 TTATAGGCTATGAGAAATGAGAACGAGAGTACTCATGTGGATTCCAGAAAAC 1620
OY 1621 CTGACTAATGCTGCCACTGCTGGCAATGGTGAATGATGATTAATTCCTCCAGAGAGAGC 1680
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Db 1621 CTGACTAATGCTGCCACTGCTGGCAATGGTGAATGATGATTAATTCCTCCAGAGAGAGC 1680
OY 1681 ABAACACCTGAAAAGCCAGCAATTTCTGACACTGAGATGAAGATATACAGTACGAA 1740
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Db 1681 ABAACACCTGAAAAGCCAGCAATTTCTGACACTGAGATGAAGATATACAGTACGAA 1740
OY 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATATTAACGATGAG 1800
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Db 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATATTAACGATGAG 1800
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RESULT 4
US-09-810-936-302
; Sequence 302, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-302
Query Match 100.0%: Score 2000: DB 10: Length 2000:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 2000: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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Db 1 ATGGTGGTTGAGGTGATTCATGCCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
OY 61 AGGAGCAAGATGGGCAAGTGTGTGCTCCCTGCTTCCCTGTCAGGAGACGGCCAG 120
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Db 61 AGGAGCAAGATGGGCAAGTGTGTGCTCCCTGCTTCCCTGTCAGGAGACGGCCAG 120
OY 121 AGCAAGTGGGCACTTCTGGAAGCAAGCAAGATCTGTATGAAGACACTCAGACCAAG 180
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Db 121 AGCAAGTGGGCACTTCTGGAAGCAAGCAAGATCTGTATGAAGACACTCAGACCAAG 180
OY 181 ATGGGCAAGTGGGCAAGTGTGTGCTCCCTGCTTCCCTGTCAGGAGACGGCCAG 240
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OY 241 GGGCTTCTGAGAGACCAAGCAAGTGTGTGCTATGAAGCACTCAGAACAGATGGCCAG 300
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Db 241 GGGCTTCTGAGAGACCAAGCAAGTGTGTGCTATGAAGCACTCAGAACAGATGGCCAG 300
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OY 361 GGAGACTAGGATGACAGTGTGCTGATGAGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
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OY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATTCACATTAAT 600
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OY 601 GTCTCTGACAAACAAAAGAGAGACGCTCTGATTAAGAGCCGTACAAATGCCAGAAATGA 660
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OY 661 TGTGGCTTAATGTTGTGGAACATGAGCAGTCAAAATATTCAGATGATGATGAAT 720
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Db 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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Db	1141	CTGCATCAGAGGAGAGGTACAAAGCTTCAAAGGCGAGTGAATAATGCGACGACAGAA	1200
Qy	1201	ATGCTCAGAGCACGAAATTAATTAAGGATGGGATAGAGAGCTTGAAGAAGAAATGAG	1260
Db	1201	ATGCTCAGAGCACGAAATTAATTAAGGATGGGATAGAGAGCTTGAAGAAGAAATGAG	1260
Qy	1261	AAGCATGAAGTAAATATGTGGGATTACTAAGAAAACCTACTAAATGGTGCACCTGCGC	1320
Db	1261	AAGCATGAAGTAAATATGTGGGATTACTAAGAAAACCTACTAAATGGTGCACCTGCGC	1320
Qy	1321	AATGCTATTAATGGATTAAATCTCTCAAAGGAGCAGACACCTGAAATATCAGCAATT	1380
Db	1321	AATGCTATTAATGGATTAAATCTCTCAAAGGAGCAGACACCTGAAATATCAGCAATT	1380
Qy	1381	CCTGACACGAAAGTGAAGGTATCACAGAAATTTGGATTAATTGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACACGAAAGTGAAGGTATCACAGAAATTTGGATTAATTGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATTACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATTACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGAGAGATCACAAAGCTTTAGGGCAGTGAATAATGCGACCGCAGAGCTAGAAAT	1560
Db	1501	TCAGAGAGAGATCACAAAGCTTTAGGGCAGTGAATAATGCGACCGCAGAGCTAGAAAT	1560
Qy	1561	TTTATGGCTATTCGAAGAAATGAAGAAGCAGCGAAGTACTCATGTGGGATTCGCAGAAAC	1620
Db	1561	TTTATGGCTATTCGAAGAAATGAAGAAGCAGCGAAGTACTCATGTGGGATTCGCAGAAAC	1620
Qy	1621	CTGACTAATGGTGCCACTGCTGCGCAATGGTGAATGATGATTAAATCTCCAAAGAGAGC	1680
Db	1621	CTGACTAATGGTGCCACTGCTGCGCAATGGTGAATGATGATTAAATCTCCAAAGAGAGC	1680
Qy	1681	AGAAACACCTGAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGTATCACAGTGACAA	1740
Db	1681	AGAAACACCTGAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGTATCACAGTGACAA	1740
Qy	1741	CAAAATATATCTCAGAGCAATTTTCTGAAAGAACGAAACACTGGAAATATTACAGATAG	1800
Db	1741	CAAAATATATCTCAGAGCAATTTTCTGAAAGAACGAAACACTGGAAATATTACAGATAG	1800
Qy	1801	ATTCGTATTAATGAAAGAACAGATAGAAAGTGGTGAAGAAATAAATTCGAGCTTCT	1860
Db	1801	ATTCGTATTAATGAAAGAACAGATAGAAAGTGGTGAAGAAATAAATTCGAGCTTCT	1860
Qy	1861	CTTAGTGTAAAGAAAGAAAGACATCTTGATGAATAATAGTAGCTTGCGGGAGAAATT	1920
Db	1861	CTTAGTGTGTAAAGAAAGAAAGACATCTTGATGAATAATAGTAGCTTGCGGGAGAAATT	1920
Qy	1921	GCCATGCTAGACTCGAGCTAGACAAATGAAGAAATCAGAGCCACTAAAAA	1980
Db	1921	GCCATGCTAGACTCGAGCTAGACAAATGAAGAAATCAGAGCCACTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	
RESULT 5			
US-09-822-827-374			
; Sequence 374, Application US/09822827			
; Patent No. US20020081680A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121.534C1			
; CURRENT APPLICATION NUMBER: US/09/822, 827			

CURRENT FILING DATE: 2001-03-28									
NUMBER OF SEQ ID NOS: 982									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 374									
LENGTH: 2000									
TYPE: DNA									
ORGANISM: Homo sapien									
US-09-822-827-374									
Query Match 100.0%; Score 2000; DB 10; Length 2000;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	ATGGTGGTGGAGGTGATTCATCGCCGGCTGCCTCTTCTGTGAAGAAGCATTTGGCTTC	60						
QY	61	AGGAGCAAGATGGGCAAGTGTGTCGCCGTGGCTTCCCTGCTGCAGGAGACGGCAAG	120						
DB	61	AGGAGCAAGATGGGCAAGTGTGTCGCCGTGGCTTCCCTGCTGCAGGAGACGGCAAG	120						
QY	121	AGCAACGTGGGCACCTTCTGGAGACCAGCAGCACTCTGTATGAACAACCTCAGGAGCAAG	180						
DB	121	AGCAACGTGGGCACCTTCTGGAGACCAGCAGCACTCTGTATGAACAACCTCAGGAGCAAG	180						
QY	181	ATGGCAGATGTGGTCGGCGCACCTTCCCTGCTCAGGGGAGTGGCAAGAGCAAGCTG	240						
DB	181	ATGGCAGATGTGGTCGGCGCACCTTCCCTGCTCAGGGGAGTGGCAAGAGCAAGCTG	240						
QY	241	GGCGCTTCTGGAGACCAAGCAGCAGCTCTGTATGAAGACACTCAGACAAAGTGGGCAAG	300						
DB	241	GGCGCTTCTGGAGACCAAGCAGCAGCTCTGTATGAAGACACTCAGACAAAGTGGGCAAG	300						
QY	301	TGTGCTCTCCCACTGTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360						
DB	301	TGTGCTCTCCCACTGTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360						
QY	361	GGAGACTACGATGACAGTGGCTTCAATGAGAGCCAGCAAGTACAGCTCCGTGGAAGATCTG	420						
DB	361	GGAGACTACGATGACAGTGGCTTCAATGAGAGCCAGCAAGTACAGCTCCGTGGAAGATCTG	420						
QY	421	GACAAAGTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTCATG	480						
DB	421	GACAAAGTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTCATG	480						
QY	481	CTCAGGGACACTGACGTGACAGAAAGGACAAAGCAAAAGAGACTGCTACATCTGGCC	540						
DB	481	CTCAGGGACACTGACGTGACAGAAAGGACAAAGCAAAAGAGACTGCTACATCTGGCC	540						
QY	541	TCTGCAATGGGAATTCAGAAAGTACTAAACCTCTGCTGGACAGACGATGTCAACTTAAT	600						
DB	541	TCTGCAATGGGAATTCAGAAAGTACTAAACCTCTGCTGGACAGACGATGTCAACTTAAT	600						
QY	601	GTCCTTGCACAAACAAACAGACAGCTGTGATTAAGGCGGCTACATGCTCAGGAATGAA	660						
DB	601	GTCCTTGCACAAACAAACAGACAGCTGTGATTAAGGCGGCTACATGCTCAGGAATGAA	660						
QY	661	TGTGGCTTAATGTTCTGTGGAACATGGCACTGTATCCAAATATTCGAGATGAGATGGAAAT	720						
DB	661	TGTGGCTTAATGTTCTGTGGAACATGGCACTGTATCCAAATATTCGAGATGAGATGGAAAT	720						
QY	721	ACCACTGTGCACTACGCTATCTATATATGAAGATAAATTAATGCGCAAAAGCACTGCTTTA	780						
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QY	781	TATGTTGCTGATATGATCAAAAAACAAGCATGGCCTCACACCACCTGTATCTTGGTGTGA	840						
DB	781	TATGTTGCTGATATGATCAAAAAACAAGCATGGCCTCACACCACCTGTATCTTGGTGTGA	840						
QY	841	CATGAGCAAAAAACAGCAAGTGGTGAATTTTAACTCAAGAAAAAGCAATTTAATATGCA	900						
DB	841	CATGAGCAAAAAACAGCAAGTGGTGAATTTTAACTCAAGAAAAAGCAATTTAATATGCA	900						

Qy	901	CTGATGATGATGAGAGACTGCTCCTCACTACTGTGATATGTTGGATCAGCAAGTATA	960
Dp	901	CTTGATGATATGTAAGAGAC TGCTCTCAACTTGCTGATATGTTGGATCAGCAAGTATA	960
Qy	961	GTCAGCCCTTACTTACAGCAAAATATTGAATGATATCTTCTCAAAGATCTATCTGCAGACG	1020
Dp	961	GTCAGCCCTTACTTACAGCAAAATATTGAATGATATCTTCTCAAAGATCTATCTGCAGACG	1020
Qy	1021	GCCAGAGATGATGCTGTTTCTTACTCATCATGTAATTTGCCATTTACTTCTGACTAC	1080
Dp	1021	GCCAGAGATGATGCTGTTTCTTACTCATCATGTAATTTGCCATTTACTTCTGACTAC	1080
Qy	1081	AAAGAAAAAACAAGATGCTAAAAATCTTCTTGAAAACAGCAATCCGAACAAGACTTAAG	1140
Dp	1081	AAAGAAAAAACAAGATGCTAAAAATCTTCTTGAAAACAGCAATCCGAACAAGACTTAAG	1140
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Dp	1141	CTGCATCAGAGAGAAGCTCACAAAGCTTCAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
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Dp	1201	ATGCTTCAGAACCCAGAAATTAATAAGATGGTGTAGAGAGTTGAAGAAATGAG	1260
Qy	1261	AAGCATGAAGTAAATATATGGGGATTACTAGAAAACCCTGACTAATGGTGTCACTGGC	1320
Dp	1261	AAGCATGAAGTAAATATATGGGGATTACTAGAAAACCCTGACTAATGGTGTCACTGGC	1320
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Dp	1321	AATGGTATATATGATTAATATCCCTCAAAGAGAGAGACAACCTCGAAATACAGCAATTT	1380
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Dp	1381	CCTGACACAGAAAGTGAAGATATCACAGAAATTTGCGAATTAGTTTCTGACTACAAAGAA	1440
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Dp	1441	AAACAGATGCCAAATATATCTTCTTGAAAACAGCAACCAGAAACAAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGAAAGATCACAAAGGCTTGAGGGCAGTGAANAATGGCCAGCCAGAGCTGAAANAAT	1560
Dp	1501	TCAGAGAAAGATCACAAAGGCTTGAGGGCAGTGAANAATGGCCAGCCAGAGCTGAAANAAT	1560
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Dp	1561	TTTTATGGCTATCGAAGAAATGAAGAAAGCAAGGAAGTACTCATGTGCGATTTCCCAGAAAAA	1620
Qy	1621	CTGACTAATGCTGCCACTGCTGGCAATGGTATGATGATTAATTTCTTCCAAGAACAGC	1680
Dp	1621	CTGACTAATGCTGCCACTGCTGGCAATGGTATGATGATTAATTTCTTCCAAGAACAGC	1680
Qy	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGGAAGTAAGAAAGATATCACAGTGAAGAA	1740
Dp	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGGAAGTAAGAAAGATATCACAGTGAAGAA	1740
Qy	1741	CAAAATGATACTCAGAAAGCAATTTTCTGGAAGAACAGAACACTGGAATTTATACAGATGAG	1800
Dp	1741	CAAAATGATACTCAGAAAGCAATTTTCTGGAAGAACAGAACACTGGAATTTATACAGATGAG	1800
Qy	1801	ATTCTGATTTATGAGAAAAGCAAGCATAGATGAGATGGTTGAANAATGAATTTCTGAGCTTCT	1860
Dp	1801	ATTCTGATTTATGAGAAAAGCAAGCATAGATGAGATGGTTGAANAATGAATTTCTGAGCTTCT	1860
Qy	1861	CTTATGTTGTAGAAAAGAAAAGCAATCTTGACATGAAAATATAGTACGTTGCGGGAAGAAAT	1920
Dp	1861	CTTATGTTGTAGAAAAGAAAAGCAATCTTGACATGAAAATATAGTACGTTGCGGGAAGAAAT	1920
Qy	1921	GCCATGCTAAGACTGAGCTAGACACAATGAAGAAACATCAGAGCCAGCTAAAAA	1980
Dp	1921	GCCATGCTAAGACTGAGCTAGACACAATGAAGAAACATCAGAGCCAGCTAAAAA	1980
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Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 6
US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match          100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps

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DB      1 ATGGGCGTGAAGTGTGATTCATGCCCGGCTCTTCTGTGAAGAAGCATTTGGTCTC 60

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DB      61 AGGAGCAAGATGGCCAAAGTGCTGCTGCCTTCCCTGCTGCAAGGAGAGGGCCAG 120

QY      121 AGCAACGCGGCGCACTTGTGAGAACCAAGACACTGCTATGAAGCACTCAGAGCAG 180
DB      121 AGCAACGCGGCGCACTTGTGAGAACCAAGACACTGCTATGAAGCACTCAGAGCAG 180

QY      181 ATGGGCAAGTGTCGCCCACTGCTTCCCCTGCTGTCAGGGGAGTAGGCAAGCAACGTG 240
DB      181 ATGGGCAAGTGTCGCCCACTGCTTCCCCTGCTGTCAGGGGAGTAGGCAAGCAACGTG 240

QY      241 GGCGCTTGTGAGACCAAGCAAGCACTGCTATGAGACACTAGAGAACAGATGGCCAG 300
DB      241 GGCGCTTGTGAGACCAAGCAAGCACTGCTATGAGAACACTAGAGAACAGATGGCCAG 300

QY      301 TGGTGTCGGCCACTGCTTCCCCTGCTGTCAGGGGAGCGCAAGCAAGTGCGGCTTGG 360
DB      301 TGGTGTCGGCCACTGCTTCCCCTGCTGTCAGGGGAGCGCGCAAGCAAGTGCGGCTTGG 360

QY      361 GGAGACTACGATGACAGTGCCTTCATGAGACCAGAGTACCAAGTCCGTGAGAGAGATTG 420
DB      361 GGAGACTACGATGACAGTGCCTTCATGAGACCAGAGTACCAAGTCCGTGAGAGAGATTG 420

QY      421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480
DB      421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480

QY      481 CTCAGGGACACTGACGTAACAGAAAGAGCAACAAAAGAGACGTCTCACATCTGGCC 540
DB      481 CTCAGGGACACTGACGTAACAGAAAGAGCAACAAAAGAGACGTCTCACATCTGGCC 540

QY      541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGATGTCAACTTAAAT 600
DB      541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGATGTCAACTTAAAT 600

QY      601 GTCTCTGCAACAAAAGAGAGACAGCTGTGATAAAGCCGCTACATTCGCAAGAGATCAA 660

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Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAACAAGAAAAAGCAATTTAAATGCA 900
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Db 961 GTACGCTTCTACTTGAACAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
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QY 1561 TTTATGCTTATCGAAGAAATGAAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TTTATGCTTATCGAAGAAATGAAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTGACTATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1621 CTGACTATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 AGAAGACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740

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Db 1681 AGAAGACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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QY 1801 ATTCTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 ATTCTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
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QY 1921 GCCATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GCCATGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-825-301-7
; Sequence 7, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE OF INVENTION: AND MONITORING OF BREAST CANCER
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825.301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-825-301-7

Query Match 77.5%; Score 1551; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTAGGTTGATTCATGCGCGCTGCTCTCTGTAAGAGAGAGAGAGAGAGAG 60
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QY 241 GGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
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Db 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGAAATTAATTTCTGACTCAAGAA 1440

QY 1441 AAGACATGCCAAATATCTTCTGAAAAACAGAACCCAGAACAGACTTAAAGTGACA 1500
Db 1441 AAGACATGCCAAATATCTTCTGAAAAACAGAACCCAGAACAGACTTAAAGTGACA 1500
QY 1501 TCAGAGAAAGATGACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAG 1551
Db 1501 TCAGAGAAAGATGACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAG 1551

RESULT 8
US-09-759-143-375
; Sequence 375, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Wang, Aljun
; APPLICANT: L1, Samuel
; APPLICANT: Skelky, Yashir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-375

Query Match 77.5%; Score 151; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGGTTGAGTGTATTCATGCGCGGCTGCTTCTGTGAAGAACATTTGCTTC 60
Db 1 ATGTTGGTTGAGTGTATTCATGCGCGGCTGCTTCTGTGTGAAGAACATTTGCTTC 60
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Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCGTTCCTGCTGCAAGGAGAGCGCAAG 120
QY 121 AGCAACGTGGGCACTCTGGAAGACAGAGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTCTGGAAGACAGAGACTGCTATGAAGACACTCAGAGCAAG 180
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QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACACACGTCCTGTGAGAGATCTG 420
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Db 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGCG 1020
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Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTTACTTTCTGACTAC 1080
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RESULT 9
US-09-780-669-375
: Sequence 375, Application US/09780669
: Patent No. US2002051977A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqi
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hurst, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C24
: CURRENT APPLICATION NUMBER: US/09/780.669
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-780-669-375
Query Match 77.5% Score 1551 DB 10 Length 2040:
Best Local Similarity 100.0% Pred. No. 0 Mismatches 0 Gaps 0
Matches 1551 Conservative 0 Indels 0
QY 1 ATGCTGTTGAGTGTGATTCATCCATCCGCGTGCCTCTCTGTGAAGAGCCATTGTGCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATCCATCCGCGTGCCTCTCTGTGAAGAGCCATTGTGCTC 60
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RESULT 10
US-09-810-936-303
; Sequence 303, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yashir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-303
Query Match 77.5%; Score 151; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGTTGTTGAGTTGATTCATGATCCGCGCTGCTTCTGTGAAAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
| | | | |
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
QY 121 AGCAAGTGGGCACTCTGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
| | | | |
DB 121 AGCAAGTGGGCACTCTGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
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DB 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
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DB 241 GCGCTTCTGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
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DB 301 TGTGTTGTCACATGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACACAGTCCCTGGAGAAATCTG 420
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DB 361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACACAGTCCCTGGAGAAATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
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DB 421 GACAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480


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Db 721 ACCACTCTGCACCTACGCTATCTATATGATGAATTAATTAATGAGCCAAAGCAGCTGCTCTTA 780
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Db 781 TATGGTGTGATATGCAATCAAAAAAACAAGCATGGGCTCACACCACTGTTACTTGGTGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
Oy 901 CTGGATATGATATGGAAGAGCTGCTCATCTTCTGTATGTGTGGATCAGCAAGTATA 960
Db 901 CTGGATATGATATGGAAGAGCTGCTCATCTTCTGTATGTGTGGATCAGCAAGTATA 960
Oy 961 GTACAGCTTCTATGAGCAAAATATGATATGATCTTCAAGATCTATCTGAGCAGAGAG 1020
Db 961 GTACAGCTTCTATGAGCAAAATATGATATGATCTTCAAGATCTATCTGAGCAGAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTGCCAGTTACTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTTAATAATCTCTCTGTAAGAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTTAATAATCTCTCTGTAAGAACAGCAATCCAGAACAGACTTAAAG 1140
Oy 1141 CTGATATCAGAGAGAGTCAAAAGTTCAAGGCAAGTGAATAATGAGCCAGCAGAGAA 1200
Db 1141 CTGATATCAGAGAGAGTCAAAAGTTCAAGGCAAGTGAATAATGAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCAAGAAATAATAAGATGGTGTATAGAGAGTTGAGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATAATAAGATGGTGTATAGAGAGTTGAGAAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGATTAATATGTGGGATTAAGAAACCTGACTAATATGTCTGCTGCTGCGC 1320
Db 1261 AAGCATGAAGATTAATATGTGGGATTAAGAAACCTGACTAATATGTCTGCTGCTGCGC 1320
Oy 1321 AATGATGATATGATTAATCTCTCAAGAGAGAGCAGAACCTGAAATATGAGCAATTT 1380
Db 1321 AATGATGATATGATTAATCTCTCAAGAGAGAGCAGAACCTGAAATATGAGCAATTT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCAGAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Oy 1441 AAACGAGATGCCAAATTAATCTTCTGTAAGAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGAGATGCCAAATTAATCTTCTGTAAGAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 12
US-09-429-755-303
; Sequence 303. Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303

Query Match      77.5%; Score 1551; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTGTGTTGAGGTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGGTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Oy 61 AAGAGCAAGATGAGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGTGGCAAG 120
Db 61 AAGAGCAAGATGAGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGTGGCAAG 120
Oy 121 ACCAAGTGGGCACTTCTGGAACCAAGCAGACGCTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 ACCAAGTGGGCACTTCTGGAACCAAGCAGACGCTGCTATGAAAGCACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGGTCCCGCAGCTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGGTCCCGCAGCTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGT 240
Oy 241 GGGCGTCTGGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGTCTGGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
Oy 301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGAGGCAAGCAAGTGGGCGCTTG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGAGGCAAGCAAGTGGGCGCTTG 360
Oy 361 GGAGACTACGATGACAGTCCCTCATGAGGCCAGGATCACAGCTCCGTGGAGAAGTCTG 420
Db 361 GGAGACTACGATGACAGTCCCTCATGAGGCCAGGATCACAGCTCCGTGGAGAAGTCTG 420
Oy 421 GCAAGCTCCAGAGAGCTGCTGGGGTAAAGTCCAGAAAGATCTCATCTGCAAG 480
Db 421 GCAAGCTCCAGAGAGCTGCTGGGGTAAAGTCCAGAAAGATCTCATCTGCAAG 480
Oy 481 CTCAGGACACTGAGCTGTAACAAGAGCAAGCAAAAGAGCACTGCTACATCTGGCC 540
Db 481 CTCAGGACACTGAGCTGTAACAAGAGCAAGCAAAAGAGCACTGCTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAACTGTAAGAACTCTGCTGAGCAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTGTAAGAACTCTGCTGAGCAGAGATGCAACTTAAT 600
Oy 601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATTAAGGCCGTACATGCCAGAAATGTA 660
Db 601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATTAAGGCCGTACATGCCAGAAATGTA 660
Oy 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTCTGCACCTACGCTATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACCTACGCTATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Oy 781 TATGTGTGATATGCAATCAAAAAAACAAGCATGGGCTCACACCACTGTTACTTGGTGTGA 840
Db 781 TATGTGTGATATGCAATCAAAAAAACAAGCATGGGCTCACACCACTGTTACTTGGTGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
Oy 901 CTGGATATGATATGGAAGAGCTGCTCATCTTCTGTATGTGTGGATCAGCAAGTATA 960
Db 901 CTGGATATGATATGGAAGAGCTGCTCATCTTCTGTATGTGTGGATCAGCAAGTATA 960
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Oy	961	GTACCTTTTACCTTGAGCAAAATTTGATGTAATCTTCGAAGATCTATCTGGACAGACG	1020
Db	961	GTACCTTTTACCTTGAGCAAAATTTGATGTAATCTTCGAAGATCTATCTGGACAGACG	1020
Oy	1021	GCCACAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTACTTTCTGACTAC	1080
Db	1021	GCCACAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTACTTTCTGACTAC	1080
Oy	1081	AAAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Oy	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGCAGTGAATAATAGCCACGACAGAAA	1200
Db	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGCAGTGAATAATAGCCACGACAGAAA	1200
Oy	1201	ATGTCCTCAAGAACCGAATAATAAAGATGATGATAGAGAGTGAAGAAATAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCGAATAATAAAGATGATGATAGAGAGTGAAGAAATAATGAAG	1260
Oy	1261	AAGCATGAAGATTAATATGTGGGATTACTAGAAAACTGACTAATAGTGTTCACTGCTGC	1320
Db	1261	AAGCATGAAGATTAATATGTGGGATTACTAGAAAACTGACTAATAGTGTTCACTGCTGC	1320
Oy	1321	AATGCTGATTAATGATTAATTTCTCTAAGGAAGACGACGACACCTGAAAAATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGATTAATTTCTCTAAGGAAGACGACGACACCTGAAAAATCAGCAATTT	1380
Oy	1381	CCTGCAACGAAAGTGAAGAGATATACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGCAACGAAAGTGAAGAGATATACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
Oy	1441	AAACGATGCCCCAAATACTCTCTGAAAAACAGCAACCCGAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCCCAAATACTCTCTGAAAAACAGCAACCCGAGAACAGACTTAAAGCTGACA	1500
Oy	1501	TCAGAGGAAGAGTCAACAAAGCCTTAGGGCAGTGAATAATGGCCAGCCAGAG	1551
Db	1501	TCAGAGGAAGAGTCAACAAAGCCTTAGGGCAGTGAATAATGGCCAGCCAGAG	1551
RESULT 13			
US-09-825-301-5			
Sequence 5, Application US/09825301			
Patent No. US20020009738A1			
GENERAL INFORMATION:			
APPLICANT: Houghton, Raymond L.			
APPLICANT: Dillon, Davin A.			
APPLICANT: Molesh, David A.			
APPLICANT: Xu, Jiangchun			
APPLICANT: Zehentner, Barbara			
APPLICANT: Persing, David H.			
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION			
FILE REFERENCE: 210121.513			
CURRENT APPLICATION NUMBER: US/09/825,301			
CURRENT FILING DATE: 2001-04-02			
NUMBER OF SEQ ID NOS: 77			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 5			
LENGTH: 1155			
TYPE: DNA			
ORGANISM: Homo sapien			
US-09-825-301-5			

Query Match	56.4%	Score 1128	DB 10	Length 1155
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1128:	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	ATGTGCTTGAGCTTGATTCATGCGCGCTGCTCTTCTGTGAGAGACCATTTGTC	60	
	1	ATGCGCTTGAGCTTGATTCATGCGCGCTGCTCTTCTGTGAGAGACCATTTGTC	60	
Ob	1	ATGTGCTTGAGCTTGATTCATGCGCGCTGCTCTTCTGTGAGAGACCATTTGTC	60	

QY	61	AGGAGCAAGATGGGCAAGTGTGTCGCGCTGCTCCGTCCTCCGTCGACGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGTGTCGCGCTGCTCCGTCCTCCGTCGACGGAGAGCGGCAAG	120
QY	121	AGCAACGTGGGCACTTCTGGAGACACAGACGACTGCTGATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGGAGACACAGACGACTGCTGATGAAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGTGTCGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	240
Db	181	ATGGGCAAGTGTGTCGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	240
QY	241	GGCGCTTCTGGAGACACAGACGACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	300
Db	241	GGCGCTTCTGGAGACACAGACGACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	300
QY	301	TGTGTCTGACACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	360
Db	301	TGTGTCTGACACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	360
QY	361	GGAGACTACGATGACGATGCTTCATGAGACCCAGGACACAGTCCGCTGGACAAATCTG	420
Db	361	GGAGACTACGATGACGATGCTTCATGAGACCCAGGACACAGTCCGCTGGACAAATCTG	420
QY	421	GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTATGCTCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTATGCTCATG	480
QY	481	CTCAGGACACTGACGTCGACAGAAAGAGACAAACAAAGAGACGTCCTACATCTGGCC	540
Db	481	CTCAGGACACTGACGTCGACAGAAAGAGACAAACAAAGAGACGTCCTACATCTGGCC	540
QY	541	TCTGCAATGGGAATTCAGAAAGTATGTTAAACTCTGCTGACAGACGATGTCAACTTAAT	600
Db	541	TCTGCAATGGGAATTCAGAAAGTATGTTAAACTCTGCTGACAGACGATGTCAACTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCGGTACATGCCAGAAATGAA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACAGCTCTGATTAAGGCGGTACAAAGCCAGGAAATGAA	660
QY	661	TGTGCTTAATGTTGTCGGAACATGAGCACTGATCCAAATATTCACATCAGATGGAAT	720
Db	661	TGTGCTTAATGTTGTCGGAACATGAGCACTGATCCAAATATTCACATCAGATGGAAT	720
QY	721	ACCACTGTCACACTGCTATCTATATGAAGATAAATTAAATGGCCAAAGCACTGCTTGA	780
Db	721	ACCACTGTCACACTGCTATCTATATGAAGATAAATTAAATGGCCAAACACTGCTTGA	780
QY	781	TATGCTGCTGATATCGAATCAAAAACAAACATGGGCTCACACACTGTTACTTGCTGA	840
Db	781	TATGCTGCTGATATCGAATCAAAAACAAACATGGGCTCACACACTGTTACTTGCTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCTGTAATTTTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCTGTAATTTTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGAGACTGCTCTATACCTGGCTGATATGTTGGATCACCAAGTATA	960
Db	901	CTGATATGATATGGAAGAGACTGCTCTATACCTGGCTGATATGTTGGATCACCAAGTATA	960
QY	961	GTCAGCCTTCTACTGAGCAAAATATGATGATATCTTCACAGATCTATCTGACAGACG	1020
Db	961	GTCAGCCTTCTACTGAGCAAAATATGATGATATCTTCACAGATCTATCTGACAGACG	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGATATTTGGCAGATTACTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGATATTTGGCAGATTACTTCTGACTAC	1080
QY	1081	AAAGAAAAACGATCTAAAAAATCTCTCGAAGAAACAGCAATCCAGAA	1128
Db	1081	AAAGAAAAACGATCTAAAAAATCTCTCGAAGAAACAGCAATCCAGAA	1128


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RESULT 14
US-09-759-143-373
; Sequence 373: Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-373

Query Match          56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGTTGAGTGTGATTCATGCGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGTGTTGAGTGTGATTCATGCGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60

OY 61 AGGACAGAGATGGGGAAGTGGTCCGCTTCCCTGCTCAGGGGAGTGGCAAGCAACG 120
Db 61 AGGACAGAGATGGGGAAGTGGTCCGCTTCCCTGCTCAGGGGAGTGGCAAGCAACG 120

OY 121 AGCAAGCTGGGCACTTCTGGAGACGACGACGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGGAGACGACGACGACTGCTATGAAGACACTCAGAGCAAG 180

OY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTCAGGGGAGTGGCAAGCAACG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTCAGGGGAGTGGCAAGCAACG 240

OY 241 GGGCGTTCTGGAGACGACGACGACTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300
Db 241 GGGCGTTCTGGAGACGACGACGACTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300

OY 301 TGGTCTGCCACTGCTTCCCTGCTCAGGGGAGCGCAAGAGTGGCGCTTGG 360
Db 301 TGGTCTGCCACTGCTTCCCTGCTCAGGGGAGCGCAAGAGTGGCGCTTGG 360

OY 361 GGAGACTAGATGACAGTGCCTTTCATGAGCCAGGTACCAAGTCCGTGAGAAATCTG 420
Db 361 GGAGACTAGATGACAGTGCCTTTCATGAGCCAGGTACCAAGTCCGTGAGAAATCTG 420

OY 421 GACAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATCGTCAG 480
Db 421 GACAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATCGTCAG 480

OY 481 CTCAGGAGACTGAGTGTAACAAGAGCAAAAGAGAGACTGCTCATCTGAGCC 540
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Db 481 CTCAGGAGACTGAGTGTAACAAGAGCAAAAGAGAGACTGCTCATCTGAGCC 540

OY 541 TCTGCCAATGGGAATTCAGAGTAAGTAAACTCTGCTGGACAGCATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTAAGTAAACTCTGCTGGACAGCATGTCACTTAAT 600

OY 601 GTCCCTTGACAAACAAAAGGACAGCTGATGAAGGGCGTGCATATGCGAGAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGGACAGCTGATGAAGGGCGTGCATATGCGAGAGATGAA 660

OY 661 TGTGGCTTAATGTTCTGGAACATGGCACTGATCCCAATATTCAGATGAGTGAAT 720
Db 661 TGTGGCTTAATGTTCTGGAACATGGCACTGATCCCAATATTCAGATGAGTGAAT 720

OY 721 ACCACTCTGCACTACGCTATCTATATGAGTAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATATGAGTAATTAATGAGCCAAAGCACTGCTTA 780

OY 781 TATGGTGTGATATGATCAAAAAAAGCATGGGCTCACACACTGTACTGTGTA 840
Db 781 TATGGTGTGATATGATCAAAAAAAGCATGGGCTCACACACTGTACTGTGTA 840

OY 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCGAATTTAATGCA 900

OY 901 CTGATATGATATGAGAGCACTGCTCATACTTCTGTATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAGAGCACTGCTCATACTTCTGTATGTTGGATCAGCAAGTATA 960

OY 961 GTACAGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTACAGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020

OY 1021 GCCAGAGATATGATGTTTCTATGATCATCATGTAATTTGCCATTAATCTGACTAC 1080
Db 1021 GCCAGAGATATGATGTTTCTATGATCATCATGTAATTTGCCATTAATCTGACTAC 1080

OY 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 15
US-09-780-669-373
; Sequence 373: Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurl, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
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; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-373

Query Match      56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGTG 240
DB 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGTG 240
QY 241 GGGGCTTCTGGAGACACAGAGACTGCTGTGAAGACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGGAGACACAGAGACTGCTGTGAAGACACTCAGAGCAAGTGGCAAG 300
QY 301 TGGGCTGACACTGCTTCCCTGCTGACAGGGGAGGCAAGGAGTGGGCGCTTGG 360
DB 301 TGGGCTGACACTGCTTCCCTGCTGACAGGGGAGGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAAGACTAGATGACAGTGGCTTCTATGAGAGCCAGTACACAGTCCGCTGAGAAAGATCTG 420
DB 361 GGAAGACTAGATGACAGTGGCTTCTATGAGAGCCAGTACACAGTCCGCTGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGGCTGTGGGTAAGTCCCGAGAAAGATCTCATGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGGCTGTGGGTAAGTCCCGAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGCACTGACGTGAGCAAGAGAGACAGCAAGAGAGTGTGCTACATCTGACC 540
DB 481 CTCAGGCACTGACGTGAGCAAGAGAGACAGCAAGAGAGTGTGCTACATCTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCCTGCTGACAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCCTGCTGACAGACAGATGTCAACTTAAT 600
QY 601 GTCCTTACACAACAAAAAGAGAGACAGCTGTGATAAGGCCGTGACATATCCAGGAAGATGAA 660
DB 601 GTCCTTACACAACAAAAAGAGAGACAGCTGTGATAAGGCCGTGACATATCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGTGGAACATGGCAGTGTCAATAATTCAGATGAGTATGAAAT 720
DB 661 TGTGCGTTAATGTTGTGGAACATGGCAGTGTCAATAATTCAGATGAGTATGAAAT 720
QY 721 ACCACTGTGACACTACCTATCTATTAATGAATTAATTAATGACCAAGCACTGCTTTA 780
DB 721 ACCACTGTGACACTACCTATCTATTAATGAATTAATTAATGACCAAGCACTGCTTTA 780
QY 781 TATGTGCTGATATGATCAATAAAGACAGATGGCTCACACCACTGTTACTTGGTGA 840
DB 781 TATGTGCTGATATGATCAATAAAGACAGATGGCTCACACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAGATTTTAAAGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAGATTTTAAAGCA 900
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QY 901 CTGATAGATATGGAAGAGACTGCTCTCATACTGCTGTATGTTGGATCAGCAAGTATA 960
DB 901 CTGATAGATATGGAAGAGACTGCTCTCATACTGCTGTATGTTGGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTTGGACAAAATATGATGATATCTTCAAGATCTATCTGGACAGC 1020
DB 961 GTCAGCCTTCTACTTGGACAAAATATGATGATATCTTCAAGATCTATCTGGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGATTAATTTGCCAGTACTTTCAGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGATTAATTTGCCAGTACTTTCAGACTAC 1080
QY 1081 AAAGAAAAACAGATGTAAAAATCTCTTGTGAAGAACAGCAATCCAGAA 1128
DB 1081 AAAGAAAAACAGATGTAAAAATCTCTTGTGAAGAACAGCAATCCAGAA 1128

RESULT 16
US-09-810-936-301
; Sequence 301, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-301

Query Match      56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGTG 240
DB 181 ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGTG 240
QY 241 GGGGCTTCTGGAGACACAGAGACTGCTGTGAAGACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGGAGACACAGAGACTGCTGTGAAGACACTCAGAGCAAGTGGCAAG 300
QY 301 TGGGCTGACACTGCTTCCCTGCTGACAGGGGAGGCAAGGAGTGGGCGCTTGG 360
DB 301 TGGGCTGACACTGCTTCCCTGCTGACAGGGGAGGCAAGGAGTGGGCGCTTGG 360
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Qy 361 GGAGACTAGATGAGAGTCCCTTACATGGAGCCAGGTACACGCTCCGTGGAGAGATCTG 420
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Db 361 GGAGACTAGATGAGAGTCCCTTACATGGAGCCAGGTACACGCTCCGTGGAGAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATTCATCTCATG 480
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Db 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATTCATCTCATG 480
Qy 481 CTCAGGAGACTGAGCTGTAACAAGAGCAAGCAAAAGAGAGAGTCTCTACATCTGGCC 540
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Db 481 CTCAGGAGACTGAGCTGTAACAAGAGCAAGCAAAAGAGAGAGTCTCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGAGAGAGATGTCACCTTAAT 600
    |||||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGAGAGAGATGTCACCTTAAT 600
Qy 601 GTCTTTGACACAAAAGAGACAGCTGTGATAAAGCCGTCAATGCCAGAGATGAA 660
    |||||
Db 601 GTCTTTGACACAAAAGAGACAGCTGTGATAAAGCCGTCAATGCCAGAGATGAA 660
Qy 661 TGTGGTTAATGTGTGTAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
    |||||
Db 661 TGTGGTTAATGTGTGTAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATATGCGCAAGCACTGCTTA 780
    |||||
Db 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATATGCGCAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGGAATCAAAAAGCAAGATGGCTCAGACCACTGTTACTGTGTA 840
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Db 781 TATGCTGCTGATATGGAATCAAAAAGCAAGATGGCTCAGACCACTGTTACTGTGTA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTAATGA 900
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Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTAATGA 900
Qy 901 CTGATAGATATGAAGAGCTGCTCATATCTGCTGATGTGTGGATCAGCAATATA 960
    |||||
Db 901 CTGATAGATATGAAGAGCTGCTCATATCTGCTGATGTGTGGATCAGCAATATA 960
Qy 961 GTCAACCTTCTACTGAGCAAAATATGATGATCTTCCAAAGATCTATCTGACAGAG 1020
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Db 961 GTCAACCTTCTACTGAGCAAAATATGATGATCTTCCAAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTTCTCATCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
    |||||
Db 1021 GCCAGAGATATGCTTCTCATCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
Qy 1081 AAGAGAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAA 1128
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Db 1081 AAGAGAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAA 1128

RESULT 17
US-09-827-373
; Sequence 373, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: us/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-827-373
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Query Match 56.4%; Score 1128; DB 10; Length 1155;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGTTGAGTGGATTCATGCCGCTGCTCTTGTGAAGAACCATTTGGTCTC 60
    |||||
Db 1 ATGGTGTTGAGTGGATTCATGCCGCTGCTCTTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGCGCAAGGAGTGTGCGCTTCCCTGCTCCCTGTCAGAGAGAGCGCAAG 120
    |||||
Db 61 AGGAGCAAGATGGCGCAAGGAGTGTGCGCTTCCCTGCTCCCTGTCAGAGAGAGCGCAAG 120
Qy 121 AGCAAGGTGGGCACTTCTGGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
    |||||
Db 121 AGCAAGGTGGGCACTTCTGGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGAGGGAGTGGCAAGCAAGCTG 240
    |||||
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGAGGGAGTGGCAAGCAAGCTG 240
Qy 241 GCGGCTTCTGGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
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Db 241 GCGGCTTCTGGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
Qy 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGGTGGGCGCTTG 360
    |||||
Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGGTGGGCGCTTG 360
Qy 361 GGAGACTACGATGACAGTGCCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
    |||||
Db 361 GGAGACTACGATGACAGTGCCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGATGAAGCAAGCAAGCAAGCAAGTCTCATCTGAGC 480
    |||||
Db 421 GACAAGCTCCACAGAGCTGCTGATGAAGCAAGCAAGCAAGCAAGTCTCATCTGAGC 480
Qy 481 CTCAGGAGACTGAGCTGTAACAAGAGCAAGCAAGCAAGCAAGTCTCATCTGAGC 540
    |||||
Db 481 CTCAGGAGACTGAGCTGTAACAAGAGCAAGCAAGCAAGCAAGTCTCATCTGAGC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGAGAGAGAGATCACTTAAT 600
    |||||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGAGAGAGAGATCACTTAAT 600
Qy 601 GTCTTTGACACAAAAGAGACAGCTGTGATAAAGCCGTCAATGCCAGAGATGAA 660
    |||||
Db 601 GTCTTTGACACAAAAGAGAGAGCTGTGATAAAGCCGTCAATGCCAGAGAGTGA 660
Qy 661 TGTGGTTAATGTGTGTAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
    |||||
Db 661 TGTGGTTAATGTGTGTAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATATGCGCAAGCACTGCTTA 780
    |||||
Db 721 ACCACTCTGCACTACGCTATCTATATGAAGATTAATATGCGCAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGGAATCAAAAAGCAAGATGGCTCAGACCACTGTTACTGTGTA 840
    |||||
Db 781 TATGCTGCTGATATGGAATCAAAAAGCAAGATGGCTCAGACCACTGTTACTGTGTA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTAATGA 900
    |||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAGCGAATTAATGA 900
Qy 901 CTGATAGATATGAAGAGCTGCTCATATCTGCTGATGTGTGGATCAGCAATATA 960
    |||||
Db 901 CTGATAGATATGAAGAGCTGCTCATATCTGCTGATGTGTGGATCAGCAATATA 960
Qy 961 GTCAACCTTCTACTGAGCAAAATATGATGATCTTCCAAAGATCTATCTGACAGAG 1020
    |||||
Db 961 GTCAACCTTCTACTGAGCAAAATATGATGATCTTCCAAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTTCTCATCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
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Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTCTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 18

US-09-429-755-301
; Sequence 301, Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-301

Query Match 56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGTTGATTCATCCCGCTCCCTCTTCTGTGAAGAACCAATTTGCTCTC 60
Db 1 ATGCTGTTGAGTTGATTCATCCCGCTCCCTCTTCTGTGAAGAACCAATTTGCTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTGCTCCCTCTGACAGGGAAGGGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTGCTCCCTCTGACAGGGAAGGGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 240
Db 181 ATGGGCAAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 240
QY 241 GGGCTTCTGGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGACAGTGGGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGACAGTGGGCTTGG 360
QY 361 GGAACACTACGATGACAGTGGCTTCTGAGAGCCAGGTACCGTCCGTGGAGAAATCTG 420
Db 361 GGAACACTACGATGACAGTGGCTTCTGAGAGCCAGGTACCGTCCGTGGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGTGGCTGGTGGGGAATCCGCCAGAAAGAAATCATGTCATG 480
Db 421 GACAAGCTCCACAGAGTGGCTGGTGGGGAATCCGCCAGAAAGAAATCATGTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAGAGAGACAAAGAGAGTGGCTCTACATCTGCGCC 540
Db 481 CTCAGGGACACTGACGTGAACAGAGAGACAAAGAGAGTGGCTCTACATCTGCGCC 540
QY 541 TCTGCCAATGGGAATTAAGAATTAATAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTAAGAATTAATAAATCTCTGCTGACAGAGATGTCAACTTAAT 600

Db 541 TCTGCCAATGGGAATTAAGAATTAATAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
QY 601 GTCTTGCACAAACAAAGAGAGACAGCTCTGATTAAGGCCCTACATGCGCAAGATGAA 660
Db 601 GTCTTGCACAAACAAAGAGAGAGACAGCTCTGATTAAGGCCCTACATGCGCAAGATGAA 660
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGAAAT 720
QY 721 ACCACTGTGCACTACGCTATATTAAGATTAATTAATGAGCCAAAGCACTGCTCTA 780
Db 721 ACCACTGTGCACTACGCTATATTAAGATTAATTAATGAGCCAAAGCACTGCTCTA 780
QY 781 TATGTCGTGATATGCAATCAAAAACAGATGGCCCTACACCACTGTTACTGTGTA 840
Db 781 TATGTCGTGATATGCAATCAAAAACAGATGGCCCTACACCACTGTTACTGTGTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCATACTTCTGATGTTGGATGACGAAGTATA 960
Db 901 CTGATAGATATGGAAGAGACTGCTCATACTTCTGATGTTGGATGACGAAGTATA 960
QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTCTCTCAAGATCTATCGACAGACG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTCTCTCAAGATCTATCGACAGACG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 19

US-09-810-936-323
; Sequence 323, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 323
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-323

Query Match 52.2%; Score 1044; DB 10; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAACCAATTTGCTCTGAGAGCAAGATGGGCAAGTGGCTGCTGCTGCTG 93
Db 34 TCTTCTGTAAGAACCAATTTGCTCTGAGAGCAAGATGGGCAAGTGGCTGCTGCTGCTG 93

Db 469 TCTTCTGTGAAGAACCATTTGGTCTCTAGAGACAAAGATGGGCAAGTGGTGTCTGCCCTTGC 528
OY 94 TTCCCTCTGTGAGAGAGGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAGCAGC 153
Db 529 TTCCCTCTGTGAGAGAGGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAGCAGC 588
OY 154 TCTGTATGAAGACACTCAGAGNCAAGATGGGCAAGTGGGCACTTCTGGAGACCAGCAGC 213
Db 589 TCTGTATGAAGACACTCAGAGNCAAGATGGGCAAGTGGGCACTTCTGGAGACCAGCAGC 648
OY 214 TGCAGGGGAGTGGCAAGACACTGGGCGCTTCTGGAGACCAGCAGCAGCAGCAGTATG 273
Db 649 TGCAGGGGAGTGGCAAGACACTGGGCGCTTCTGGAGACCAGCAGCAGCAGCAGTATG 708
OY 274 AAGACATCAGGAACAAGTGGGCAAGTGGTGTCTGCCCACTGCTTCCCTGCGCAGGGG 333
Db 709 AAGACATCAGGAACAAGTGGGCAAGTGGTGTCTGCCCACTGCTTCCCTGCGCAGGGG 768
OY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGACTAGCAAGTGGCTTCTGAGGCC 393
Db 769 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGACTAGCAAGTGGCTTCTGAGGCC 828
OY 394 AGGTACCAAGTCTGAGAGAGATGGCAAGTCTGCACAGAGTGGCTGAGGGGTAA 453
Db 829 AGGTACCAAGTCTGAGAGAGATGGCAAGTCTGCACAGAGTGGCTGAGGGGTAA 888
OY 454 GTCCCAAGAAAGATCTAGTGTCTGAGGACACTGAGCTAACAAGAAAGCAAG 513
Db 889 GTCCCAAGAAAGATCTAGTGTCTGAGGACACTGAGCTAACAAGAAAGCAAG 948
OY 514 CAAAGAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAAAGTAAAGCTC 573
Db 949 CAAAGAGAGACTGCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAAAGTAAAGCTC 1008
OY 574 CTGTGACAGACGATGTCTACCTAATGTCTTGGACAAACAAAGAGACAGCTCTGAT 633
Db 1009 CTGTGACAGACGATGTCTAATGTCTTGGACAAACAAAGAGACAGCTCTGAT 1068
OY 634 AAGGCGGTACATGGCAGAGAGATGAATGTGGTTAATGTCTGGAACATGGCAGTAT 693
Db 1069 AAGGCGGTACATGGCAGAGAGATGAATGTGGTTAATGTCTGGAACATGGCAGTAT 1128
OY 694 CCAATATTCAGATGAGATGGAATACCACTGCTGACATGCTATCTATATGAAGAT 753
Db 1129 CCAATATTCAGATGAGATGGAATACCACTGCTGACATGCTATCTATATGAAGAT 1188
OY 754 AAATTAATGGCCAAAGACACTGCTTATATGTGTGATATGGAATCAAAAACAAGCAT 813
Db 1189 AAATTAATGGCCAAAGACACTGCTTATATGTGTGATATGGAATCAAAAACAAGCAT 1248
OY 814 GGCCCTCACACCACTGTACTTGGTGTACATGAGCAAAAACAGCAAGTGTGAATTTT 873
Db 1249 GGCCCTCACACCACTGTACTTGGTGTACATGAGCAAAAACAGCAAGTGTGAATTTT 1308
OY 874 ATCAAGAAAAAAGCAATTTAATGACACTGATAGATGAGAGAGCTGCTCTCATACT 933
Db 1309 ATCAAGAAAAAAGCAATTTAATGACACTGATAGATGAGAGAGCTGCTCTCATACT 1368
OY 934 GCTGTATGTGTGATCAGCAAGTATAGTACAGCTTCTTATGAGCAAAAATATGATGA 993
Db 1369 GCTGTATGTGTGATCAGCAAGTATAGTACAGCTTCTTATGAGCAAAAATATGATGA 1428
OY 994 TCTTCTCAAGATCTATCTGAGAGAGAGGCGCAGAGTATGCTTCTGATCATCAT 1053
Db 1429 TCTTCTCAAGATCTATCTGAGAGAGAGGCGCAGAGTATGCTTCTGATCATCAT 1488
OY 1054 GTAAATTTGCACTTCTTCTGACTACAAAGAAAAACAGATCTTAAATCTCTTGAA 1113
Db 1489 GTAAATTTGCACTTCTTCTGACTACAAAGAAAAACAGATCTTAAATCTCTTGAA 1548
OY 1114 AACAGCAATCCAGAA 1128
Db 1549 AACAGCAATCCAGAA 1563

RESULT 20
US-09-810-936-328
; Sequence 328, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-328

Query Match 48.8%; Score 975; DB 10; Length 1155;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ATGTGTGTTGAGTGTGATTCATGCCGGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGTGTGTTGAGTGTGATTCATGCCGGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
OY 61 AGGAGCAAGATGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
OY 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCAAGTGTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCAAGTGTCTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
OY 241 GGCGTCTTCTGGAGACCAAGCAAGTGTCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGCGTCTTCTGGAGACCAAGCAAGTGTCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
OY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGTGGGCAAG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGTGGGCAAG 360
OY 361 GGAGACTACGATGACAGTGTCTTATGAGCCAGGTACCAAGTGGGCAAGTGGGCAAG 420
Db 361 GGAGACTACGATGACAGTGTCTTATGAGCCAGGTACCAAGTGGGCAAGTGGGCAAG 420
OY 421 GACAACTTCCAGAGAGTGGTGGGTTAAAGTCCCAAGAAAGATGCTATGCTGCAAG 480
Db 421 GACAACTTCCAGAGAGTGGTGGGTTAAAGTCCCAAGAAAGATGCTATGCTGCAAG 480
OY 481 CTCAGGAGACACTGAGTGAAGCAAGCAAGCAAGAAAGAGTGTCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGAGTGAAGCAAGCAAGCAAGAAAGAGTGTCTTACATCTGGCC 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGAGAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGAGAGAGATGTCAACTTAAT 600

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QY 601 GTCCTTGACAAACAAAAGAGACAGCTGTGATTAAGCCGTACAAATCCAGAGATGAA 660
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Db 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGCCGTACAAATCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGCATCAATATTTCCAGATGAGTGAAT 720
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGCATCAATATTTCCAGATGAGTGAAT 720
QY 721 ACCACTGTGCACTACGCTATCTATTAATGAATTAATTAATGGCAAGACCTGCTTA 780
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Db 721 ACCACTGTGCACTACGCTATCTATTAATGAATTAATTAATGGCAAGACCTGCTTA 780
QY 781 TATGTCGTGATATCGAATCAAAAACACAGATGGCCTCACACACTGTTACTGTGTA 840
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Db 781 TATGTCGTGATATCGAATCAAAAACACAGATGGCCTCACACACTGTTACTGTGTA 840
QY 841 CATGACGAAAAACAGACAGTGTGTAATTTTAAATCAAGAAAAAGGAATTTAAATGCA 900
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Db 841 CATGACGAAAAACAGACAGTGTGTAATTTTAAATCAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGGAATGATATGGAAGAGACTGTCTATCTGCTGATGTTGGATCAGCAAGTATA 960
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Db 901 CTGGAATGATATGGAAGAGACTGTCTATCTGCTGATGTTGGATCAGCAAGTATA 960
QY 961 GTGACCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGACAGAGC 1020
      |||
Db 961 GTGACCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATGCTGTTTGTAGCATCATCAGTATTTGCCAGTACTTCTGACTAC 1080
      |||
Db 1021 GCCAGAGATGCTGTTTGTAGCATCATCAGTATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATCTCTTGAAGAACAGCAATCCAGAA 1128
      |||
Db 1081 AAGAAAAACAGATGCTAAATCTCTTGAAGAACAGCAATCCAGAA 1128

RESULT 21
US-09-759-143-368
; Sequence 368, Application US/09759143
; Patient No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Wang, Aijun
; APPLICANT: Li, Samuel
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-368
```

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Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2,9e-175;
Matches 691; Conservatve 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAGAACCCATTGCTCAGAGACAAGTTGGGCAAGTGTGCTGCCGTGC 93
      |||
Db 256 TCTTCTGTAAGAACCCATTGCTCAGAGACAAGTTGGGCAAGTGTGCTGCCGTGC 315
QY 94 TTCCCTGCTGCAAGGAGAGACGGCAAGAGCAAGTGGGCACTTCTGAGACCAAGAC 153
      |||
Db 316 TTCCCTGCTGCAAGGAGAGACGGCAAGAGCAAGTGGGCACTTCTGAGACCAAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGACAGATGGCAAGTGTGTCGCCCACTCTCCCTGC 213
      |||
Db 376 TCTGCTATGAAGACACTCAGAGACAGATGGCAAGTGTGTCGCCCACTCTCCCTGC 435
QY 214 TGCAGGGGGAGTGGCAAGCAACGTGGGGCTTCTGGAGACCAAGCAAGCACTGCTG 273
      |||
Db 436 TGCAGGGGGAGTGGCAAGCAACGTGGGGCTTCTGGAGACCAAGCAAGCACTGCTG 495
QY 274 AAGCACTCAGAAACAAGATGGCAAGTGGTGTGCTGCACTGCTCCCTGCTGAGGGGG 333
      |||
Db 496 AAGCACTCAGAAACAAGATGGCAAGTGGTGTGCTGCACTGCTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGACCAAGTGGGGCTTGGGGAGACTAGCATACAGTGCCTTCATGAGACCC 393
      |||
Db 556 AGCGGCAAGACCAAGTGGGGCTTGGGGAGACTAGCATACAGTGCCTTCATGAGACCC 615
QY 394 AGGTACCAAGTCCGTGGAGAAGATCTGACAAAGTCCACAGAGTGCCTGCTGGGGTAA 453
      |||
Db 616 AGGTACCAAGTCCGTGGAGAAGATCTGACAAAGTCCACAGAGTGCCTGCTGGGGTAA 675
QY 454 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGACACTGACGTGAACAAGAGACAG 513
      |||
Db 676 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGACACTGACGTGAACAAGAGACAG 735
QY 514 CAAAAGAGACGTGCTACATCTGCGCTTCCCAATGGGAATTCAGAAATGTAATCTC 573
      |||
Db 736 CAAAAGAGACGTGCTACATCTGCGCTTCCCAATGGGAATTCAGAAATGTAATCTC 795
QY 574 CTGCTGACAGACAGATGCTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGATA 633
      |||
Db 796 CTGCTGACAGACAGATGCTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGATA 855
QY 634 AAGCCCTGACATGCCAGAAATGATGCGTTAATGTTGCTGGAACATGCACTGAT 693
      |||
Db 856 AAGCCCTGACATGCCAGAAATGATGCGTTAATGTTGCTGGAACATGCACTGAT 915
QY 694 CCAAAATTTCCAGATGAGTGAATTAATCACTCT 728
      |||
Db 916 CCAAAATTTCCAGATGAGTGAATTAATCACTCT 950

RESULT 22
US-09-780-669-368
; Sequence 368, Application US/09780669
; Patient No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
```

APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 368
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-368

Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2.9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

34 TCTTGTGAGAACCATTTGGTCTCAGAGCAAGATGGCAAGTGGTGGCCGTTGC 93
DB TCTTGTGAGAACCATTTGGTCTCAGAGCAAGATGGCAAGTGGTGGCCGTTGC 315
94 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGCACTTCTGGAGACCAAGCAGC 153
DB TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGCACTTCTGGAGACCAAGCAGC 375
154 TCTGCTATGAAACACTCAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCA 213
DB TCTGCTATGAAACACTCAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCA 435
214 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 273
DB TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
436 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
274 AAGACTCAGAACAGATGGGCAAGTGGGCAAGTGGGCACTTCTGGAGACCAAG 333
DB AAGACTCAGAACAGATGGGCAAGTGGGCAAGTGGGCACTTCTGGAGACCAAG 555
436 AAGACTCAGAACAGATGGGCAAGTGGGCAAGTGGGCACTTCTGGAGACCAAG 555
334 AGCGCAAGAGCAAGTGGGCTTGGGAGACTAGATGACAGTGGCTTCTGAGACCC 393
DB AGCGCAAGAGCAAGTGGGCTTGGGAGACTAGATGACAGTGGCTTCTGAGACCC 615
556 AGCGCAAGAGCAAGTGGGCTTGGGAGACTAGATGACAGTGGCTTCTGAGACCC 615
394 AGCTACCACTCCGTCGAGAGATGTGACAAAGTCCACAGAGTCCCTGTTGAGG 453
DB AGCTACCACTCCGTCGAGAGATGTGACAAAGTCCACAGAGTCCCTGTTGAGG 675
616 AGCTACCACTCCGTCGAGAGATGTGACAAAGTCCACAGAGTCCCTGTTGAGG 675
454 GTCCCAAGAAAGATCTCATGTCATGCTCAGGACACTGACGTGAACAAAGAGCAAG 513
DB GTCCCAAGAAAGATCTCATGTCATGCTCAGGACACTGACGTGAACAAAGAGCAAG 735
676 GTCCCAAGAAAGATCTCATGTCATGCTCAGGACACTGACGTGAACAAAGAGCAAG 735
514 CAAAAGAGAGTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAAATTAATAACTC 573
DB CAAAAGAGAGTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAAATTAATAACTC 795
726 CAAAAGAGAGTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAAATTAATAACTC 795
574 CTGCTGAGACAGATGTCACTTAATGTCTTGACAAACAAAGAGAGCAGCTTGATA 633
DB CTGCTGAGACAGATGTCACTTAATGTCTTGACAAACAAAGAGAGCAGCTTGATA 855
796 CTGCTGAGACAGATGTCACTTAATGTCTTGACAAACAAAGAGAGCAGCTTGATA 855
634 AAGCCGTACCAATGCGCAGAGATGAATGTGGTAAATGCTGGAACATGGCACTGAT 693
DB AAGCCGTACCAATGCGCAGAGATGAATGTGGTAAATGCTGGAACATGGCACTGAT 915
856 AAGCCGTACCAATGCGCAGAGATGAATGTGGTAAATGCTGGAACATGGCACTGAT 915
694 CCAATATTCAGATGATGGAATACCACTCT 728
DB CCAATATTCAGATGATGGAATACCACTCT 950

US-09-780-669-368

Sequence 294, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 294
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-294

Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2.9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

34 TCTTGTGAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGTTGC 93
DB TCTTGTGAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGTTGC 315
256 TCTTGTGAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGTTGC 315
94 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGCACTTCTGGAGACCAAGCAGC 153
DB TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGGCACTTCTGGAGACCAAGCAGC 375
154 TCTGCTATGAAACACTCAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCA 213
DB TCTGCTATGAAACACTCAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCA 435
316 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
214 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
436 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
214 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
436 TGCAGGGGAGTGGCAAGACAGTGGGCTTCTGAGACCAAGCACTTCTGATG 495
274 AAGACTCAGAACAGATGGGCAAGTGGGCAAGTGGGCACTTCTGGAGACCAAG 333
DB AAGACTCAGAACAGATGGGCAAGTGGGCAAGTGGGCACTTCTGGAGACCAAG 555
496 AAGACTCAGAACAGATGGGCAAGTGGGCAAGTGGGCACTTCTGGAGACCAAG 555
334 AGCGCAAGAGCAAGTGGGCTTGGGAGACTAGATGACAGTGGCTTCTGAGACCC 393
DB AGCGCAAGAGCAAGTGGGCTTGGGAGACTAGATGACAGTGGCTTCTGAGACCC 615
556 AGCGCAAGAGCAAGTGGGCTTGGGAGACTAGATGACAGTGGCTTCTGAGACCC 615
394 AGCTACCACTCCGTCGAGAGATGTGACAAAGTCCACAGAGTCCCTGTTGAGG 453
DB AGCTACCACTCCGTCGAGAGATGTGACAAAGTCCACAGAGTCCCTGTTGAGG 675
616 AGCTACCACTCCGTCGAGAGATGTGACAAAGTCCACAGAGTCCCTGTTGAGG 675
454 GTCCCAAGAAAGATCTCATGTCATGCTCAGGACACTGACGTGAACAAAGAGCAAG 513
DB GTCCCAAGAAAGATCTCATGTCATGCTCAGGACACTGACGTGAACAAAGAGCAAG 735
676 GTCCCAAGAAAGATCTCATGTCATGCTCAGGACACTGACGTGAACAAAGAGCAAG 735
514 CAAAAGAGAGTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAAATTAATAACTC 573
DB CAAAAGAGAGTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAAATTAATAACTC 795
736 CAAAAGAGAGTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAAATTAATAACTC 795
574 CTGCTGAGACAGATGTCACTTAATGTCTTGACAAACAAAGAGAGCAGCTTGATA 633
DB CTGCTGAGACAGATGTCACTTAATGTCTTGACAAACAAAGAGAGCAGCTTGATA 855
796 CTGCTGAGACAGATGTCACTTAATGTCTTGACAAACAAAGAGAGCAGCTTGATA 855
634 AAGCCGTACCAATGCGCAGAGATGAATGTGGTAAATGCTGGAACATGGCACTGAT 693
DB AAGCCGTACCAATGCGCAGAGATGAATGTGGTAAATGCTGGAACATGGCACTGAT 915
856 AAGCCGTACCAATGCGCAGAGATGAATGTGGTAAATGCTGGAACATGGCACTGAT 915

QY 694 CCAATATTCAGATGATGAAATACCACTCT 728
|
Db 916 CCAATATTCAGATGATGAAATACCACTCT 950

RESULT 24
US-09-822-827-368
; Sequence 368, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-368

Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2.9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGCAAGTGTGCTGCCGTTGC 93
|
Db 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 153
|
Db 316 TTCCCTGTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375
QY 154 TCTGCTATGAAGACACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 213
|
Db 376 TCTGCTATGAAGACACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 435
QY 214 TGCAGGGGGAGTGGCAAGACAGCAAGCTTCTGAGACACAGCAAGCTTCTGATG 273
|
Db 436 TGCAGGGGGAGTGGCAAGACAGCAAGCTTCTGAGACACAGCAAGCTTCTGATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGCACAGCTTCCCTGCTGAGGGGG 333
|
Db 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGCACAGCTTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGAGCAAGATGGGCGCTTTGGGGAAGTACAGATGACAGTGCCTTCATGAGGCC 393
|
Db 556 AGCGGCAAGAGCAAGATGGGCGCTTTGGGGAAGTACAGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGGACACAGCTCGTGGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGGGTAA 453
|
Db 616 AGGACACAGCTCGTGGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGGGTAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGATCTCAGGAGCACTGACGTGAACAGAAAGAGCAAG 513
|
Db 676 GTCCCGAAGAAAGATCTCATGCTGATCTCAGGAGCACTGACGTGAACAGAAAGAGCAAG 735
QY 514 CAAAAGAGAGTCTCATGCTGATCTGAGGAGCACTGACGTGAACAGAAAGAGCAAG 573
|
Db 736 CAAAAGAGAGTCTCATGCTGATCTGAGGAGCACTGACGTGAACAGAAAGAGCAAG 795
QY 574 CTGCTGACAGAGCATGTCACTTAATGCTCTTGACAAAGAAAGAGAGAGAGCTGATA 633
|
Db 796 CTGCTGACAGAGCATGTCACTTAATGCTCTTGACAAAGAAAGAGAGAGAGCTGATA 855
QY 634 AAGGCGCTTAAGATCCAGAGAGATGATGCTTAATGTTGCTGGAACATGGAGCTGAT 693
|
Db 856 AAGGCGCTTAAGATCCAGAGAGATGATGCTTAATGTTGCTGGAACATGGAGCTGAT 915

QY 694 CCAATATTCAGATGATGAAATACCACTCT 728
|
Db 916 CCAATATTCAGATGATGAAATACCACTCT 950

RESULT 25
US-09-429-755-294
; Sequence 294, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429.755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 294
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-294

Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2.9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 93
|
Db 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 153
|
Db 316 TTCCCTGTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375
QY 154 TCTGCTATGAAGACACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 213
|
Db 376 TCTGCTATGAAGACACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 435
QY 214 TGCAGGGGGAGTGGCAAGACAGCAAGCTTCTGAGACACAGCAAGCTTCTGATG 273
|
Db 436 TGCAGGGGGAGTGGCAAGACAGCAAGCTTCTGAGACACAGCAAGCTTCTGATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGCACAGCTTCCCTGCTGAGGGGG 333
|
Db 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGCACAGCTTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGAGCAAGATGGGCGCTTTGGGGAAGTACAGATGACAGTGCCTTCATGAGGCC 393
|
Db 556 AGCGGCAAGAGCAAGATGGGCGCTTTGGGGAAGTACAGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGGACACAGCTCGTGGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGGGTAA 453
|
Db 616 AGGACACAGCTCGTGGAGAAAGATCTGGACAAAGCTCCACAGAGCTGCTGGGGTAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGATCTCAGGAGCACTGACGTGAACAGAAAGAGCAAG 513
|
Db 676 GTCCCGAAGAAAGATCTCATGCTGATCTCAGGAGCACTGACGTGAACAGAAAGAGCAAG 735
QY 514 CAAAAGAGAGTCTCATGCTGATCTGAGGAGCACTGACGTGAACAGAAAGAGAGAGCTGATA 573
|
Db 736 CAAAAGAGAGTCTCATGCTGATCTGAGGAGCACTGACGTGAACAGAAAGAGAGAGCTGATA 795
QY 574 CTGCTGACAGAGCATGTCACTTAATGCTCTTGACAAAGAAAGAGAGAGAGCTGATA 633
|
Db 796 CTGCTGACAGAGCATGTCACTTAATGCTCTTGACAAAGAAAGAGAGAGAGCTGATA 855

APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Smith, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-295

Query Match 12.6%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.8e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGAGGAGGCGGCAAGACAGTGGGCACTTCTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGCAAGAGGAGGCGGCAAGACAGTGGGCACTTCTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACATGAGCAAGATGGGCAAGTGGGCGGCACTTCTGAGAGC 213
DB 376 TCTGCTATGAAGACACACATGAGCAAGATGGGCAAGTGGGCGGCACTTCTGAGAGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGAGAGTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGAGAGTGTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 29
US-09-822-827-369
Sequence 369, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TREATMENT OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 369
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-822-827-369

Query Match 12.6%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.8e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGAGGAGGCGGCAAGACAGTGGGCACTTCTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGCAAGAGGAGGCGGCAAGACAGTGGGCACTTCTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACATGAGCAAGATGGGCAAGTGGGCGGCACTTCTGAGAGC 213
DB 376 TCTGCTATGAAGACACACATGAGCAAGATGGGCAAGTGGGCGGCACTTCTGAGAGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGAGAGTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGAGAGTGTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 30
US-09-429-755-295
Sequence 295, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-295

Query Match 12.6%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.8e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGAGGAGGCGGCAAGACAGTGGGCACTTCTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGCAAGAGGAGGCGGCAAGACAGTGGGCACTTCTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACATGAGCAAGATGGGCAAGTGGGCGGCACTTCTGAGAGC 213
DB 376 TCTGCTATGAAGACACACATGAGCAAGATGGGCAAGTGGGCGGCACTTCTGAGAGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGAGAGTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGAGAGTGTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555

```
OY 334 AGC 336
    |||
Db 556 AGC 558

RESULT 31
US-09-759-143-531
; Sequence 531, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-531

Query Match 6.0%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
    |||||||
Db 333 GGACAAGCAAAAGAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 392

OY 567 AAAACTCGTGTGACAGACGATGCACTTAATGCTTGACACAAAAAGAGACAGC 626
    |||||||
Db 393 AAAACTCGTGTGACAGACGATGCACTTAATGCTTGACACAAAAAGAGACAGC 452

OY 627 TCTGATTAAGGCCGTCACATGTCAGAGAGATGATGTGGTGAATGTTGCTGGAACATGG 686
    |||||
Db 453 TCTGATTAAGGCCGTCACATGTCAGAGAGATGATGTGGTGAATGTTGCTGGAACATGG 512

OY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
    |||||||
Db 513 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 554

RESULT 32
US-09-780-669-531
; Sequence 531, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
```

```
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-531

Query Match 6.0%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
    |||||||
Db 333 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 392

OY 567 AAAACTCGTGTGACAGACGATGCACTTAATGCTTGACACAAAAAGAGACAGC 626
    |||||||
Db 393 AAAACTCGTGTGACAGACGATGCACTTAATGCTTGACACAAAAAGAGACAGC 452

OY 627 TCTGATTAAGGCCGTCACATGTCAGAGAGATGATGTGGTGAATGTTGCTGGAACATGG 686
    |||||
Db 453 TCTGATTAAGGCCGTCACATGTCAGAGAGATGATGTGGTGAATGTTGCTGGAACATGG 512

OY 687 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 728
    |||||||
Db 513 CACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 554

RESULT 33
US-09-810-936-314
; Sequence 314, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 314
; LENGTH: 879
; TYPE: DNA
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Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 566
|||||
Db 276 GGACAGCAAAAGAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 335

QY 567 AAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGGACACAAAAGAGAGACAGC 626
|||||
Db 336 AAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGGACACAAAAGAGAGACAGC 395

QY 627 TCTGATTAAGGCCGCTACATGCGCAGAGATGATGCGTTAAATGTTGCTGGAACATGG 686
|||||
Db 396 TCTGATTAAGGCCGCTACATGCGCAGAGATGATGCGTTAAATGTTGCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCAGATGAGATGGAATACCACTCT 728
|||||
Db 456 CACTGATCCAAATATTCAGATGAGATGGAATACCACTCT 497

RESULT 37

US-09-780-669-372
; Sequence 372; Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriok
; APPLICANT: Wang, Aljun
; APPLICANT: Li, Samuel
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-372

Query Match 6.0%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 566
|||||
Db 276 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 335

QY 567 AAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGGACACAAAAGAGAGACAGC 626
|||||
Db 336 AAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGGACACAAAAGAGAGACAGC 395

QY 627 TCTGATTAAGGCCGCTACATGCGCAGAGATGATGCGTTAAATGTTGCTGGAACATGG 686
|||||
Db 396 TCTGATTAAGGCCGCTACATGCGCAGAGATGATGCGTTAAATGTTGCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCAGATGAGATGGAATACCACTCT 728
|||||
Db 456 CACTGATCCAAATATTCAGATGAGATGGAATACCACTCT 497

RESULT 38

US-09-810-936-298
; Sequence 298; Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 298
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-298

Query Match 6.0%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 566
|||||
Db 276 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 335

QY 567 AAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGGACACAAAAGAGAGACAGC 626
|||||
Db 336 AAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGGACACAAAAGAGAGACAGC 395

QY 627 TCTGATTAAGGCCGCTACATGCGCAGAGATGATGCGTTAAATGTTGCTGGAACATGG 686
|||||
Db 396 TCTGATTAAGGCCGCTACATGCGCAGAGATGATGCGTTAAATGTTGCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCAGATGAGATGGAATACCACTCT 728
|||||
Db 456 CACTGATCCAAATATTCAGATGAGATGGAATACCACTCT 497

RESULT 39

US-09-822-827-372
; Sequence 372; Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.53A1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-372

Query Match 6.0%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
DB 276 GGACAAAGCAAAAGAGGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 335
QY 567 AAAACTCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 395
QY 627 TCTGATTAAGGCGGTACATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGG 686
DB 396 TCTGATTAAGGCGGTACATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCACATGATGTGAATATCCACTCT 728
DB 456 CACTGATCCAAATATTCACATGATGTGAATATCCACTCT 497

RESULT 40

US-09-429-755-298
; Sequence 298, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 298
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-298

Query Match 6.0%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
DB 276 GGACAAAGCAAAAGAGGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 335
QY 567 AAAACTCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 395
QY 627 TCTGATTAAGGCGGTACATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGG 686
DB 396 TCTGATTAAGGCGGTACATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCACATGATGTGAATATCCACTCT 728
DB 456 CACTGATCCAAATATTCACATGATGTGAATATCCACTCT 497

RESULT 41
US-09-825-301-1/C
; Sequence 1, Application US/09825301
; Patent No. US20020009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, Davin C.

; APPLICANT: Molesch, David A.
; APPLICANT: Xu, Jianshun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-1

Query Match 6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
DB 791 GGACAAAGCAAAAGAGGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 732
QY 567 AAAACTCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 626
DB 731 AAAACTCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 672
QY 627 TCTGATTAAGGCGGTACATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGG 686
DB 671 TCTGATTAAGGCGGTACATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGG 612
QY 687 CACTGATCCAAATATTCACATGATGTGAATATCCACTCT 728
DB 611 CACTGATCCAAATATTCACATGATGTGAATATCCACTCT 570

RESULT 42

US-09-759-143-366/C
; Sequence 366, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hendersen, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-366

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Query Match          6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 566
      |||||||
Db 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 732

Oy 567 AAAACTCTGCTGGACAGACAGATGCACACTTAATGCTTGACACAAAAGAGACAGC 626
      |||||||
Db 731 AAAACTCTGCTGGACAGACAGATGCACACTTAATGCTTGACACAAAAGAGAGACAGC 672

Oy 627 TCTGATAAAGCCCGTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 686
      |||||
Db 671 TCTGACAAAGGCCCTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 612

Oy 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
      |||||||
Db 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 43
US-09-780-669-366/c
; Sequence 366, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-366

Query Match          6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 566
      |||||||
Db 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 732

Oy 567 AAAACTCTGCTGGACAGACAGATGCACACTTAATGCTTGACACAAAAGAGACAGC 626
      |||||||
Db 731 AAAACTCTGCTGGACAGACAGATGCACACTTAATGCTTGACACAAAAGAGACAGC 672

Oy 627 TCTGATAAAGCCCGTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 686
      |||||||
Db 671 TCTGATAAAGCCCGTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 612
```

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Db 671 TCTGCAAAAGCCGTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 612
Oy 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
      |||||||
Db 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 44
US-09-810-936-291/c
; Sequence 291, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 291
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-291

Query Match          6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 566
      |||||||
Db 791 GGACAGCAAAAGAGAGACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 732

Oy 567 AAAACTCTGCTGGACAGACAGATGCACACTTAATGCTTGACACAAAAGAGACAGC 626
      |||||||
Db 731 AAAACTCTGCTGGACAGACAGATGCACACTTAATGCTTGACACAAAAGAGACAGC 672

Oy 627 TCTGATAAAGCCCGTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 686
      |||||
Db 671 TCTGACAAAGGCCCTACATCCAGAGAGATGATGCTGTTAATGTTGCTGGAACATG 612

Oy 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
      |||||||
Db 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 45
US-09-810-936-292/c
; Sequence 292, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-292
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; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-292

Query Match      6.08; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGACTGCTTACATCTGGCCCTTGGCCAATGGGAATTCAGAACTAGT 566
Db 791 GGACAAAGCAAAAGAGACTGCTTACATCTGGCCCTTGGCCAATGGGAATTCAGAACTAGT 732
QY 567 AAAACTCTGCTGTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
Db 731 AAAACTCTGCTGTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGCCGTACAAATGCCAGAGATGAATGTGCGTTAATGTTGCTGGAACATGG 686
Db 671 TCTGACAAAGCCGTACAAATGCCAGAGATGAATGTGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTGATCCAATATTCAGATGAGTATGGAAATACCACTCT 728
Db 611 CACTGATCCAATATTCAGATGAGTATGGAAATACCACTCT 570
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OM nucleic - nucleic search, using sw model

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12754.351 Million cell updates/sec

Title: US-09-924-400-302
Perfect score: 2000
Sequence: 1 atgttggttgagtgatc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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41: /cgn2_6/ptodata/1/pna/US0950_COMB.seq:*
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Result				SUMMARIES	
No.	Score	% Match	Query Length	ID	Description
1	2000	100.0	2000	1 PCT-US02-24917-302	Sequence 302, App
2	2000	100.0	2000	1 US-09-288-946-374	Sequence 374, App
3	2000	100.0	2000	1 US-09-289-198-302	Sequence 302, App
4	2000	100.0	2000	1 US-09-429-755-302	Sequence 302, App
5	2000	100.0	2000	18 US-09-443-686-374	Sequence 374, App
6	2000	100.0	2000	18 US-09-463-672A-374	Sequence 374, App
7	2000	100.0	2000	20 US-09-534-825A-302	Sequence 302, App
8	2000	100.0	2000	20 US-09-536-857-374	Sequence 374, App
9	2000	100.0	2000	22 US-09-568-100A-374	Sequence 374, App
10	2000	100.0	2000	22 US-09-577-505B-302	Sequence 302, App
11	2000	100.0	2000	22 US-09-580-583-302	Sequence 302, App
12	2000	100.0	2000	22 US-09-593-793A-374	Sequence 374, App
13	2000	100.0	2000	23 US-09-605-783A-374	Sequence 374, App
14	2000	100.0	2000	24 US-09-651-215-374	Sequence 374, App
15	2000	100.0	2000	25 US-09-651-236-374	Sequence 374, App
16	2000	100.0	2000	25 US-09-657-279-374	Sequence 374, App
17	2000	100.0	2000	26 US-09-679-272-374	Sequence 374, App
18	2000	100.0	2000	26 US-09-679-426-374	Sequence 374, App
19	2000	100.0	2000	27 US-09-685-166-374	Sequence 374, App
20	2000	100.0	2000	27 US-09-685-166A-374	Sequence 374, App
21	2000	100.0	2000	27 US-09-699-295-302	Sequence 302, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22 2000 100.0 2000 28 US-09-709-729-374 Sequence 374, App
23 2000 100.0 2000 29 US-09-759-143-374 Sequence 374, App
24 2000 100.0 2000 30 US-09-780-669-374 Sequence 374, App
25 2000 100.0 2000 31 US-09-810-936-302 Sequence 302, App
26 2000 100.0 2000 31 US-09-822-827-374 Sequence 374, App
27 2000 100.0 2000 32 US-09-825-301-6 Sequence 6, Appli
28 2000 100.0 2000 32 US-09-852-911-374 Sequence 374, App
29 2000 100.0 2000 33 US-09-895-793-374 Sequence 374, App
30 2000 100.0 2000 33 US-09-895-814-374 Sequence 374, App
31 2000 100.0 2000 34 US-09-924-400-302 Sequence 302, App
32 2000 100.0 2000 38 US-10-006-920-374 Sequence 374, App
33 2000 100.0 2000 38 US-10-010-940-374 Sequence 374, App
34 2000 100.0 2000 38 US-10-012-896-374 Sequence 374, App
35 2000 100.0 2000 39 US-10-079-137B-302 Sequence 302, App
36 2000 100.0 2000 40 US-10-144-678A-374 Sequence 374, App
37 2000 100.0 2000 42 US-10-212-679-302 Sequence 302, App
38 1551 77.5 2040 16 PCT-US02-24917-303 Sequence 303, App
39 1551 77.5 2040 16 US-09-288-946-375 Sequence 375, App
40 1551 77.5 2040 16 US-09-289-198-303 Sequence 303, App
41 1551 77.5 2040 18 US-09-429-755-303 Sequence 303, App
42 1551 77.5 2040 18 US-09-443-686-375 Sequence 375, App
43 1551 77.5 2040 18 US-09-483-672A-375 Sequence 375, App
44 1551 77.5 2040 20 US-09-534-825A-303 Sequence 303, App
45 1551 77.5 2040 20 US-09-536-857-375 Sequence 375, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-302
; Sequence 302, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-302
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Query Match 100.0%; Score 2000; DB 1; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6, 6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGTGGTGGAGTGGATTCATCCGCGGCTCTCTGTGAAGAGCCATTGGCTC 60
Db 1 ATGGTGGTGGAGTGGATTCATCCGCGGCTCTCTGTGAAGAGCCATTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGCTGGGCACTTCTGGAGACACGACGACTCTCTATGAAGACACTCAGAGAG 180
Db 121 AGCAAGCTGGGCACTTCTGGAGACACGACGACTCTCTATGAAGACACTCAGAGAG 180
QY 181 ATGGGCAAGTGGTGGCGCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGAGCAAGCTG 240
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QY 241 GGGCGCTTCTGGAGACGACGAGCTCTGTATGAAGACTCAGAGAAAGATGGCAAG 300
Db 241 GGGCGCTTCTGGAGACGACGAGCTCTGTATGAAGACTCAGAGAAAGATGGCAAG 300
QY 301 TGGTGGTGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 301 TGGTGGTGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 361 GGAGACTACGATGACATGCTGCTTATGAGAGCCAGTACAGCTCTGAGAGAGATCTG 420
Db 361 GGAGACTACGATGACATGCTGCTTATGAGAGCCAGTACAGCTCTGAGAGAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGAGAAAGATCTCATCTGATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGACACATGACGTGAACAGAGACAGCAAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGACACATGACGTGAACAGAGACAGCAAGAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGTCGACAGCATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGTCGACAGCATGTCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGACGCTCTGTATTAAGGCCCTACAAATGCCAGAAAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGAGCTCTGTATTAAGGCCCTGTACAAATGCCAGAAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTATCCAAATTTCCAGTATGATGCAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTATCCAAATTTCCAGTATGATGCAAT 720
QY 721 ACCACCTGACACTGCTATCTATTAATGAAGATTAATTAAGGCAAGAGAGCTCTTA 780
Db 721 ACCACCTGACACTGCTATCTATTAATGAAGATTAATTAAGGCAAGAGAGCTCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAACAGATGCGCTCACACACCTGTTACTTGGTGA 840
Db 781 TATGTCCTGATATGCAATCAAAAACAGATGCGCTCACACACCTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATATCAAGAAAAAGGATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATATCAAGAAAAAGGATTTAAATGCA 900
QY 901 CTGATATGATATGAGAGAGCTGCTCATCTGCTATGTTGTGTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAGAGAGCTGCTCATCTGCTATGTTGTGTGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTTGAAGCAAAATATTTATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTCAGCCTTCTACTTGAAGCAAAATATTTATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTATGATCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTATGATCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACGAATCAGAAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACGAATCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGTTCAAAAGCAGTGAATAATAGCCAGCAAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAAGTTCAAAAGCAGTGAATAATAGCCAGCAAGAGAAA 1200
QY 1201 ATGTCTCAAGACACAGAAATTAATTAAGATGATGATGAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGACACAGAAATTAATTAAGATGATGATGAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTATATATATGAGGATTAATCTAGAAAACCTGACTAATGGTGTCACTGGCTGGC 1320
Db 1261 AAGCATGAAGTATATATATGAGGATTAATCTAGAAAACCTGACTAATGGTGTCACTGGCTGGC 1320
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QY	1321	AAAGGATTAATGATTTAATTCCTCAAAAGAGACAGACAACCAGAAATACCAATTT	1380
Db	1321	AAATGGTATATAGATTAAATTCCTCAAAAGGAAGACAGAACCTCGAAATACCAATTT	1380
QY	1381	CTTGACACGAAAGTAGAAGATATCAGAAATTTGCGAATTAGTTCTGACTACAAAGAA	1440
Db	1381	CTTGACACGAAAGTAGAAGATATCAGAAATTTGCGAATTAGTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCAGAACAAAGACTTAAAGTACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCAGAACAAAGACTTAAAGTACA	1500
QY	1501	TCAGAGAAAGTACACAAAGGCTTTGAGGCGACTGAAAAATGGCCAGCCAGACTAGAAAT	1560
Db	1501	TCAGAGAAAGTACACAAAGGCTTTGAGGCGACTGAAAAATGGCCAGCCAGACTAGAAAT	1560
QY	1561	TTTATGTGCTATCGAAGAAATGAAAGACGCGAAGTACTCATGTGGAATCCCGAAGAAC	1620
Db	1561	TTTATGTGCTATCGAAGAAATGAAAGACGCGAAGTACTCATGTGGAATCCCGAAGAAC	1620
QY	1621	CTGACTAATGCGTCCACTCGTGGCAATGGTGATGATGATTAATTCCTCCAAAGGAAGAC	1680
Db	1621	CTGACTAATGCGTCCACTCGTGGCAATGGTGATGATGATTAATTCCTCCAAAGGAAGAC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGGAATGAAAGATATCACAGTGACGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGGAATGAAAGATATCACAGTGACGAA	1740
QY	1741	CAAAATGATCTCAGAAAGCAATTTGTGAAAGAACAGACATGGAATTTACAGATGAG	1800
Db	1741	CAAAATGATCTCAGAAAGCAATTTGTGAAAGAACAGACATGGAATTTACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAAGAAAGCAGATAGAGTGTGAAAAAATGAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAAAGAAAGCAGATAGAGTGTGAAAAAATGAATTCGAGCTTCT	1860
QY	1861	CTTAGTGTGAAGAAAGAAAAAGCATCTTGATGAAATATAGTACTTGGGGAGGAATTT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAAAGCATCTTGATGAAATATAGTACTTGGGGAGGAATTT	1920
QY	1921	GCCATGCTAAGACTGAGCTAGACACAAATGAAGAACATCAGAGCCACCTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGCTAGACACAAATGAAGAACATCAGAGCCACCTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000	1980
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	1980

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RESULT 2
US-09-288-946-374
Sequence 374, Application US/09288946
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C7
CURRENT APPLICATION NUMBER: US/09/288, 946
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-288-946-374

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Query Match	100.0%;	Score 2000;	DB 16;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 6.6e-226;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATGCGTGTGAGTGTGATTCATGCGGGCTGCTCTTGTGTGAGAAACCCATTGGTCTC	60
OY	1	ATGGGTGTGAGTGTGATTCATGCGGGCTGCTCTTGTGTGAGAAACCCATTGGTCTC	60
Db	1	ATGGGTGTGAGTGTGATTCATGCGGGCTGCTCTTGTGTGAGAAACCCATTGGTCTC	60
OY	61	AGGACCAAGATGGCAATGGTGGCGCGTTGGCTTCCCTGCTGCAAGGAGACGGCCAAAG	120
Db	61	AGGACCAAGATGGCAATGGTGGCGCGTTGGCTTCCCTGCTGCAAGGAGACGGCCAAAG	120
OY	121	AGCAACGTGGGCACTTGTGAGAGACCAGACGACTCTGTATGAAGACACTGAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTGTGAGAGACCAGACGACTCTGTATGAAGACACTGAGAGCAAG	180
OY	181	ATGGGCAAGTGTGGCGGCACTGCTTCCCTGGCTGACAGGGGAGAGGGGAACGACAGTG	240
Db	181	ATGGGCAAGTGTGGCGGCACTGCTTCCCTGGCTGACAGGGGAGAGGGGAACGACAGTG	240
OY	241	GCGCGTTTGTGAGACACGACGACTCTGTATGAAGACACTGAGAAACAATGGGCAAG	300
Db	241	GCGCGTTTGTGAGACACGACGACTCTGTATGAAGACACTGAGAAACAATGGGCAAG	300
OY	301	TGGTGTCCCACTGCTTCCCTGCTGACAGGGGGAGGCGCAAGACGAGTGGGCGTTGG	360
Db	301	TGGTGTCCCACTGCTTCCCTGCTGACAGGGGGAGGCGCAAGACGAGTGGGCGTTGG	360
OY	361	GGAAGCACTACGATGACAGAGTGCCTTCATGGAAGCCAGAGTACGAGTCCGTGGAGAAATCTG	420
Db	361	GGAAGCACTACGATGACAGAGTGCCTTCATGGAAGCCAGAGTACGAGTCCGTGGAGAAATCTG	420
OY	421	GACAAGCTCCACAGAGCTGCGTGGGGGTAAAGTCCCGAGAAAGATCTCATCTGCATNG	480
Db	421	GACAAGCTCCACAGAGCTGCGTGGGGGTAAAGTCCCGAGAAAGATCTCATCTGCATNG	480
OY	481	CTCAGGGCACTGACGTGAACAAGAGACAAAGCAAGCAAAAGAGACTGCTACATCTGGCC	540
Db	481	CTCAGGGCACTGACGTGAACAAGAGACAAAGCAAGCAAAAGAGACTGCTACATCTGGCC	540
OY	541	TCTGCCAATGGGAATTTCAGAACTACTTCTGCTGGACACGATGTCACTTAAT	600
Db	541	TCTGCCAATGGGAATTTCAGAACTACTTCTGCTGGACACGATGTCACTTAAT	600
OY	601	GTCCTTGACAAACAAAAGAGGACGACCTCGATTAAGGCCGATCAATGGCAGAGAACTGAA	660
Db	601	GTCCTTGACAAACAAAAGAGGACGACCTCGATTAAGGCCGATCAATGGCAGAGAACTGAA	660
OY	661	TGTGGCTTAATGTTGCTGGAAACATGGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
Db	661	TGTGGCTTAATGTTGCTGGAAACATGGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
OY	721	ACCACTGTGCACTACGCTATCTATATATGAGATAATTAATGAGCCAAAGCACTGCTTTA	780
Db	721	ACCACTGTGCACTACGCTATCTATATATGAGATAATTAATGAGCCAAAGCACTGCTTTA	780
OY	781	TATGTCGTGATATGCAATCAAAAACAAGCATGGCCCTCACACCACTGTACTTGGSTTA	840
Db	781	TATGTCGTGATATGCAATCAAAAACAAGCATGGCCCTCACACCACTGTACTTGGSTTA	840
OY	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900
OY	901	CTGGATAGATATGAGAGACTGCTCTCAATCTGCTGATGTGTTGGATCAGCAAGTATA	960
Db	901	CTGGATAGATATGAGAGACTGCTCTCAATCTGCTGATGTGTTGGATCAGCAAGTATA	960
OY	961	GTCACACTTCTACTGTGACCAAAATTTGATGTAATCTTCAAGAGCTATCTGGAAGAGCG	1020
Db	961	GTCACACTTCTACTGTGACCAAAATTTGATGTAATCTTCAAGAGCTATCTGGAAGAGCG	1020
OY	1021	GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCCAATCTTCTGATCTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCCAATCTTCTGATCTAC	1080
OY	1081	AAAGAAAAACAGATCTTAAAAATCTTCTGTGAAAAACAGCAATCCAGAAACAAGATTAAAG	1140


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|||||
Db 661 TGTGGTAAATGTCTGGAAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACCTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTT 780
Db 721 ACCACTCTGCACCTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTT 780
Qy 781 TATGCTGATATGATCAAAAAACAAGCATGGCGCTCACACCTGTTACTTGGTGA 840
Db 781 TATGCTGATATGATCAAAAAACAAGCATGGCGCTCACACCTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAACGCAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAACGCAATTTAAATGA 900
Qy 901 CTGGATATGATGGAAGCACTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGGATATGATGGAAGCACTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
Qy 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCAGAGATCTATCTGGACAGC 1020
Db 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCAGAGATCTATCTGGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGCTTAA 1140
Db 1081 AAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGCTTAA 1140
Qy 1141 CTGACATCGAGAGAGAGCAAAAGTCAAAAGGAGGAGGAAATATGCGACAGAGAA 1200
Db 1141 CTGACATCGAGAGAGAGCAAAAGTCAAAAGGAGGAGGAAATATGCGACAGAGAA 1200
Qy 1201 ATGCTCAGAAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAAGAAATGAAG 1260
Db 1201 ATGCTCAGAAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGTTGGATTAAGAAACCTGACTAAATGCTCAGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGTTGGATTAAGAAACCTGACTAAATGCTCAGCTGGC 1320
Qy 1321 AATGATATGATGATTAATCTCAAGAGAGAGAGAAACCTGAAATATGAGCAATT 1380
Db 1321 AATGATATGATGATTAATCTCAAGAGAGAGAGAAACCTGAAATATGAGCAATT 1380
Qy 1381 CCTGACAAAGAGTGAAGAGTATCAGAAATTTGGAAATAGTTTCTGACTACAAAGA 1440
Db 1381 CCTGACAAAGAGTGAAGAGTATCAGAAATTTGGAAATAGTTTCTGACTACAAAGA 1440
Qy 1441 AAGCAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGA 1500
Db 1441 AAGCAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGA 1500
Qy 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGAGTGAAGAGGCGACAGAGTAGAAAT 1560
Db 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGAGTGAAGAGGCGACAGAGTAGAAAT 1560
Qy 1561 TTATGCTATGAGAAATGAAGAGCAAGCAAGTACTCATGCTGATTTCCAGAAAAC 1620
Db 1561 TTATGCTATGAGAAATGAAGAGCAAGCAAGTACTCATGCTGATTTCCAGAAAAC 1620
Qy 1621 CTGACTAATGCTGCCACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAC 1680
Db 1621 CTGACTAATGCTGCCACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAC 1680
Qy 1681 AAGAACCTGGAAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGTGCGAA 1740
Db 1681 AAGAACCTGGAAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGTGCGAA 1740
Qy 1741 CAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Db 1741 CAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800

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Db 1741 CAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Qy 1801 ATTCGATTCATGAAGAAAGAGATAGAGGTTGAAAAATGAATTCAGCTTCT 1860
Db 1801 ATTCGATTCATGAAGAAAGAGATAGAGGTTGAAAAATGAATTCAGCTTCT 1860
Qy 1861 CTAGTGTGAAGAAAGAAAGACATCTGATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
Db 1861 CTAGTGTGAAGAAAGAAAGACATCTGATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACAAATGAATCAATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACAAATGAATCAATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-429-755-302
; Sequence 302, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGATGTTGAGGTGATTCATGCGCGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGATGTTGAGGTGATTCATGCGCGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AAGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AAGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AAGACGTGGGCACTTCTGAGACACAGCAGACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AAGACGTGGGCACTTCTGAGACACAGCAGACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGTG 240
Db 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGTG 240
Qy 241 GGGCGTTCTGGAGACGACGACACTCTGATGAAGACACTAGAGAACAAATGGGCAAG 300
Db 241 GGGCGTTCTGGAGACGACGACACTCTGATGAAGACACTAGAGAACAAATGGGCAAG 300
Qy 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGGAGGAGGAGGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGGAGGAGGAGGCAAGAGTGGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTCCCTTCATGAGAGCCAGGATACCAAGTCCGTGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGAGAGCCAGGATACCAAGTCCGTGAGAAATCTG 420

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QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTGATG 480
    |||||||
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTGATG 480
QY 481 CTCAGGACACTGACGTGAAACAGAAAGACAGCAAAAGAGGACTGCTTCATCTGACC 540
    |||||||
Db 481 CTCAGGACACTGACGTGAAACAGAAAGACAGCAAAAGAGGACTGCTTCATCTGACC 540
QY 541 TCTGCCAATGGAATTCAGAAAGTAGTAAAGTCTGCTGGACAGACAGATGCACTTAAT 600
    |||||||
Db 541 TCTGCCAATGGAATTCAGAAAGTAGTAAAGTCTGCTGGACAGACAGATGCACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGACAGCTGTGATAAAGCCGTACATGCCAGGAAGATGAA 660
    |||||||
Db 601 GTCCCTGACAAACAAAAGAGAGACAGCTGTGATAAAGCCGTACATGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGGAAACATGACATGATCCAAATATTCAGATGAGTATGAAAT 720
    |||||||
Db 661 TGTGCGTTAATGTTGCTGGGAAACATGACATGATCCAAATATTCAGATGAGTATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTATATGAAAGATTAATGAGCAAGACACTGCTCTTA 780
    |||||||
Db 721 ACCACTGTGACACTACGCTATCTATATGAAAGATTAATGAGCAAGACACTGCTCTTA 780
QY 781 TATGCTCTGATATCGAATCAAAAACAGCAGTGGCTCACACCACTGTACTTGTGTTA 840
    |||||||
Db 781 TATGCTCTGATATCGAATCAAAAACAGCAGTGGCTCACACCACTGTACTTGTGTTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGGAATTTAAAGCA 900
    |||||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGGAATTTAAAGCA 900
QY 901 CTGATGATGATGAGAAAGAGACTGCTCTCATCTTGTATGTTGATGATCAGCAATGATA 960
    |||||||
Db 901 CTGATGATGATGAGAAAGAGACTGCTCTCATCTTGTATGTTGATGATCAGCAATGATA 960
QY 961 GTACGCTTCTACTTGAACAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
    |||||||
Db 961 GTACGCTTCTACTTGAACAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGATTTTGGCCAGTACTTCTGACTAC 1080
    |||||||
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGATTTTGGCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAAACAGACTTAAAG 1140
    |||||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGGAGAGTCAAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGGAGAGTCAAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAAA 1200
QY 1201 ATGCTTCAGAACAGCAAAATTAATAGATGATGATGATGATGATGATGATGATGATGATG 1260
    |||||||
Db 1201 ATGCTTCAGAACAGCAAAATTAATAGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
    |||||||
Db 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
    |||||||
Db 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
QY 1381 CCGACACACAGAAAGTGAAGAGTATCAGAGATTTGGCAATTAATGTTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCGACACACAGAAAGTGAAGAGTATCAGAGATTTGGCAATTAATGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTTCTGAAAGACAGCAACCCAGCAAGCAAGCTTAAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCAAAATCTCTTCTGAAAGACAGCAACCCAGCAAGCAAGCTTAAAGCTGACA 1500

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QY 1501 TCAGAGGAGAGATCACAAGAGCTTGAAGGACATGAAAAATGGCCAGCCAGCTAGAAAAT 1560
    |||||||
Db 1501 TCAGAGGAGAGATCACAAGAGCTTGAAGGACATGAAAAATGGCCAGCCAGCTAGAAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAAACACAGGAAGTCTCATGTGCGATTTCCAGAAAAC 1620
    |||||||
Db 1561 TTTATGGCTATCGAAGAAATGAAGAAACACAGGAAGTCTCATGTGCGATTTCCAGAAAAC 1620
QY 1621 CTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
    |||||||
Db 1621 CTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 AGAACCCTGAAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCACAGTACGAA 1740
    |||||||
Db 1681 AGAACCCTGAAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCACAGTACGAA 1740
QY 1741 CAAAATGATATCTGAGAGCAATTTTGAAGAACAGCACTGGAAATATACAGATGAG 1800
    |||||||
Db 1741 CAAAATGATATCTGAGAGCAATTTTGAAGAACAGCACTGGAAATATACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGTGAAAAATGAATTCGAGCTTTCT 1860
    |||||||
Db 1801 ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGTGAAAAATGAATTCGAGCTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATTTGCAATGAAATATGATGATGATGATGATGATGATG 1920
    |||||||
Db 1861 CTTAGTTGTAAGAAAGAAAGACATTTGCAATGAAATATGATGATGATGATGATGATGATG 1920
QY 1921 GCCATGCTAAGACTGAGAGTACAGCAATGAAATGATGAGCCAGCTTAAAGAAAAA 1980
    |||||||
Db 1921 GCCATGCTAAGACTGAGAGTACAGCAATGAAATGATGAGCCAGCTTAAAGAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 5
US-09-443-686-374
; Sequence 374, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443,686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 551
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-374

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Query Match 100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTGAATTCATGCGGCGCTCTCTGTAAGAAAGCAATTTGGCTC 60
Db 1 ATGGTGGTGAAGTGAATTCATGCGGCGCTCTCTGTAAGAAAGCAATTTGGCTC 60

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Oy 61 AGGACGAAGATGGGCAAGTGGTGTGCTGCCGTTGCTTCCCTGCTGCAGGAGGAGCGGCAAG 120
    |||
Db 61 AGGACGAAGATGGGCAAGTGGTGTGCTGCCGTTGCTTCCCTGCTGCAGGAGGAGCGGCAAG 120
Oy 121 AGCAAGTGGGCACTTCTGGAGACCAAGACGACTGCTGTATGAAAGACACTCAGAGCAAG 180
    |||
Db 121 AGCAAGTGGGCACTTCTGGAGACCAAGACGACTGCTGTATGAAAGACACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGGTGGCGGCACATGCTTCCCTGCTGCAGGAGGAGTGGCAAGACGCTG 240
    |||
Db 181 ATGGGCAAGTGGTGGCGGCACATGCTTCCCTGCTGCAGGAGGAGTGGCAAGACGCTG 240
Oy 241 GCGCGTTCTGGAGACCAAGACGACTGCTGTATGAAAGACACTCAGAGCAAGTGGGCAAG 300
    |||
Db 241 GCGCGTTCTGGAGACCAAGACGACTGCTGTATGAAAGACACTCAGAGCAAGTGGGCAAG 300
Oy 301 TGGTCTGCCACTGCTTCCCTGCTGCAGGAGGAGCGGCAAGGAGTGGCGCTTGG 360
    |||
Db 301 TGGTCTGCCACTGCTTCCCTGCTGCAGGAGGAGCGGCAAGGAGTGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGAGTCCCTTCATGAGAGCCAGGTACACAGTCCGTTGAGAAATCTG 420
    |||
Db 361 GGAGACTACGATGACAGAGTCCCTTCATGAGAGCCAGGTACACAGTCCGTTGAGAAATCTG 420
Oy 421 GACAAGCTCCACAGAGTGCCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
    |||
Db 421 GACAAGCTCCACAGAGTGCCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
Oy 481 CTCAGGAGACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
    |||
Db 481 CTCAGGAGACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
Oy 541 TGTGCATGGGAATTCGAAGTACTTAAACCTCGTGGAGAGAGAGTCACTTAT 600
    |||
Db 541 TGTGCATGGGAATTCGAAGTACTTAAACCTCGTGGAGAGAGTCACTTAT 600
Oy 601 GTCTTGAACAACAAAAGAGAGACAGCTGTATGAAGGCGTACAAATGCCAGGAAGTGA 660
    |||
Db 601 GTCTTGAACAACAAAAGAGAGAGACAGCTGTATGAAGGCGTACAAATGCCAGGAAGTGA 660
Oy 661 TGTGCGTTAATGTTCTGTGACATGGCACTGTATCCAAATATTCAGATAGTAAAT 720
    |||
Db 661 TGTGCGTTAATGTTCTGTGACATGGCACTGTATCCAAATATTCAGATAGTAAAT 720
Oy 721 ACCACTGCACTAGCTATCTATATGAGATTAATTAATGAGCCAAACCACTGCTTA 780
    |||
Db 721 ACCACTGCACTAGCTATCTATATGAGATTAATTAATGAGCCAAACCACTGCTTA 780
Oy 781 TATGCTGTATATGAAATCAAAAAAAGCATGGCTCACACCACTGTACTTGGTGA 840
    |||
Db 781 TATGCTGTATATGAAATCAAAAAAAGCATGGCTCACACCACTGTACTTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
    |||
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
Oy 901 CTGGATAGATATGAAAGAGCTGCTCATACTGCTATGTTGGTGGAGACACAGTATA 960
    |||
Db 901 CTGGATAGATATGAAAGAGCTGCTCATACTGCTATGTTGGTGGAGACACAGTATA 960
Oy 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
    |||
Db 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
Oy 1021 GCCAAGAGTATGCTGTTTCTATGATCATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
    |||
Db 1021 GCCAAGAGTATGCTGTTTCTATGATCATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
Oy 1081 AAAAAAACAATGATGTAATCTCTGTAAGACAGAAATCCAGAAACAAACTTAAAG 1140
    |||
Db 1081 AAAAAAACAATGATGTAATCTCTGTAAGACAGAAATCCAGAAACAAACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGAGTGAAGAAATAGCCAGCCAGAGAA 1200

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Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAAGAAATAGCCAGCAGAGAA 1200
    |||
Oy 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTGTATGAGAGCTTGAAGAAATGAAG 1260
    |||
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTGTATGAGAGCTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGATTAATGATGGGATTTACTATGAAAAACCTGACATATGTTGCTGCTGGC 1320
    |||
Db 1261 AAGCATGAAGATTAATGATGGGATTTACTATGAAAAACCTGACATATGTTGCTGCTGGC 1320
Oy 1321 AATGCTGAATATGATTAATTCCTCAAGAGAGACAGAACCTGAAATATGCAATTT 1380
    |||
Db 1321 AATGCTGAATATGATTAATTCCTCAAGAGAGACAGAACCTGAAATATGCAATTT 1380
Oy 1381 CCTGACAAAGAAATGTAAGATATACAGAAATTTGCCAATTAATGTTTCTGACTACAAAGAA 1440
    |||
Db 1381 CCTGACAAAGAAATGTAAGATATACAGAAATTTGCCAATTAATGTTTCTGACTACAAAGAA 1440
Oy 1441 AAGCATGCCCCAATATCTCTGTAAGAACCAACCCAGAACAAAGACTTAAGCTGACA 1500
    |||
Db 1441 AAGCATGCCCCAATATCTCTGTAAGAACCAACCCAGAACAAAGACTTAAGCTGACA 1500
Oy 1501 TCAGAGAGAGTCAACAAAGCCTGAGGCACTGAGAAATGGCCACAGAGCTAGAAAT 1560
    |||
Db 1501 TCAGAGAGAGTCAACAAAGCCTGAGGCACTGAGAAATGGCCACAGAGCTAGAAAT 1560
Oy 1561 TTTATGCTATGAGAAATGTAAGAACCAAGCAAGTACTCATGTGCTATCCACAGAAAC 1620
    |||
Db 1561 TTTATGCTATGAGAAATGTAAGAACCAAGCAAGTACTCATGTGCTATCCACAGAAAC 1620
Oy 1621 CTGACTAATGTTGCTGCACTGCTGCAATGGTGTATGATGATTAATTCCTCAAGAGAGAC 1680
    |||
Db 1621 CTGACTAATGTTGCTGCACTGCTGCAATGGTGTATGATGATTAATTCCTCAAGAGAGAC 1680
Oy 1681 AGAACACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAGATATCACAGTACGAA 1740
    |||
Db 1681 AGAACACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAGATATCACAGTACGAA 1740
Oy 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATTTACACGATGAG 1800
    |||
Db 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATTTACACGATGAG 1800
Oy 1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGTGTGAAGAAATGAATTCGAGCTTCT 1860
    |||
Db 1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGTGTGAAGAAATGAATTCGAGCTTCT 1860
Oy 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGAAATATGATGCTTGGGGAGAAATTT 1920
    |||
Db 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGAAATATGATGCTTGGGGAGAAATTT 1920
Oy 1921 GCCATGCTTAAGCTGAGCTAGACACATGAACATCAGAGCCAGCTAAAAA 1980
    |||
Db 1921 GCCATGCTTAAGCTGAGCTAGACACATGAACATCAGAGCCAGCTAAAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAA 2000
    |||
Db 1981 AAAAAAAAAAAAAAAAAA 2000

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RESULT 6
US-09-483-672A-374
; Sequence 374. Application US/09483672A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.

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; APPLICANT: Solk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Wang, Aljun
; APPLICANT: Mesner, Madeleine
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42711C11
; CURRENT APPLICATION NUMBER: US/09/483,672A
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-483-672A-374

Query Match      100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTGGTATTCATCCGCGCTCTCTGTGAAAGCCATTGGCTC 60
DB 1 ATGGTGGTTGAGTGGTATTCATCCGCGCTCTCTGTGAAAGCCATTGGCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGGAGCGGCAAG 120
QY 121 AGCAACCTGGGCACTTCTGTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACCTGGGCACTTCTGTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGGGCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
QY 241 GGGCTTCTGTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGCTTCTGTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAGTGGCAAG 300
QY 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
DB 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACATGCTGCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAAGATCTG 420
DB 361 GGAGACTACGATGACATGCTGCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTGAGGACACTGACGTGAACAGAAAGACAAAGAGAGTCTTACATCTGACC 540
DB 481 CTGAGGACACTGACGTGAACAGAAAGACAAAGAGAGTCTTACATCTGACC 540
QY 541 TCTGCAATGGGAATTCAGAAATGTAATAATCTGCTGGACAGAGATGCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGTAATAATCTGCTGGACAGAGATGCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAGAGAGAGAGCTCTGTATTAAGGCGGTACAAATCCAGGAAGTAA 660
DB 601 GTCCCTTGACAAACAAAGAGAGAGAGCTCTGTATTAAGGCGGTACAAATCCAGGAAGTAA 660
QY 661 TGTGCTGTAATGTTGCTGGAACATGGCAGTCAATATATTCAGATGAGTATGAAT 720
DB 661 TGTGCTGTAATGTTGCTGGAACATGGCAGTCAATATATTCAGATGAGTATGAAT 720
QY 721 AACACCTGACATACGCTATCTATTAAGAGATTAATATGGCCAAAGCACTGCTCTTA 780
DB 721 AACACCTGACATACGCTATCTATTAAGAGATTAATATGGCCAAAGCACTGCTCTTA 780
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QY 781 TATGCTGCTGATATCGAATCAAAAACAGATGGCCCTCACACCAGTACTTGGTGA 840
DB 781 TATGCTGCTGATATCGAATCAAAAACAGATGGCCCTCACACCAGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATATGAGAGAGCTGCTCATATCTGCTATGTTGGTATGAGCAAGTATA 960
DB 901 CTGATGATATATGAGAGAGCTGCTCATATCTGCTATGTTGGTATGAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTCAGCCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTGTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTGTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATAATCTCTGAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAATAATCTCTGAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAAGAGAGAGTCAAAAAGGTTCAAAAGGCAAGTAAATAATGAGCCAGAGAAA 1200
DB 1141 CTGACATCAAGAGAGAGTCAAAAAGGTTCAAAAGGCAAGTAAATAATGAGCCAGAGAAA 1200
QY 1201 ATGCTCTAAGACACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATTAAG 1260
DB 1201 ATGCTCTAAGACACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATTAAG 1260
QY 1261 AAGCATGAAGTATATATGTTGGGATTAAGTAAACCTGACTATGTTGTCAGTGGC 1320
DB 1261 AAGCATGAAGTATATATGTTGGGATTAAGTAAACCTGACTATGTTGTCAGTGGC 1320
QY 1321 AATGCTATATATGATTAATTTCTCAAAAGAGAGCAAGACACTGAAATTCAGCAATTT 1380
DB 1321 AATGCTATATATGATTAATTTCTCAAAAGAGAGCAAGACACTGAAATTCAGCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAATTTGACTACAAAGAA 1440
DB 1381 CTTGACACAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAATTTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAAAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCCAGAGCTAGAAAAT 1560
DB 1501 TCAGAGGAAGAGTCAAAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGCTATCCAGAAAGATGAAGAGACAGGAAGTCTATGTGCGATTTCCAGAAAAC 1620
DB 1561 TTTATGCTATCCAGAAAGATGAAGAGACAGGAAGTCTATGTGCGATTTCCAGAAAAC 1620
QY 1621 CTGACTAATGATGGCACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGAGC 1680
DB 1621 CTGACTAATGATGGCACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGAACACCTGAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACTAGAGAA 1740
DB 1681 AGAACACCTGAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACTAGAGAA 1740
QY 1741 CAAAATGATATCTAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
DB 1741 CAAAATGATATCTAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATGATGAAGAAAGCAAGATGAGTGGTTGAATAATGAAATCTGAGCTTCT 1860
DB 1801 ATTCTGATGATGAAGAAAGCAAGATGAGTGGTTGAATAATGAAATCTGAGCTTCT 1860
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1861 CTTAGTTGTAGAAAGAAAAAGACATCTTGCATGAAATAGTACGTGGCGGAGAAAT 1920
1861 CTTAGTTGTAGAAAGAAAAAGACATCTTGCATGAAATAGTACGTGGCGGAGAAAT 1920
1921 GCCATGCTAGACCTGGAGCTAGACACATGAAACATCAGAGCCAGCTAAACAAAAA 1980
1921 GCCATGCTAGACCTGGAGCTAGACACATGAAACATCAGAGCCAGCTAAACAAAAA 1980
1981 AAAAAAAAAAAAAAAAAAAAAA 2000
1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-534-825A-302
Sequence 302, Application US/09534825A
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C7
CURRENT APPLICATION NUMBER: US/09/534, 825A
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 317
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-534-825A-302

Query Match 100.0%; Score 2000; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGTGCTTGTAGAGTTGATTCATGCGGCTGCTCTTGTGTAAGAACCATTTGCTC 60
1 ATGGTGCTTGTAGAGTTGATTCATGCGGCTGCTCTTGTGTAAGAACCATTTGCTC 60
61 AGGAGCAATGGGCAAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
61 AGGAGCAATGGGCAAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
121 ACCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
121 ACCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
181 ATGGGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 ATGGGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241 GGGGCTTGTGAGACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
241 GGGGCTTGTGAGACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
361 GGAAGCTAGATGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 GGAAGCTAGATGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGCACTGCTGCTGCTGCTGCTGCT 540

481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGGAGCTGCTGCTGCTGCTGCTGCT 540
481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGGAGCTGCTGCTGCTGCTGCTGCT 540
541 TCTGCCAATGGCAATTCAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 TCTGCCAATGGCAATTCAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
601 GTCCCTGACAAACAAAGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601 GTCCCTGACAAACAAAGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
661 TGTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
661 TGTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
781 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
841 CATGACCAAAACAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
841 CATGACCAAAACAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
901 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
901 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
961 CTCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
961 CTCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
1021 GCCAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1021 GCCAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1081 AAGAAACAAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1081 AAGAAACAAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1141 CTGACATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
1141 CTGACATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGCTGATGAGAGGCTGGAAGAAATGAAG 1260
1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGCTGATGAGAGGCTGGAAGAAATGAAG 1260
1261 AAGCATGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
1261 AAGCATGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
1321 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
1321 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
1381 CTTGACAAAGCAAGTGAAGTATCAAGAAATTTGCAATTTGCTGCTGCTGCTGCTGCTGCTGCT 1440
1381 CTTGACAAAGCAAGTGAAGTATCAAGAAATTTGCAATTTGCTGCTGCTGCTGCTGCTGCTGCT 1440
1441 AAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1441 AAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1501 TCAGAGGAGAGTCAAGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
1501 TCAGAGGAGAGTCAAGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
1561 TTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1561 TTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

Db 1561 TTATGCTATCGAAGAAATGAAGACGAGAGTACTCATGTGCGATTCCTCCAGAAAAC 1620
QY 1621 CTGACTAATGGTGGCCTGCTGCAATGGTATGATGATTAATTCCTCCAAGAAAGAGC 1680
Db 1621 CTGACTAATGGTGGCCTGCTGCAATGGTATGATGATTAATTCCTCCAAGAAAGAGC 1680
QY 1661 AGAACACCTGAAGACGCAATTTCTGACACTGTGAAGTGAAGATACAGTGCAGAA 1740
Db 1661 AGAACACCTGAAGACGCAATTTCTGACACTGTGAAGTGAAGATACAGTGCAGAA 1740
QY 1741 CAAATGATCTAGCAACCAATTTTGTGAACAGCAACACTGGAATTTACAGATAG 1800
Db 1741 CAAATGATCTAGCAACCAATTTTGTGAACAGCAACACTGGAATTTACAGATAG 1800
QY 1801 ATTCTGATCTAGCAACCAATTTTGTGAACAGCAACACTGGAATTTACAGATAG 1860
Db 1801 ATTCTGATCTAGCAACCAATTTTGTGAACAGCAACACTGGAATTTACAGATAG 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAGTTCGCGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAGTTCGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACGCTGACCTGACACATGAACATGACGACGCTAAAAAAGAA 1980
Db 1921 GCCATGCTAAGACGCTGACCTGACACATGAACATGACGACGCTAAAAAAGAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
US-09-536-857-374

; Sequence 374, Application US/09536857

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuhui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kelos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42712C12
; CURRENT APPLICATION NUMBER: US/09/536, 857
; NUMBER OF SEQ ID NOS: 592
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-536-857-374

Query Match 100.0%; Score 2000; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6, 6e-726;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTGTGATTCATCCGCTGCTCTCTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGTGTTGAGTGTGATTCATCCGCTGCTCTCTCTCTGTAAGAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGAGCAAGATGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGTGGGCACTTCTGGAGACGACGACCTCTGTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGGAGACGACGACCTCTGTATGAAGACACTGAGAGCAAG 180

Db 121 AGCAAGTGGGCACTTCTGGAGACGACGACCTCTGTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 ATGGGCAAGTGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 GGGCTTCTGGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
Db 241 GGGCTTCTGGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
QY 301 TGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 GGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 GACAAAGTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAAGTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGACACTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACG 540
Db 481 CTCAGGACACTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACG 540
QY 541 TCTGCAATGGGAATTCAGAGTGAATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TCTGCAATGGGAATTCAGAGTGAATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTCCCTGACAAACAAAAGAGGACGCTGATTAAGAGGCTGACATGCTGCAATTAAT 660
Db 601 GTCCCTGACAAACAAAAGAGGACGCTGATTAAGAGGCTGACATGCTGCAATTAAT 660
QY 661 TGTGCGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TGTGCGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 TATGCTGCTGATATGCAATCAAAAACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGAAAGAAATTAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGAAAGAAATTAATGA 900
QY 901 CTGATAGATATGGAAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 CTGATAGATATGGAAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 GTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 GTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 GCCAGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 GCCAGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 AAGAGAAACAGATGCTTAAATATCTCTTCTGAAACAGCAATTCAGAAACAGATTAAG 1140
Db 1081 AAGAGAAACAGATGCTTAAATATCTCTTCTGAAACAGCAATTCAGAAACAGATTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGAGTGAATAATAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGAGTGAATAATAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGACCAAGAAATTAATTAAGATGCTGATAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGACCAAGAAATTAATTAAGATGCTGATAGAGGTTGAAGAAATGAAG 1260

```
QY 1261 AAGCATGAAGTAATATGTTGGATTACTAGAAAACCTGACTAATGTTCTACTGCTGCG 1320
    |||||||
Db 1261 AAGCATGAAGTAATATGTTGGATTACTAGAAAACCTGACTAATGTTCTACTGCTGCG 1320
QY 1321 AATGCTGTAATGATTAATTCCTCAAGAGAGACAGAACCTGGAATATCAGCAATTT 1380
    |||||||
Db 1321 AATGCTGTAATGATTAATTCCTCAAGAGAGACAGAACCTGGAATATCAGCAATTT 1380
QY 1381 CCTGCAACGAAAGTGAAGAGATATCACAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCTGCAACGAAAGTGAAGAGATATCACAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTCTGTAAGAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCCAAATTAATCTCTGTAAGAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGACTCACAAGGCTTGAGGGCAGTGAATAATGCCACCCAGAGCTAGAAAAT 1560
    |||||||
Db 1501 TCAGAGGAAGACTCACAAGGCTTGAGGGCAGTGAATAATGCCACCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGCGTATGAGAAATGAGAAGACGGAAGTACTCATGTGGATTTCCACAGAAAAC 1620
    |||||||
Db 1561 TTTATGCGTATGAGAAATGAGAAGACGGAAGTACTCATGTGGATTTCCACAGAAAAC 1620
QY 1621 CTGACTAATGCTGCCACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAGAAAGC 1680
    |||||||
Db 1621 CTGACTAATGCTGCCACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAGAAAGC 1680
QY 1681 AGACACCTGAAAGCCAGCAATTTCTGACACTGGAATGAAGATATCACAGTACGAA 1740
    |||||||
Db 1681 AGACACCTGAAAGCCAGCAATTTCTGACACTGGAATGAAGATATCACAGTACGAA 1740
QY 1741 CAAATGATACCTACAAGCAATTTGTGAAGACAGACCTGGAATATTAACAGATGAG 1800
    |||||||
Db 1741 CAAATGATACCTACAAGCAATTTGTGAAGACAGACCTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAGAGATAGAAAGTGTGAATAATGAATCTGAGCTTTCT 1860
    |||||||
Db 1801 ATTCTGATTCATGAGAAAGAGATAGAAAGTGTGAATAATGAATCTGAGCTTTCT 1860
QY 1861 CTTAGCTTAAAGAAAGAAAGACATCTTGCATGAAATATGATGCTTGGGGAGAAAT 1920
    |||||||
Db 1861 CTTAGCTTAAAGAAAGAAAGACATCTTGCATGAAATATGATGCTTGGGGAGAAAT 1920
QY 1921 GCCATGCTAAAGCTGAGCTATACACATGAAACATCAGAGCCAGCTAAAAAATTTT 1980
    |||||||
Db 1921 GCCATGCTAAAGCTGAGCTATACACATGAAACATCAGAGCCAGCTAAAAAATTTT 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||||
```

RESULT 9
US-09-568-100A-374
Sequence 374, Application US/09568100A

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun

```
; APPLICANT: Skelky, Yasil A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.42713c13  
; CURRENT APPLICATION NUMBER: US/09/568.100A  
; NUMBER OF SEQ ID NOS: 701  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 374  
; LENGTH: 2000  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-568-100A-374
```

Query Match 100.0% Score 2000: DB 22: Length 2000:
Best Local Similarity 100.0%: Pred. No. 6.6e-226;
Matches 2000: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AATGCTGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
    |||||||
Db 1 AATGCTGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGACAGATGGCGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
    |||||||
Db 61 AGGACAGATGGCGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
    |||||||
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACGTTG 240
    |||||||
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACGTTG 240
QY 241 GCGCTTCTGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
    |||||||
Db 241 GCGCTTCTGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTCTGCTGCACTGCTTCCCTGCTGAGGGGAGCGCAAGCAAGTGGCGCTTG 360
    |||||||
Db 301 TGGTCTGCTGCACTGCTTCCCTGCTGAGGGGAGCGCAAGCAAGTGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTGTCTTCAATGAGCCAGGTACACGCTCGTGAAGATCTG 420
    |||||||
Db 361 GGAGACTACGATGACAGTGTCTTCAATGAGCCAGGTACACGCTCGTGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTCATGCTATG 480
    |||||||
Db 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
    |||||||
Db 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTCTGCTGAGAGAGATGCAACTTAAT 600
    |||||||
Db 541 TCTGCCAATGGGAATTCAGAACTCTGCTGAGAGAGATGCAACTTAAT 600
QY 601 GTCTTGACACAAAAAGAGACAGCTGTGATTAAGGCCCTGCAATGCCAGAGATGAA 660
    |||||||
Db 601 GTCTTGACACAAAAAGAGAGACAGCTGTGATTAAGGCCCTGCAATGCCAGAGATGAA 660
QY 661 TGTGCTTAATTTGCTGGAACATGGCAATCCAAATATCCAGATAGTATGGAAT 720
    |||||||
Db 661 TGTGCTTAATTTGCTGGAACATGGCAATCCAAATATCCAGATAGTATGGAAT 720
QY 721 ACCACTCTGCACTAGCTTCTATATGAAGTAATTAATGAGCAAGCAAGCTGCTTA 780
    |||||||
Db 721 ACCACTCTGCACTAGCTTCTATATGAAGTAATTAATGAGCAAGCAAGCTGCTTA 780
QY 781 TATGCTGTGATATGAATCAAAAAAAGCAATGGCTTACACCACTGTTACTGCTGA 840
    |||||||
Db 781 TATGCTGTGATATGAATCAAAAAAAGCAATGGCTTACACCACTGTTACTGCTGA 840
```

QY	841	CATAGCAAAAAACGCAAGTCGTAATTTTAAATCAAAAAAGCCAAATTTAAATGCA	900
Db	841	CATAGCAAAAAACGCAAGTCGTAATTTTAAATCAAAAAAGCCAAATTTAAATGCA	900
QY	901	CTGATAGATATGGAAGAGTGCCTCATACTTGTCTGTATGTTGTGATCAGCAAGTATA	960
Db	901	CTGATAGATATGGAAGAGTGCCTCATACTTGTCTGTATGTTGTGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAGCAAAATATTGATGATCTCTTCAGAGATCTATCTGACAGCG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTGATGATCTCTTCAGAGATCTATCTGACAGCG	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTTACATCAATATGTATTTGGCAGTTACTTTCCTACATC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTTACATCAATATGTATTTGGCAGTTACTTTCCTACATC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTTCTTGAAACAGCAATCCAGAACACACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTTCTTGAAACAGCAATCCAGAACACACTTAAAG	1140
QY	1141	CTGACATCAGAGGAAGGTACCAAGGTTCAAAAGGACAGTAAATAATAGCAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAGGTACCAAGGTTCAAAAGGACAGTAAATAATAGCAGCCAGAGAAA	1200
QY	1201	ATGTCCTCAAGAACCCAGAAATTAATTAAGGATGGTATAGAGAGGTTGAAGAAAGAAATGAG	1260
Db	1201	ATGTCCTCAAGAACCCAGAAATTAATTAAGGATGGTATAGAGAGGTTGAAGAAAGAAATGAG	1260
QY	1261	AAGCATGAAAGTATATATGTGGGATTAAGTAAAAACCTGACATTAATGTGTCTACCTGTGC	1320
Db	1261	AAGCATGAAAGTATATATGTGGGATTAAGTAAAAACCTGACATTAATGTGTCTACCTGTGC	1320
QY	1321	AATGATATATGATTAATTTCTCTCAAGGAGAGCAGAACCTCGAAATAATCAGCAATTT	1380
Db	1321	AATGATATATGATTAATTTCTCTCAAGGAGAGCAGAACCTCGAAATAATCAGCAATTT	1380
QY	1381	CCTGACAAACGAAAGTGAAGGTATCACAGAAATTTGGGAATTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGGTATCACAGAAATTTGGGAATTAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACGATGCCAAATTTCTTCTTGAAAAACAGAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCAAATTTCTTCTTGAAAAACAGAACCCAGAACAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAGAGATCACAAAGGCTTTGAGGCGATGAAATATGSCCAGCCAGAGCTAGAAAAT	1560
Db	1501	TCAGAGAGAGATCACAAAGGCTTTGAGGCGATGAAATATGSCCAGCCAGAGCTAGAAAAT	1560
QY	1561	TTTATGGCTATCGAAGAAATGAAGAAGCACAGGAATGACTCATGTGGGAATTTCCCAAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGCACAGGAATGACTCATGTGGGAATTTCCCAAGAAAC	1620
QY	1621	CTGACTAATGGTGCACACTGCTGGCAATGTGATGATGATTAATCTCCCAAGAAAGAC	1680
Db	1621	CTGACTAATGGTGCACACTGCTGGCAATGTGATGATGATTAATCTCCCAAGAAAGAC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATCACAGTACGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATCACAGTACGAA	1740
QY	1741	CAAAATGATACTCGAAGCAATTTTGTGAAAGAACACAACTGGAATATTCACAGATAG	1800
Db	1741	CAAAATGATACTCGAAGCAATTTTGTGAAAGAACACAACTGGAATATTCACAGATAG	1800
QY	1801	ATTCGTATTCATGAAGAAAGACAGATAGAAGTGGTTGAAAAAATGAATTCGTGAGCTTCT	1860
Db	1801	ATTCGTATTCATGAAGAAAGACAGATAGAAGTGGTTGAAAAAATGAATTCGTGAGCTTCT	1860
QY	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGTCATGAATAATAGTACTGTGCGGGAGAAATTT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGTCATGAATAATAGTACTGTGCGGGAGAAATTT	1920

```

OY      1921 GCATGCGTAAGCTGGAGCTAGACACAACTGAACAATTCAGAGCCACTTAAAAA 1980
DB      1921 GCGATGCTTAGAGCTGGAGCTAGACACAACTGAACAATTCAGAGCCACTTAAAAA 1980

OY      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
        ||| ||||| ||||| |||||
DB      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-09-577-505B--302
; Sequence 302, Application US/09577505B
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Mishner, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419CB
CURRENT APPLICATION NUMBER: US/09/577, 505B
CURRENT FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-577-505B--302
```

Query Match	Similarity	100.0%	Score	2000:	DB	22:	Length	2000:
Best Local	Similarity	100.0%	Pred.	No.	6	6e	22:	
Matches	2000:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
QY	1	ATGGTGGTTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAAGCCATTGTGGTCTC	60					
DB	1	ATGGTGGTTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAAGCCATTGTGGTCTC	60					
QY	61	AGGACCAAGATGGGCAAGTGGTGGCCGTTTCCCTTGGTGAAGGAGCCGGCAAG	120					
DB	61	AGGACCAAGATGGGCAAGTGGTGGCCGTTTCCCTTGGTGAAGGAGCCGGCAAG	120					
QY	121	AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAACAACATCAGAGCAAG	180					
DB	121	AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAACAACATCAGAGCAAG	180					
QY	181	ATGGGCAAGTGGTGGCCGACACTGCTTCCCTCTGCAGAGGGGAGTGGCAAGACAACTGT	240					
DB	181	ATGGGCAAGTGGTGGCCGACACTGCTTCCCTCTGCAGAGGGGAGTGGCAAGACAACTGT	240					
QY	241	GGCGCTTTGGAGACCAGAGCACTCTGCTATGAAGACACTAGGAACAAGATGGGCAAG	300					
DB	241	GGCGCTTTGGAGACCAGAGCACTCTGCTATGAAGACACTAGGAACAAGATGGGCAAG	300					
QY	301	TGGTCTGTGCAATGCTTCCCTCCCTGTCAGAGGGGAGCGGCAAGGCAAGGTGGGCTTTGG	360					
DB	301	TGGTCTGTGCAATGCTTCCCTCCCTGTCAGAGGGGAGCGGCAAGGCAAGGTGGGCTTTGG	360					
QY	361	GGAGACTAGATGACAGTGGCTTCTCATGTGAGAGCCAGCAGTACCACTCGTGGAGAAATCTG	420					
DB	361	GGAGACTAGATGACAGTGGCTTCTCATGTGAGAGCCAGCAGTACCACTCGTGGAGAAATCTG	420					
QY	421	GACAAAGCTCCACAGAGCTGGCTGTGGGGTAAAGTCCCCAGAAAGATCTCATGTCATG	480					
DB	421	GACAAAGCTCCACAGAGCTGGCTGTGGGGTAAAGTCCCCAGAAAGATCTCATGTCATG	480					
QY	481	CTCAGGGACACTGACAGTGAACAAGAACCAAGCAAAAGAGATGCTCTACATCTGGCC	540					
DB	481	CTCAGGGACACTGACAGTGAACAAGAACCAAGCAAAAGAGATGCTCTACATCTGGCC	540					

QY 241 GGGCTTCTGGAGACGACGACTCTGATGAAAGACACTCAGAGCAAGATGGGCAAG 300
|||||
Db 241 GGGCTTCTGGAGACGACGACTCTGATGAAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGGTGCTCCAGCTCTCCCTGCTGAGGGGGGAGCGGCAAGAGCAAGGTGGGCTTGG 360
|||||
Db 301 TGGGTGCTCCAGCTCTCCCTGCTGAGGGGGGAGCGGCAAGAGCAAGGTGGGCTTGG 360
QY 361 GGAGACTACGATGACATGCTTCATGAGCCAGGTACCAAGCTCCCTGGAGAAATCTG 420
|||||
Db 361 GGAGACTACGATGACATGCTTCATGAGCCAGGTACCAAGCTCCCTGGAGAAATCTG 420
QY 421 GACAGCTCCAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGATCTCATGTCATG 480
|||||
Db 421 GACAGCTCCAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGATCTCATGTCATG 480
QY 481 CTGAGGACACTGACGTGAACAGAGACAGCAAGAAAGAGACTGCTTCATCTGCTGCC 540
|||||
Db 481 CTGAGGACACTGACGTGAACAGAGACAGCAAGAAAGAGACTGCTTCATCTGCTGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATCTCTGCTGGACAGACGATGCAACTTAAT 600
|||||
Db 541 TCTGCCAATGGGAATTCAGAAATCTCTGCTGGACAGACGATGCAACTTAAT 600
QY 601 GTCTTACACAACAAAAAGAGACAGCTCTGATTAAGGCCCTACATGCCAGGAATGAA 660
|||||
Db 601 GTCTTACACAACAAAAAGAGACAGCTCTGATTAAGGCCCTACATGCCAGGAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTCAATATTCAGATGAGTAATGAAAT 720
|||||
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTCAATATTCAGATGAGTAATGAAAT 720
QY 721 ACCACTCTGCACACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTA 780
|||||
Db 721 ACCACTCTGCACACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTA 780
QY 781 TATGCTCTGATATCGAATCAAAAAACAGCAGTGGCTCACACAGCTTACTTGGTGA 840
|||||
Db 781 TATGCTCTGATATCGAATCAAAAAACAGCAGTGGCTCACACAGCTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACGCAAGTCGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
|||||
Db 841 CATGAGCAAAAAACGCAAGTCGTAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATGATATGGAAGAGACTGCTCATCTTGTCTGATGTTGGATCAGCAATGATA 960
|||||
Db 901 CTGATGATATGGAAGAGACTGCTCATCTTGTCTGATGTTGGATCAGCAATGATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGC 1020
|||||
Db 961 GTGAGCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTTCCCGATTCTTCTGACTAC 1080
|||||
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTTCCCGATTCTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATCTCTCTGAAAAACAGCAATCCAGAAACAGACTTAAAG 1140
|||||
Db 1081 AAAGAAAAACAGATGCTAAATCTCTCTGAAAAACAGCAATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCAAGTGAATTAAGCCAGAGAAAA 1200
|||||
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCAAGTGAATTAAGCCAGAGAAAA 1200
QY 1201 ATGTCCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGGTGTAAGAAATGAAG 1260
|||||
Db 1201 ATGTCCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGGTGTAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATATGTTGGATTTACTAGAAAACTGACTAATGTTGCTACTGCTGC 1320
|||||
Db 1261 AAGCATGAAGTAATATGTTGGATTTACTAGAAAACTGACTAATGTTGCTACTGCTGC 1320

QY 1321 AATGCTAATATGATTAATTTCTCTCAAGAGACGCAAAACCTGTAAATTCAGCAATTT 1380
|||||
Db 1321 AATGCTAATATGATTAATTTCTCTCAAGAGAGAGCAAAACCTGTAAATTCAGCAATTT 1380
QY 1381 CCTGACACGAAATGAAAGTATACAGAAATTTGCAATTAATTTGATGCTCAAGAA 1440
|||||
Db 1381 CCTGACACGAAATGAAAGTATACAGAAATTTGCAATTAATTTGATGCTCAAGAA 1440
QY 1441 AAACGATGCCCCAAATATCTTCTGAAAAACAGCAACCCAGCAAGACTTAAAGCTGACA 1500
|||||
Db 1441 AAACGATGCCCCAAATATCTTCTGAAAAACAGCAACCCAGCAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGTACAAAAGCTTGGAGGCAAGTAAAAATGGCCAGCCAGACTTGAAT 1560
|||||
Db 1501 TCAGAGAGAGTACAAAAGCTTGGAGGCAAGTAAAAATGGCCAGCCAGACTTGAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAACAGGAAATCTCATGTCGATTTCCCGAAGAAC 1620
|||||
Db 1561 TTTATGCTATCGAAGAAATGAAGAACAGGAAATCTCATGTCGATTTCCCGAAGAAC 1620
QY 1621 CTGACATATGCTGCTGCTGCTGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGC 1680
|||||
Db 1621 CTGACATATGCTGCTGCTGCTGCTGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATTCACAGTGAAGAA 1740
|||||
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATTCACAGTGAAGAA 1740
QY 1741 CAAATATGATCTCGAAGCAATTTTGTGAAGAACAGAACTGGAATTTTACACAGTAGAG 1800
|||||
Db 1741 CAAATATGATCTCGAAGCAATTTTGTGAAGAACAGAACTGGAATTTTACACAGTAGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGTAAGAAATTTCTGACCTTTCT 1860
|||||
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGTAAGAAATTTCTGACCTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTCTGATGAAATTAATGATGTTGGGGAAGAAAT 1920
|||||
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTCTGATGAAATTAATGATGTTGGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACCAATGAATGAAATCAGAGCCAGCTAAAAA 1980
|||||
Db 1921 GCCATGCTAAGACTGAGAGCTAGACCAATGAATGAAATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
|||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 12
US-09-593-793A-374
; Sequence 374, Application US/09593793A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Helper, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: DINGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42715C15

/ CURRENT APPLICATION NUMBER: US/09/593,793A
/ CURRENT FILING DATE: 2000-06-13
/ NUMBER OF SEQ ID NOS: 814
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-593-793A-374

Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGTGAGGTGATTCATGCCGCTCTTGTGAAGAAAGCATTTGGTCTC 60
DB 1 ATGGTGTGAGGTGATTCATGCCGCTCTTGTGAAGAAAGCATTTGGTCTC 60
OY 61 AGGAGCAGATGGGCAAGTGTGCTGCGTTGCTCCCTGCTGCAGGAGACGGCAAG 120
DB 61 AGGAGCAGATGGGCAAGTGTGCTGCGTTGCTCCCTGCTGCAGGAGACGGCAAG 120
OY 121 AGCAAGTGGGCACTTCTGGAAGCAGCAGCAGCTGCTATGAAGACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAAGCAGCAGCAGCTGCTATGAAGACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGGTGGCGGCACTGCTCCCTGCTGCAGGAGGAGTGGCAAGCAAGTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTCCCTGCTGCAGGAGGAGTGGCAAGCAAGTG 240
OY 241 GCGGCTTCTGGAAGCAGCAGCAGCTGCTATGAAGACTCAGAGCAAGTGGGCAAG 300
DB 241 GCGGCTTCTGGAAGCAGCAGCAGCTGCTATGAAGACTCAGAGCAAGTGGGCAAG 300
OY 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
OY 361 GGAGACTAGATGACAGTCTTCTGATGAGAGCAGTACAGTCCCTGGAGAGAGTCTG 420
DB 361 GGAGACTAGATGACAGTCTTCTGATGAGAGCAGTACAGTCCCTGGAGAGAGTCTG 420
OY 421 GACAAAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
OY 481 CTCAGGAGACCTGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CTCAGGAGACCTGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGAGAGAGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGAGAGAGAGATGTCAACTTAAT 600
OY 601 GTCTCTTGACAAAG 660
DB 601 GTCTCTTGACAAAG 660
OY 661 TGTGGGTAAATGCTGTGAAGACATGGCAGTCCAAATATTTCCAAATGATGTGAAT 720
DB 661 TGTGGGTAAATGCTGTGAAGACATGGCAGTCCAAATATTTCCAAATGATGTGAAT 720
OY 721 ACCACTCTGACCTAGCTATCTATATGAAGATTAATTAATGAGCAAGAGAGAGAGAG 780
DB 721 ACCACTCTGACCTAGCTATCTATATGAAGATTAATTAATGAGCAAGAGAGAGAGAG 780
OY 781 TATGGTCTGATATGATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGGTCTGATATGATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
OY 841 CATGAGCAAAAAAG 900
DB 841 CATGAGCAAAAAAG 900

OY 901 CTGATAGATATGAG 960
DB 901 CTGATAGATATGAG 960
OY 961 GTGAGCCTTCTACTTGAAG 1020
DB 961 GTGAGCCTTCTACTTGAAG 1020
OY 1021 GCCAGAGATATGCTGTTCTGATCATCATGATTAATTTGCCAGTTACTTTTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTGATCATCATGATTAATTTGCCAGTTACTTTTGACTAC 1080
OY 1081 AAG 1140
DB 1081 AAG 1140
OY 1141 CTGACATCAG 1200
DB 1141 CTGACATCAG 1200
OY 1201 ATGCTCAAG 1260
DB 1201 ATGCTCAAG 1260
OY 1261 AAGCATGAAGATTAATGATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 AAGCATGAAGATTAATGATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
OY 1321 AATGATGAATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGATGAATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
OY 1381 CCTGACAAAG 1440
DB 1381 CCTGACAAAG 1440
OY 1441 AAACAGATGCAAAATACCTCTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AAACAGATGCAAAATACCTCTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
OY 1501 TCAG 1560
DB 1501 TCAG 1560
OY 1561 TTTATGCTATGCAAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 TTTATGCTATGCAAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
OY 1621 CTGACTAATGAGTCCAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 CTGACTAATGAGTCCAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
OY 1681 AGAAGACCTGAAAGCCAG 1740
DB 1681 AGAAGACCTGAAAGCCAG 1740
OY 1741 CAAAATGATACCTGAG 1800
DB 1741 CAAAATGATACCTGAG 1800
OY 1801 ATTCTGATTCATGAAG 1860
DB 1801 ATTCTGATTCATGAAG 1860
OY 1861 CTTAGTTGTAAG 1920
DB 1861 CTTAGTTGTAAG 1920
OY 1921 GCCATGCTAAG 1980
DB 1921 GCCATGCTAAG 1980

QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 13

US-09-605-783A-374
; Sequence 374, Application US/09605783A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,783A
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-783A-374

Query Match 100.0%; Score 2000; DB 23; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGCTC 60
Db 1 ATGGTGGTGAAGTGTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGCGGGGACATCTGAGACACAGACAGACTCTGCTATGAAGACACTGAGGCAAG 180
Db 121 AGCAAGCGGGGACATCTGAGACACAGACAGACTCTGCTATGAAGACACTGAGGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCCGCTGCTCCCTGCTGTCAGAGGGGAGTGGCAAGAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCTGCCGCTGCTCCCTGCTGTCAGAGGGGAGTGGCAAGAGCAAGCTG 240
QY 241 GGGCTTCTGGAGACACAGAGACTCTGCTATGAAGACACTGAGAACAGATGGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGAGACTCTGCTATGAAGACACTGAGAACAGATGGGCAAG 300
QY 301 TGGTGGTGGCAGCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGATGGGCTTGG 360
Db 301 TGGTGGTGGCAGCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGATGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCAAGTCCGCTGAGAGAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCAAGTCCGCTGAGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480

Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGACACTGACGTGAACAGAGACAGCAAGAGAGAGTGTCTACATCTGACC 540
Db 481 CTCAGGACACTGACGTGAACAGAGACAGCAAGAGAGAGTGTGTCTACATCTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGATGTCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGACAGCTGTGATTAAGGGCCGTCACATGACAGAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGACAGCTGTGATTAAGGGCCGTCACATGACAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGACACTAGCTATCTATTAATGAAGATTAATTAATGCGCAAGACCTGCTTA 780
Db 721 ACCACTGACACTAGCTATCTATTAATGAAGATTAATTAATGCGCAAGACCTGCTTA 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAGATGGCCCTCACACACCTTACTGCTGA 840
Db 781 TATGCTGTGATATGCAATCAAAAAACAGATGGCCCTCACACACCTTACTGCTGA 840
QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGAGCAATTAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGAGCAATTAATGCA 900
QY 901 CTGATAGATATGGAAGAGAGCTGCTCATCTGCTGATGTTGATGATGCAAGATTA 960
Db 901 CTGATAGATATGGAAGAGAGCTGCTCATCTGCTGATGTTGATGATGCAAGATTA 960
QY 961 GTGAGCCTTCTACTTGAACAAATATGATGATCTCTCAAGATCTATCTGAGACAGCG 1020
Db 961 GTGAGCCTTCTACTTGAACAAATATGATGATCTCTCAAGATCTATCTGAGACAGCG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTCCAGTTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATTCAGAGAGAGTCAAAAGTTCAAAGGCAAGTGAATTAATGACCCAGAGAAA 1200
Db 1141 CTGACATTCAGAGAGAGTCAAAAGTTCAAAGGCAAGTGAATTAATGACCCAGAGAAA 1200
QY 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATAGAGAGTGAAGAAAGATGAAG 1260
Db 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATAGAGAGTGAAGAAAGATGAAG 1260
QY 1261 AAGCATGAATTAATTAATGATGATTAAGTAACTGCTGAAACCTGACTTAATGCTGCTG 1320
Db 1261 AAGCATGAATTAATTAATGATGATTAAGTAACTGCTGAAACCTGACTTAATGCTGCTG 1320
QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAAGAACCTGGAATTAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAAGAACCTGGAATTAATTT 1380
QY 1381 CCTGACAAAGCAAGTGAAGAGTATCAAGATTTGCGAATTAATTTGCTGACTACAAAAGAA 1440
Db 1381 CCTGACAAAGCAAGTGAAGAGTATCAAGATTTGCGAATTAATTTGCTGACTACAAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAACCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAACCTGACA 1500
QY 1501 TCAGAGGAGAGAGTACAAAGGCTTGAAGGCAAGTGAATTAATGAGAGAGCTTGAATTAAT 1560
Db 1501 TCAGAGGAGAGAGTACAAAGGCTTGAAGGCAAGTGAATTAATGAGAGAGCTTGAATTAAT 1560

```
OY 1561 TTTATGCTATCGAAGAAATGAAGACAGAGAGTACTCATGTGGATTCCAGAAAC 1620
    |||
Db 1561 TTTATGCTATCGAAGAAATGAAGACAGAGAGTACTCATGTGGATTCCAGAAAC 1620
OY 1621 CTGACTAATGTCGCCACTGCTGGCAATGTGATGATTAATTCCTCAAGAAAGAC 1680
    |||
Db 1621 CTGACTAATGTCGCCACTGCTGGCAATGTGATGATTAATTCCTCAAGAAAGAC 1680
OY 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAATATACAGTACGAA 1740
    |||
Db 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAATATACAGTACGAA 1740
OY 1741 CAAATGATACCTAGAGCAATTTGTGAGAAAGCAAGACGATATTAACAGTGAAG 1800
    |||
Db 1741 CAAATGATACCTAGAGCAATTTGTGAGAAAGCAAGACGATATTAACAGTGAAG 1800
OY 1801 ATCTGATTCATGAAGAAAGCAGATAGAAGTGTGAAAAATGAATTCAGCTTTCT 1860
    |||
Db 1801 ATCTGATTCATGAAGAAAGCAGATAGAAGTGTGAAAAATGAATTCAGCTTTCT 1860
OY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAATAATGTCGCGGGAAGAAAT 1920
    |||
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAATAATGTCGCGGGAAGAAAT 1920
OY 1921 GCCATGCTAGAGCTGAGCTAGACACAAATGAACATCAGAGCGCTAAAAA 1980
    |||
Db 1921 GCCATGCTAGAGCTGAGCTAGACACAAATGAACATCAGAGCGCTAAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAA 2000
    |||
Db 1981 AAAAAAAAAAAAAAAAAA 2000
```

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RESULT 14
US-09-636-215-374
; Sequence 374, Application US/09636215
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-374
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```
Query Match 100.0%; Score 2000; DB 24; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 ATGGTGTTGAGTTGATTCATGCGGCTGCTTCTGTGTAAGAACCATTTGGTCTC 60
```

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Db 1 ATGGTGTTGAGTTGATTCATGCGGCTGCTTCTGTGTAAGAACCATTTGGTCTC 60
    |||
OY 61 AGAGCAGATGAGCAATGTGTGTCCTGCTTCCCTGTCAGAGGAGCGGCAAG 120
    |||
Db 61 AGAGCAGATGAGCAATGTGTGTCCTGCTTCCCTGTCAGAGGAGCGGCAAG 120
OY 121 AGCAACGTGGGCACTTCTGAGAACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
    |||
Db 121 AGCAACGTGGGCACTTCTGAGAACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
OY 181 ATGGGCAATGTGTGCGCCACTGCTTCCCTGTCAGAGGAGAGTGGCAAGCAAGCTG 240
    |||
Db 181 ATGGGCAATGTGTGCGCCACTGCTTCCCTGTCAGAGGAGAGTGGCAAGCAAGCTG 240
OY 241 GGGGCTTCTGAGACACAGCAGCACTCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
    |||
Db 241 GGGGCTTCTGAGACACAGCAGCACTCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
OY 301 TGGTGCTGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCGCTTG 360
    |||
Db 301 TGGTGCTGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCGCTTG 360
OY 361 GGAGACTAGATGACAGTCTTCATGAGAGCCAGGTACAGGTCCTGGAGAAATCTG 420
    |||
Db 361 GGAGACTAGATGACAGTCTTCATGAGAGCCAGGTACAGGTCCTGGAGAAATCTG 420
OY 421 GACAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCAG 480
    |||
Db 421 GACAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCAG 480
OY 481 CTCAGGAGACTGAGCTGTAAGCAAGAGCAAGCAAGAGGAGCTCTACATCTGGCC 540
    |||
Db 481 CTCAGGAGACTGAGCTGTAAGCAAGAGCAAGCAAGAGGAGCTCTACATCTGGCC 540
OY 541 TCTGCCAATGGGAATTCAGAAATGTAATCTCTGCTGAGAGAGATGTCAACTTAAT 600
    |||
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATCTCTGCTGAGAGAGATGTCAACTTAAT 600
OY 601 GTCTTGTGACACAAAAGAGGACAGCTCTGATTAAGGCGCTACATCCAGCAAGTGA 660
    |||
Db 601 GTCTTGTGACACAAAAGAGGACAGCTCTGATTAAGGCGCTACATCCAGCAAGTGA 660
OY 661 TGTGCTTAATGTGTGTGGAACATGGCAGTCCAAATATTCACATGATGATGAAT 720
    |||
Db 661 TGTGCTTAATGTGTGTGGAACATGGCAGTCCAAATATTCACATGATGATGAAT 720
OY 721 ACCACTGTCACCTACCTATCTATATGAAGATTAATTAATGAGCCAAAGCAGCTCTTA 780
    |||
Db 721 ACCACTGTCACCTACCTATCTATATGAAGATTAATTAATGAGCCAAAGCAGCTCTTA 780
OY 781 TATGTGTGATATGATTAATCAAAAAAACAAGATGGCTCACACACTGTTACTGGTGA 840
    |||
Db 781 TATGTGTGATATGATTAATCAAAAAAACAAGATGGCTCACACACTGTTACTGGTGA 840
OY 841 CATGAGCAAAAACAGCAAGCTGGAATTTTAATCAAAAAAAGCAATTAATGA 900
    |||
Db 841 CATGAGCAAAAACAGCAAGCTGGAATTTTAATCAAAAAAAGCAATTAATGA 900
OY 901 CTGAGATAGATGAGAGAGCTGCTCATACTGCTGATGTTGTGATCAGCAAGTATA 960
    |||
Db 901 CTGAGATAGATGAGAGAGCTGCTCATACTGCTGATGTTGTGATCAGCAAGTATA 960
OY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
    |||
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
OY 1021 GCCAGAGATATGCTTCTATGATCATCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
    |||
Db 1021 GCCAGAGATATGCTTCTATGATCATCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
OY 1081 AAGGAAACAGATGCTAAATAATCTCTTGAAGAACAGAAATCCAAAGACTTAAG 1140
    |||
```

Db	1081	AAACAAAACAGATGCTTAAATTAATCTCTTCTGAAACAGCAATTCACAGAACAGACTTAAG	11440
Qy	1141	CTGACATCAGAGGAAGAGTGTACAAAGTTCAAAGGCAGTGAATAATGACCACGAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGAGTGTACAAAGTTCAAAGGCAGTGAATAATGACCACGAGAGAA	1200
Qy	1201	ATGCTCTAAGACCCAGAAATTAATTAAGATGATGATAGAGAGTGTGAAGAAGAAATGAAG	1260
Db	1201	ATGCTCTAAGACCCAGAAATTAATTAAGATGATGATAGAGAGTGTGAAGAAGAAATGAAG	1260
Qy	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAACTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAACTGACTAATGTGTCACTGTGGC	1320
Qy	1321	AATGCTGTATATGATTAATTCCTCAAAGAGAGCAGAACCCGTGAATAATGACATATT	1380
Db	1321	AATGCTGTATATGATTAATTCCTCAAAGAGAGCAGAACCCGTGAATAATGACATATT	1380
Qy	1381	CCTGACACAGAAAGTGAAGATATCAGAAATTTGGGAATTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGATATCAGAAATTTGGGAATTAGTTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATTAATCTTCTGTGAACACCAACCCAGAACAGACTTAAACTGACA	1500
Db	1441	AAACAGATGCCAAATTAATCTTCTGTGAACACCAACCCAGAACAGACTTAAACTGACA	1500
Qy	1501	TCAGAGGAAGAGTGTACAAAGGCTTGAAGGCGAGTGAATAATGGCCAGACCTAGAAAT	1560
Db	1501	TCAGAGGAAGAGTGTACAAAGGCTTGAAGGCGAGTGAATAATGGCCAGACCTAGAAAT	1560
Qy	1561	TTTATGGCTATCCAGAAATTAAGAAAGCAGCAGGAATCTCATGTGGATTCCCGAGAAAC	1620
Db	1561	TTTATGGCTATCCAGAAATTAAGAAAGCAGCAGGAATCTCATGTGGATTCCCGAGAAAC	1620
Qy	1621	CTGACTAATGGTGCCACTGCTGCGCATGGTGAATGATTAATTCCTCCAAGAGAGAGC	1680
Db	1621	CTGACTAATGGTGCCACTGCTGCGCATGGTGAATGATTAATTCCTCCAAGAGAGAGC	1680
Qy	1681	AGAAACCTTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTGAGAA	1740
Db	1681	AGAAACCTTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTGAGAA	1740
Qy	1741	CAAAATGATCTCAGAAAGCAATTTGTGAAGAACGAACACATGGAATTTACACAGATGAG	1800
Db	1741	CAAAATGATCTCAGAAAGCAATTTGTGAAGAACGAACACATGGAATTTACACAGATGAG	1800
Qy	1801	ATTCGTATTCATGAAGAAAGCAGATAGAGTGGTTGAATAATGAATTCGACCTTCT	1860
Db	1801	ATTCGTATTCATGAAGAAAGCAGATAGAGTGGTTGAATAATGAATTCGACCTTCT	1860
Qy	1861	CTTAGTGTATGAAGAAAGAAAGCATCTGTCATGAAATAATAGTACTGCGGGAAGAAATT	1920
Db	1861	CTTAGTGTATGAAGAAAGAAAGCATCTGTCATGAAATAATAGTACTGCGGGAAGAAATT	1920
Qy	1921	GCCATGCTTAAGACTGAGACTAGACACAAATGAACAATCAAGAGCCAGACTAAAAAATGAA	1980
Db	1921	GCCATGCTTAAGACTGAGACTAGACACAAATGAACAATCAAGAGCCAGACTAAAAAATGAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 15			
US-09-651-236-374			
; Sequence 374, Application US/09651236			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yugu			
; APPLICANT: Henderson, Robert A.			

	APPLICANT:	Fanger, Michael D.
	APPLICANT:	Rafter, Gary R.
	APPLICANT:	Reiter, Marc W.
	APPLICANT:	Stolk, John A.
	APPLICANT:	Day, Craig H.
	APPLICANT:	Vedvick, Thomas S.
	APPLICANT:	Carter, Darlick
	APPLICANT:	Li, Samuel
	APPLICANT:	Wang, Aljun
	APPLICANT:	Skelky, Yasir A.W.
	APPLICANT:	Hepfer, William
	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE THERAPY AND
	TITLE OF INVENTION:	DIAGNOSIS OF PROSTATE CANCER
	FILE REFERENCE:	210121.42718C18
	CURRENT APPLICATION NUMBER:	US/09/651.236
	CURRENT FILING DATE:	2000-08-29
	NUMBER OF SEQ ID NOS:	865
	SOFTWARE:	FastSeq for Windows Version 3.0
	SEQ ID NO 374	
	LENGTH:	2000
	TYPE:	DNA
	ORGANISM:	Homo sapien
	US-09-651-236-374	
	Query Match	100.0%; Score 2000; DB 25; Length 2000;
	Best Local Similarity	100.0%; Pred. No. 6.6e-226;
	Matches 2000; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1	ATGGGTTTGAGGTTCATTCATGCCGGCTCCCTTCTGTGAAGAAGCATTTGGTCTC 60
Db	1	ATGGGTTTGAGGTTCATTCATGCCGGCTCCCTTCTGTGAAGAAGCATTTGGTCTC 60
Oy	61	AGGACCAAGATTGGCGAAGTGTGCTGCCGTTGCTTCCCCTGCTGCAGGAGAGCGGCAAG 120
Db	61	AGGACCAAGATTGGCGAAGTGTGCTGCCGTTGCTTCCCCTGCTGCAGGAGAGCGGCAAG 120
Oy	121	AGCAACGTGGGACACTTCTTGAGAACCCAGCACACTCTGCTATGAACAACACTCAGAGCAAG 180
Db	121	AGCAACGTGGGACACTTCTTGAGAACCCAGCACACTCTGCTATGAACAACACTCAGAGCAAG 180
Oy	181	ATGGCAAGTGGTGCGCGCACACTGCTTCCCTCTCAGGGGGAGTGGCAAGAGCAAGCTG 240
Db	181	ATGGCAAGTGGTGCGCGCACACTGCTTCCCTCTCAGGGGGAGTGGCAAGAGCAAGCTG 240
Oy	241	GCGCCTTCTGAGACCAGCAGCAGCTCTGCTATGAAGAACTCAGAACATGTGGCAAG 300
Db	241	GCGCCTTCTGAGACCAGCAGCAGCTCTGCTATGAAGAACTCAGAACATGTGGCAAG 300
Oy	301	TGGTCTCTCCACTGCTTCCCCCTGCTGCAAGGGGGAGCGGCAAGAGGAAGTGGGCGCTTGG 360
Db	301	TGGTCTCTCCACTGCTTCCCCCTGCTGCAAGGGGGAGCGGCAAGAGGAAGTGGGCGCTTGG 360
Oy	361	GGAGACTACGATGACAGTGCCTTCATVGAGGCCAGGTAACACGTCCTCGTGAGAGATCTG 420
Db	361	GGAGACTACGATGACAGTGCCTTCATVGAGGCCAGGTAACACGTCCTCGTGAGAGATCTG 420
Oy	421	GACAACTCCACAGAGTGCCTGGGGGGTAAAGTCCCAAGAAAGATCTCATTCGTCATG 480
Db	421	GACAACTCCACAGAGTGCCTGGGGGGTAAAGTCCCAAGAAAGATCTCATTCGTCATG 480
Oy	481	CTCAGGGACACTGACGTACACAAAGAGACAAAGCAAAAAGAGAGACTCTCTACATCTGGCC 540
Db	481	CTCAGGGACACTGACGTACACAAAGAGACAAAGCAAAAAGAGAGACTCTCTACATCTGGCC 540
Oy	541	TCTGCCAATGGGAATTCAGAAGTAATAAACTCTCTGCTGAGACAGCATGTCAACTTAAT 600
Db	541	TCTGCCAATGGGAATTCAGAAGTAATAAACTCTCTGCTGAGACAGCATGTCAACTTAAT 600
Oy	601	GTCCTTGACACAAAAAGAGACACTCTGATTAAGGCGGTACATGTCAGAGAAATGAA 660
Db	601	GTCCTTGACACAAAAAGAGACACTCTGATTAAGGCGGTACATGTCAGAGAAATGAA 660
Oy	661	TGTGGTTAATGTGCTGGAACATGGCACTGATCCAAATATTCCAGATGATGTAGAAAT 720

Oy	241	GGCCCTTCTGGAGCCACGACGACTCGTGGTATGAAGACACTCAGAACAAAGTGGGCAAG	300
Db	241	GGCCCTTCTGGAGCCACGACGACTCGTGGTATGAAGACACTCAGAACAAAGTGGGCAAG	300
Oy	301	TGtGTGtCCACtTbCTtCCCTtGCTGCTCAGGGGGAGCGGCAAGAGCAAGTGGGCTtTGG	360
Db	301	TGtGTGtCCACtTbCTtCCCTtGCTGCTCAGGGGGAGCGGCAAGAGCAAGTGGGCTtTGG	360
Oy	361	GGAGACTACGATGACACTGCTTCATGAGAGCCAGGTACCACGTCCGTGGAGAGATCTG	420
Db	361	GGAGACTACGATGACACTGCTTCATGAGAGCCAGGTACCACGTCCGTGGAGAGATCTG	420
Oy	421	GACAAAGTCCACAGAGTGGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCTAG	480
Db	421	GACAAAGTCCACAGAGTGGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCTAG	480
Oy	481	CTCAGGACACTGACGTGAACAAGAGGACAAAGCAAAAGAGACtGCTACATCTGGCC	540
Db	481	CTCAGGAGCACTGACGTGAACAAGAGGACAAAGCAAAAGAGACtGCTACATCTGGCC	540
Oy	541	TCTGCCAATGGGAATTGAGAGTAAAGTAAACCTCTGTCGACAGACGATGTCACCTTAAT	600
Db	541	TCTGCCAATGGGAATTGAGAGTAAAGTAAACCTCTGTCGACAGACGATGTCACCTTAAT	600
Oy	601	GTCCTTGCAACAAAAGAGACAGCTGATTAAGAGCCGTACATATGCGAGGAAGATAA	660
Db	601	GTCCTTGCAACAAAAGAGAGACAGCTGATTAAGAGCCGTACATATGCGAGGAAGATAA	660
Oy	661	TGTGCGTAAATGTTGCTGCGAACAATGGCACTGATCCAAATATCCAGATAGATGAAT	720
Db	661	TGTGCGTAAATGTTGCTGCGAACAATGGCACTGATCCAAATATTCAGATAGATGAAT	720
Oy	721	ACCACCTGCACTACGCTATCTTAATGAAGATAAATTATGCGCAAAAGCACTGCTTTA	780
Db	721	ACCACCTGCACTACGCTATCTTAATGAAGATAAATTATGCGCAAAAGCACTGCTTTA	780
Oy	781	TATGTGCTGATATGCAATGAAAAAACAAGCATGGGCTCACACCACTGTTACTGTGGTGA	840
Db	781	TATGTGCTGATATGCAATGAAAAAACAAGCATGGGCTCACACCACTGTTACTGTGGTGA	840
Oy	841	CATGAGCAAAAAACAGCAAGTCTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTCTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAATGCA	900
Oy	901	CTGGATAGATATGGAGAGACTGCTCTCATCTCTGATCTGTATGTTGTGATCAGCAATGA	960
Db	901	CTGGATAGATATGGAGAGACTGCTCTCATCTCTGATCTGTATGTTGTGATCAGCAATGA	960
Oy	961	GTCAGCCTTACTGTGAGCAAAATATTGATGATCTTCCAGAGATCTATCTGGAGACAGC	1020
Db	961	GTCAGCCTTACTGTGAGCAAAATATTGATGATCTTCCAGAGATCTATCTGGAGACAGC	1020
Oy	1021	GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGGCAGTACTTCTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGGCAGTACTTCTGACATAC	1080
Oy	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAAACAAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAAACAAGACTTAAAG	1140
Oy	1141	CTGACATCAGAGGAAGGTACAAAGGTTCAAGAGCGAGTGAAGAAATGCGACAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGGTACAAAGGTTCAAGAGCGAGTGAAGAAATGCGACAGAGAA	1200
Oy	1201	ATGCTCAAGAACCAAGAAATTAATTAAGATGGGATAGAGAGGTTGAAGAAATTAAG	1260
Db	1201	ATGCTCAAGAACCAAGAAATTAATTAAGATGGGATAGAGAGGTTGAAGAAATTAAG	1260
Oy	1261	AAGCATAAAGTAAATATGTGGGATTAATGAAGAAACCTGACTAAATGCTGCTGCTGGC	1320
Db	1261	AAGCATAAAGTAAATATGTGGGATTAATGAAGAAACCTGACTAAATGCTGCTGCTGGC	1320
Oy	1321	AATGCTGATTAATGATTAATTTCTCAAGAGAGAGCAGAACCTGAAATATGACCAATTT	1380

Db	1321	AAATGCTATATATGGATTAAATTCCTCAAGAGAGAGAGACCCCTGAAATATACACAAATTT	1380
QY	1381	CCTGACACAGAAAGTGAAGATATCAACAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGATATCAACAGAAATTTGCAATTAAGTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTCTCTGTGAAAACACCAACCCAGAACCAAGACTTAAACCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTCTGTGAAAACACCAACCCAGAACCAAGACTTAAACCTGACA	1500
QY	1501	TCAGAGAGAAAGTACACAAAGGCTTGAGGGCAGTGAATAATGGCCACCCAGACCTAGAAAT	1560
Db	1501	TCAGAGAGAAAGTACACAAAGCTTGAGGGCAGTGAATAATGGCCACCCAGACCTAGAAAT	1560
QY	1561	TTTATGCGCTATCGAAGAAATGAAGAAGCACAGGAAGTACTCATGTGCGATTTCCAGAAAAC	1620
Db	1561	TTTATGCGCTATCGAAGAAATGAAGAAGCACAGGAAGTACTCATGTGCGATTTCCAGAAAAC	1620
QY	1621	CTGACTAATGGTGGCCACTGCTGGCCAAATGGTGAATGATGATTAATTCCTCCAGAAAGAGC	1680
Db	1621	CTGACTAATGGTGGCCACTGCTGGCCAAATGGTGAATGATGATTAATTCCTCCAGAAAGAGC	1680
QY	1681	AGAACACCTGAAAGCAGCAATTTCTCGACACTGGAATGAAGATATCACAGTAGAGAA	1740
Db	1681	AGAACACCTGAAAGCAGCAATTTCTCGACACTGGAATGAAGATATCACAGTAGAGAA	1740
QY	1741	CAAAATGATACCTAGAAAGCAATTTTGTGGAAGAACAGAACACTGGAAATTTACACAGATGAG	1800
Db	1741	CAAAATGATACCTAGAAAGCAATTTTGTGGAAGAACAGAACACTGGAAATTTACACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAGAAAGCAATGAGAAGTGGTTGAAAAAATGAATTCGACCTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGCAATGAGAAGTGGTTGAAAAAATGAATTCGACCTTCT	1860
QY	1861	CTTAGTGTATGAAGAAAGAAAGACATCTTGCAATGAAAATAGTACCTTCGGGGAAGAAAT	1920
Db	1861	CTTAGTGTATGAAGAAAGAAAGACATCTTGCAATGAAAATAGTACCTTCGGGGAAGAAAT	1920
QY	1921	GGCATGCTAAGACTGGAGCTAGACACACATGAAGAAACATCAGAGCCAGCTAAAAA	1980
Db	1921	GGCATGCTAAGACTGGAGCTAGACACACATGAAGAAACATCAGAGCCAGCTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

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RESULT 17
US-09-679-272-374
; Sequence 374, Application US/09679272
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven G.
; APPLICANT: Cheever, Martin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534
; CURRENT APPLICATION NUMBER: US/09/679, 272
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 476
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-679-272-374

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Query Match	100.0%;	Score 2000;	DB 26;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 6.6e-226;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTATTCATGCCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTATTCATGCCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCAAGTGTGCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAG 180
DB 121 AGCAAGTGGGCAAGTGTGCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCAAGTGTGCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAG 240
DB 181 ATGGGCAAGTGTGCGGCAAGTGTGCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAG 240
QY 241 GCGGCTTGTGAGACGACGAGCTCTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300
DB 241 GCGGCTTGTGAGACGACGAGCTCTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300
QY 301 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB 301 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
QY 361 GGAGACTAGATGACAGTGTGCTTCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAG 420
DB 361 GGAGACTAGATGACAGTGTGCTTCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAG 420
QY 421 GACAAAGCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAAAGCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACAGTGTGCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAGTGTGCAAG 540
DB 481 CTCAGGAGACAGTGTGCAAGGAGCGGCAAGTGTGCAAGGAGCGGCAAGTGTGCAAG 540
QY 541 TCTGCCAATGGGAAATTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TCTGCCAATGGGAAATTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTCCTTGACACAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 GTCCTTGACACAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 TGTGGTGAATGTGTGCTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGT 720
DB 661 TGTGGTGAATGTGTGCTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGT 720
QY 721 ACCACTGTGCACTAGCTATCTATGAAGTGAATTAATGAGCAAGTGTGCACTGCTTA 780
DB 721 ACCACTGTGCACTAGCTATCTATGAAGTGAATTAATGAGCAAGTGTGCACTGCTTA 780
QY 781 TATGTGCTGATATGAATCAAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 TATGTGCTGATATGAATCAAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 CATGAGCAAAAAGAGAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 900
DB 841 CATGAGCAAAAAGAGAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 900
QY 901 CTGATAGATATGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 CTGATAGATATGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 GTCAGCCTTCTAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGT 1020
DB 961 GTCAGCCTTCTAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGT 1020
QY 1021 GCCAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 GCCAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 AAGAAAAACAGATGTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140

DB 1081 AAGAAAAACAGATGTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGCTCACAAGGTTCAAAAGGCAAGTGAATTAATGAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAGAGCTCACAAGGTTCAAAAGGCAAGTGAATTAATGAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGTGAATTAATGAGTGTGATAGAGAGTGAAGCAAGTGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGTGAATTAATGAGTGTGATAGAGAGTGAAGCAAGTGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGAGTGTGATAGAGAGTGAAGCAAGTGAAGTGAAG 1320
DB 1261 AAGCATGAAGATTAATGATGAGTGTGATAGAGAGTGAAGCAAGTGAAGTGAAG 1320
QY 1321 AATGTGATATGATTAATCTTCAAGAGAGAGCAAGCACTGGAATTAATGCAATTT 1380
DB 1321 AATGTGATATGATTAATCTTCAAGAGAGAGCAAGCACTGGAATTAATGCAATTT 1380
QY 1381 CCGTGAACAGAGAGTGAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 CCGTGAACAGAGAGTGAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AAGCAGATGCCAAATTAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAGTGA 1500
DB 1441 AAGCAGATGCCAAATTAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAGTGA 1500
QY 1501 TCAGAGAGAGTCAACAAAGCTTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1560
DB 1501 TCAGAGAGAGTCAACAAAGCTTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1560
QY 1561 TTTATGGCTATGAAGAAATGAAGAGCAAGGAGTCAATGCTGATGCTGATGCTGATG 1620
DB 1561 TTTATGGCTATGAAGAAATGAAGAGCAAGGAGTCAATGCTGATGCTGATGCTGATG 1620
QY 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 AGAACCTGTAAGAGAGAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCA 1740
DB 1681 AGAACCTGTAAGAGAGAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCA 1740
QY 1741 CAAATGATAGTCAAGAGAAATTTGTGAAGAGCAAGTGAATTAATGATGATGATG 1800
DB 1741 CAAATGATAGTCAAGAGAAATTTGTGAAGAGCAAGTGAATTAATGATGATGATG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATGAAGTGTGGAAGAAATGAATTCGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATGAAGTGTGGAAGAAATGAATTCGAGCTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAGATTCGATGAAATTAATGATGATGATGATGATGATGAT 1920
DB 1861 CTTAGTGTGAAGAAAGAGATTCGATGAAATTAATGATGATGATGATGATGATGAT 1920
QY 1921 GCCATGCTAAGAGTGAAGTGAAGCAATGCAAGCAAGTGAAGCAAGTGAAGCAAG 1980
DB 1921 GCCATGCTAAGAGTGAAGTGAAGCAATGCAAGCAAGTGAAGCAAGTGAAGCAAG 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 18
US-09-679-426-374
; Sequence 374, Application US/09679426
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: us/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-374

Query Match 100.0%; Score 2000; DB 26; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTTAGAGTTGATTCATGCCGCTGCTTCTGTGAAGAACCTTTGGTCTC 60
Db 1 ATGTGGTTAGAGTTGATTCATGCCGCTGCTTCTGTGAAGAACCTTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCTTCTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCTTCTGAGACACGACACTCTCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCGTTGG 360
Db 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCGTTGG 360
QY 361 GAGAGTACAGTACAGTGGCTTCTATGAGACCCAGTACACAGTGGTGGTGGTGGTGG 420
Db 361 GAGAGTACAGTACAGTGGCTTCTATGAGACCCAGTACACAGTGGTGGTGGTGGTGG 420
QY 421 GACAAGTTCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 421 GACAAGTTCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
QY 481 CTCAGGAGACAGTACAGTGAAGAGAGAGAGAGAGAGAGAGAGTGGTGGTGGTGGTGG 540
Db 481 CTCAGGAGACAGTACAGTGAAGAGAGAGAGAGAGAGAGAGAGTGGTGGTGGTGGTGG 540
QY 541 TCTGGCAATGGGAATTAAGAAGTAAATCTGCTGGACAGAGATGCAACTTAAT 600
Db 541 TCTGGCAATGGGAATTAAGAAGTAAATCTGCTGGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAG 660
Db 601 GTCTTGAACAACAAAG 660

QY 661 TGGCGTTAAATGTTGGTGAACATGCGATGATCCAAATATTCAGATGAGATGAAT 720
Db 661 TGGCGTTAAATGTTGGTGAACATGCGATGATCCAAATATTCAGATGAGATGAAT 720
QY 721 ACCACTGTGACATGCTATCTATTAATGAATTAATTAATGAATGAATGAATGAAT 780
Db 721 ACCACTGTGACATGCTATCTATTAATGAATTAATTAATGAATGAATGAATGAAT 780
QY 781 TATGTCCTGATATGATCAATCAAAAAACAGATGGCTCACACACAGTTCATCTGTGTA 840
Db 781 TATGTCCTGATATGATCAATCAAAAAACAGATGGCTCACACACAGTTCATCTGTGTA 840
QY 841 CATGAGCAAAAAACAGATGCTGTAATTTTAAATCAAGAAAAACGAATTAATGA 900
Db 841 CATGAGCAAAAAACAGATGCTGTAATTTTAAATCAAGAAAAACGAATTTAAATGA 900
QY 901 CTGATATGATATGAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
Db 901 CTGATATGATATGAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
QY 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCTAATTTGCCAGTTACTTGTACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCTAATTTGCCAGTTACTTGTACTAC 1080
QY 1081 AAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Db 1081 AAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 CTGACATCAGAGAGAGTGCACAAAGTTCAAAGAGTGAATATACCCAGAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGTTCAAAGAGTGAATATACCCAGAGAGAAA 1200
QY 1201 ATGTCTCAAGACCAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 ATGTCTCAAGACCAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAGCATGAAGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGATATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGATATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CTTGACACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1381 CTTGACACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 AAACAGATGCAAAATATCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAACAGATGCAAAATATCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TCAGAGAGAGAGTGCACAAAGGCTTGGAGGAGAGTGAATGGCCAGCAGAGAGTGAAT 1560
Db 1501 TCAGAGAGAGAGTGCACAAAGGCTTGGAGGAGAGTGAATGGCCAGCAGAGAGTGAAT 1560
QY 1561 TTTATGCTATTCGAAGATTAAGAGAGACAGAGAGTACTATGTCGATTCAGAGAAAC 1620
Db 1561 TTTATGCTATTCGAAGATTAAGAGAGACAGAGAGTACTATGTCGATTCAGAGAAAC 1620
QY 1621 CTGACTAATGCTGCACTGCTGGCAAGTGGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 CTGACTAATGCTGCACTGCTGGCAAGTGGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 AGAAGACCTGAAG 1740
Db 1681 AGAAGACCTGAAG 1740
QY 1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800

Oy	1321	AAAGGTGTAATGATTAATTTCTTCCAAAGSAAAGACAGAACACCTGAAATATGCAATTT	1380
Oy	1321	AAAGGTGTAATGATTAATTTCTTCCAAAGSAAAGACAGAACACCTGAAATATGCAATTT	1380
Db	1321	AAATGTGTAATGATTAATTTCTTCCAAAGSAAAGACAGAACACCTGAAATATGCAATTT	1380
Oy	1381	CCTGACCAACGAAAGTGAAGAGATATCACAGATTTTGGCAATTAAGTTCTGACTACAAAGA	1440
Db	1381	CCTGACCAACGAAAGTGAAGAGATATCACAGATTTTGGCAATTAAGTTCTGACTACAAAGA	1440
Oy	1441	AAACAGATGCCAAATATCTCTTTGTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTTGTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
Oy	1501	TCACAGGAAGAGTTCACAAAGGCTTGAGGCGACATGGAATATGGCCAGCCAGAGCTAGAAAT	1560
Db	1501	TCACAGGAAGAGTTCACAAAGGCTTGAGGCGACATGGAATATGGCCAGCCAGAGCTAGAAAT	1560
Oy	1561	TTTATGGCTATTCGAAGAAATGAAGAACAGCAAGCAATCATGTGGAGTTCCCAAGAAAC	1620
Db	1561	TTTATGGCTATTCGAAGAAATGAAGAACAGCAAGCAATCATGTGGAGTTCCCAAGAAAC	1620
Oy	1621	CTGACTAATGTGTCCACTGCTGGCAATGTGTGATGATGATTAATTCCTCCAAAGAAAGAC	1680
Db	1621	CTGACTAATGTGTCCACTGCTGGCAATGTGTGATGATGATTAATTCCTCCAAAGAAAGAC	1680
Oy	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAGATATCACAGTGCAGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAGATATCACAGTGCAGAA	1740
Oy	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACAGACACAGGAATATACACAGATAG	1800
Db	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACAGACACAGGAATATATACACAGATAG	1800
Oy	1801	ATTCGTGATTCATGAAAGAAAGACAGATAGAAGTGGTTGAAAAAAATGAAATCTGACGTTCT	1860
Db	1801	ATTCGTGATTCATGAAAGAAAGACAGATAGAAGTGGTTGAAAAAAATGAAATCTGACGTTCT	1860
Oy	1861	CTTGACTGTGAAGAAAGAAAGACATCTTGTCATGAAATATGATGCTGGCGAGCAAAAT	1920
Db	1861	CTTGACTGTGAAGAAAGAAAGACATCTTGTCATGAAATATGATGCTGGCGAGCAAAAT	1920
Oy	1921	GCCATGCTAAGACACGTGAGACATGACAAATGAACATCACAGCCACTAAAAAAGAAAAA	1980
Db	1921	GCCATGCTAAGACACGTGAGACATGACAAATGAACATCACAGCCACTAAAAAAGAAAAA	1980
Oy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 20			
US-09-685-166A-374			
: Sequence 374, Application US/09685166A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jiang, Yuqun.			
: APPLICANT: Henderson, Robert A.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retter, Marc W.			
: APPLICANT: Stolk, John A.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Vedyick, Thomas S.			
: APPLICANT: Carter, Darlick			
: APPLICANT: Li, Samuel			
: APPLICANT: Wang, Aijun			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Hedler, William			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
: FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
: TITLE REFERENCE: 210121.427C21			

Query Match	100.0%	Score 2000:	DB 27:	Length 2000:
Best Local Similarity	100.0%	Pred. No. 6.6e-226;		
Matches 2000:	Conservative	0;	Mismatches	0; Indels
				Gaps
				0;
<pre> ; CURRENT APPLICATION NUMBER: US/09/685,166A ; CURRENT FILING DATE: 2000-10-10 ; NUMBER OF SEQ ID NOS: 898 ; SOFTWARE: FASTSEQ for Windows Version 3.0 ; SEQ ID NO 374 ; LENGTH: 2000 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-685-166A-374 </pre>				
QY	1	ATGGTGCTTGAAGTTCATTCATGCGCGCTGCTCTTCTGTGAAGAGCCATTGCTC	60	
DB	1	ATGGTGCTTGAAGTTCATTCATGCGCGCTGCTCTTCTGTGAAGAGCCATTGCTC	60	
QY	61	AGGAGCAGATGGCGAAGTGTGCTCCGCTTCCCTGCTGCAAGGAGACGGCGAAG	120	
DB	61	AGGAGCAGATGGCGAAGTGTGCTCCGCTTCCCTGCTGCAAGGAGACGGCGAAG	120	
QY	121	ACCAACGTGGGACATTCCTGGAGACCAACGACACTGCTATGAAGACACTCGAGGACAG	180	
DB	121	ACCAACGTGGGACATTCCTGGAGACCAACGACACTGCTATGAAGACACTCGAGGACAG	180	
QY	181	ATGGGCAATGTGTCGCGCAGCTGCTTCCCTCTCTGAGGGGAGTGGCAAGACAGCTG	240	
DB	181	ATGGGCAATGTGTCGCGCAGCTGCTTCCCTCTCTGAGGGGAGTGGCAAGACAGCTG	240	
QY	241	GGCGCTTGTGAGACCAACGACGACTCTGCTATGAAGACACTCAGAAACAGATGGGCAAG	300	
DB	241	GGCGCTTGTGAGACCAACGACGACTCTGCTATGAAGACACTCAGAAACAGATGGGCAAG	300	
QY	301	TGGTGCTGCACATGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCGCTTGG	360	
DB	301	TGGTGCTGCACATGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCGCTTGG	360	
QY	361	GGAGACTACGATGACAGTCCCTTCATGTGAGGCCAGGTACACGTCGCTGGAAGATCTG	420	
DB	361	GGAGACTACGATGACAGTCCCTTCATGTGAGGCCAGGTACACGTCGCTGGAAGATCTG	420	
QY	421	GACAAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATGTCATG	480	
DB	421	GACAAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATGTCATG	480	
QY	481	CTCAGGAGACACTGACGTGAACAAGAGCAAGCAAAAGAGACATCTCTACATCTGGCC	540	
DB	481	CTCAGGAGACACTGACGTGAACAAGAGCAAGCAAAAGAGACATCTCTACATCTGGCC	540	
QY	541	TCCTGCAATGGGAATTCACAAGTAGTAAATCTCTGCTGGAAGACAGATGTCAACTTAAT	600	
DB	541	TCCTGCAATGGGAATTCACAAGTAGTAAATCTCTGCTGGAAGACAGATGTCAACTTAAT	600	
QY	601	GTCCTTGAACAAAAAGAGACAGCTCTGATAAAGGCCGTACAAATGCCAGGAAGATGA	660	
DB	601	GTCCTTGAACAAAAAGAGACAGCTCTGATAAAGGCCGTACAAATGCCAGGAAGATGA	660	
QY	661	TGTGGCTTAATTTGCTGGAACATGACACTGATCCAAATATTCGAGATGATGGAAT	720	
DB	661	TGTGGCTTAATTTGCTGGAACATGACACTGATCCAAATATTCGAGATGATGGAAT	720	
QY	721	ACCACCTGACATAGCGCTATCTATATGAGATTAATTAATGGCCAAAGCACTGCTCTTA	780	
DB	721	ACCACCTGACATAGCGCTATCTATATGAGATTAATTAATGGCCAAAGCACTGCTCTTA	780	
QY	781	TATGCTGCTGATATGCAATCAAAAAAAGACATGGCTCACAACCACTGTACTTGGTGA	840	
DB	781	TATGCTGCTGATATGCAATCAAAAAAAGACATGGCTCACAACCACTGTACTTGGTGA	840	
QY	841	CATGAGCAAAAAACAGACGTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900	
DB	841	CATGAGCAAAAAACAGACGTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900	


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Db 541 TCTGCCAATGGGAATTGAGAAGTAGTAATAACTCTGCTGGACAGACGATGTCAACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGACAGCTCTGATATAAGGCCGTACATGCTCCAGAGATGAA 660
Db 601 GTCCCTGACAAACAAAAGAGACAGCTCTGATATAAGGCCGTACATGCTCCAGAGATGAA 660
QY 661 TGTGCGTTAAATGTTGCTGGAAACATGCGACGTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAAATGTTGCTGGAAACATGCGACGTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACCTGCACTGCTATCTATATATGAGATATAATTAATGGCAAAAGCACTGCTCTTA 780
Db 721 ACCACCTGCACTGCTATCTATATATGAGATATAATTAATGGCAAAAGCACTGCTCTTA 780
QY 781 TATGCTGCTATATCGAATCAAAAACAGCATGGCTCCACACACTGTTACTTGATGTA 840
Db 781 TATGCTGCTATATCGAATCAAAAACAGCATGGCTCCACACACTGTTACTTGATGTA 840
QY 841 CATGACCAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGACCAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATGATGATGGAAGAGCTGCTCATCTGCTATGCTATGCTGATGCTGACAGATATA 960
Db 901 CTGATGATGATGGAAGAGCTGCTCATCTGCTATGCTGATGCTGATGCTGACAGATATA 960
QY 961 GTCAGCCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGCTGACAGACG 1020
Db 961 GTCAGCCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGCTGACAGACG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGTATAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGTATAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAAAGAACTTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAAAGAACTTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGGTTCAAAAGCGAGTGAAATATAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGGTTCAAAAGCGAGTGAAATATAGCCAGAGAAA 1200
QY 1201 ATGCTCTAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCTAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATATGTTGGGATTTACTGAAAAAAGCTGATGATGCTGCTGCTGCTG 1320
Db 1261 AAGCATGAAGTAATATGTTGGGATTTACTGAAAAAAGCTGATGATGCTGCTGCTGCTG 1320
QY 1321 AATGCTGATATGATGATTAAATTCCTCAAGAGAGAGCAACACCTGAAATACACCAATTT 1380
Db 1321 AATGCTGATATGATGATTAAATTCCTCAAGAGAGAGCAACACCTGAAATACACCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGAGTATCACAGATTTTGGCAATTTAGTTTCTGACTACAAAGAA 1440
Db 1381 CTTGACACAGAAAGTGAAGAGTATCACAGATTTTGGCAATTTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTTCTGAAAAAGCAACCAAGAACAAAGCTTTAAACCTTGACA 1500
Db 1441 AAACAGATGCAAAATCTCTTCTGAAAAAGCAACCAAGAACAAAGCTTTAAACCTTGACA 1500
QY 1501 TCAGAGAGAGAGTCCAAAAGCTTTGAGGCGAGTGAATAATGGCCAGCCAGAGACTGAAAT 1560
Db 1501 TCAGAGAGAGAGTCCAAAAGCTTTGAGGCGAGTGAATAATGGCCAGCCAGAGACTGAAAT 1560
QY 1561 TTTATGCTCTATCGAAGAAATGAAGAGACGAGAAATGCTCATGTCGATTTCCAGAAAC 1620
Db 1561 TTTATGCTCTATCGAAGAAATGAAGAGACGAGAAATGCTCATGTCGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680

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QY 1681 AGAACACCTGAAAAGCCAGCAATTTCTGACACAGATGAGATGAAGATATCACAGTGACGAA 1740
Db 1681 AGAACACCTGAAAAGCCAGCAATTTCTGACACAGATGAGATGAAGATATCACAGTGACGAA 1740
QY 1741 CAAAATGATCTACAGAAAGCAATTTTGTGAGAGACAGAACACTGCAATATTTACAGATGAG 1800
Db 1741 CAAAATGATCTACAGAAAGCAATTTTGTGAGAGAACAGAACACTGCAATATTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAAGCAGATGAGTGGTTGAAAAAATGAATTTCTGACTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAAGCAGATGAGTGGTTGAAAAAATGAATTTCTGACTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAAGAAAGACATCTTGCTGATGAAAAATGATGCTGCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAAGAAAAGAAAGACATCTTGCTGATGAAAAATGATGCTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTTGACACATGAAATGACATGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGAGCTTGACACATGAAATGACATGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 22
US-09-709-729-374
; Sequence 374, Application us/09709729
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C22
; CURRENT APPLICATION NUMBER: US-09/709,729
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 551
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-709-729-374

Query Match 100.0%; Score 2000; DB 28; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6; 6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1921 GCCATGCTAGAGCTGAGCTAGACACAAATGAATCATCAGAGCCAGCTAATAAAAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 24
US-09-780-669-374
Sequence 374: Application US/09780669

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-374

Query Match 100.0% Score 2000: DB 30: Length 2000:
Best Local Similarity 100.0%: Pred. No. 6.6e-226:
Matches 2000: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 ATGTGCTTGAAGTATGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGTGCTTGAAGTATGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGACCAAGATGGCAAGTGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGCAAGTGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTTGAGACACAGACGACTCTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTTGAGACACAGACGACTCTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240
Qy 241 GCGCGTTCGAGACACAGACGACTCTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
Db 241 GCGCGTTCGAGACACAGACGACTCTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
Qy 301 TGGTCTGCACTGCTGCTGCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCGTTGG 360
Db 301 TGGTCTGCACTGCTGCTGCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCGTTGG 360
Qy 361 GGAGACTAGATGACAGTGCCTTCTATGAGCCAGGTACACAGTCCGTGAGCAAGATCTG 420

Db 361 GGAGACTAGATGACAGTGCCTTCTATGAGCCAGGTACACAGTCCGTGAGCAAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGCTGAGTAAAGTCCCAAGAAAGATCTCAGTCATG 480
Db 421 GACAGCTCCACAGAGCTGCTGCTGAGTAAAGTCCCAAGAAAGATCTCAGTCATG 480
Qy 481 CTCAGGACACTGAGTGAACAAAGACAAAGCAAGAGAGCTGCTTACATCTGCGC 540
Db 481 CTCAGGACACTGAGTGAACAAAGACAAAGCAAGAGAGCTGCTTACATCTGCGC 540
Qy 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGAGACAGATGTCATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGAGACAGATGTCATTAAT 600
Qy 601 GTCTTGACAAACAAAAGAGGACAGCTGATTAAGCCGCTACATGCCAGAAATGAA 660
Db 601 GTCTTGACAAACAAAAGAGGACAGCTGATTAAGCCGCTACAAATGCCAGAAATGAA 660
Qy 661 TGTGGCTTAATGTGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGCTTAATGTGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAACAAAGCATGGCTCACACACTGTTACTGCTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAACAAAGCATGGCTCACACACTGTTACTGCTGA 840
Qy 841 CATGAGCAAAAACAGCAATCGGAAATTTTAATCAAGAAAACGAATTTAATATGA 900
Db 841 CATGAGCAAAAACAGCAATCGGAAATTTTAATCAAGAAAACGAATTTAATATGA 900
Qy 901 CTGATAGATATGGAAGACTGCTCATACTGCTGATATGTTGATGATCAGCAACTATA 960
Db 901 CTGATAGATATGGAAGACTGCTCATACTGCTGATATGTTGATGATCAGCAACTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
Qy 1021 GCCAGAGTATGCTGTTCTATGTCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGTATGCTGTTCTATGTCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGAGTGAAGTCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGAGTGAAGTCCAGCAGAGAAA 1200
Qy 1201 ATGTCACAAGAACAGAAATTAATAGATGGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCACAAGAACAGAAATTAATAGATGGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGATGATTAATAGAAAACCTGAAATGCTGCTGCG 1320
Db 1261 AAGCATGAAAGTAAATATGATGATTAATAGAAAACCTGAAATGCTGCTGCG 1320
Qy 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440
Qy 1441 AAACAGATCCCAAAATACTCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATCCCAAAATACTCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500


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1141 CTGACATCAGAGAGAGTACAAAGTTCAAAAGCCAGTGAATAATAGCCAGCCAGAGANA 1200
1141 CTGACATCAGAGAGAGTACAAAGTTCAAAAGCCAGTGAATAATAGCCAGCCAGAGANA 1200
1201 ATGTCCTCAAGAACCGAAATTAATAGATGGTGTATAGAGAGCTTGAGAGAAATGAAG 1260
1201 ATGTCCTCAAGAACCGAAATTAATAGATGGTGTATAGAGAGCTTGAGAGAAATGAAG 1260
1261 AAGCATGAAGATTAATAGTGGATTTACTAGAAAACCTGACTAAATGGTCTCCTGTGCG 1320
1261 AAGCATGAAGATTAATAGTGGATTTACTAGAAAACCTGACTAAATGGTCTCCTGTGCG 1320
1321 AATGCTGATTAATGATTAATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1321 AATGCTGATTAATGATTAATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1381 CCTGCAACGAAAGTGAAGAGATATCAGAGAAATTTGGCAATTTGTTTCTGACTACAAAG 1440
1381 CCTGCAACGAAAGTGAAGAGATATCAGAGAAATTTGGCAATTTGTTTCTGACTACAAAG 1440
1441 AAACGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGAACAGACTTAAGAGTGACA 1500
1441 AAACGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGAACAGACTTAAGAGTGACA 1500
1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
1561 TTTATGCTGATTAATGAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1561 TTTATGCTGATTAATGAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1621 CTGACTAATGAGTGGCAGTGGCAGTGGTGAATGATGATTAATCTTCAAGAGAGAGAG 1680
1621 CTGACTAATGAGTGGCAGTGGCAGTGGTGAATGATGATTAATCTTCAAGAGAGAGAG 1680
1681 AGAACACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAGAGATACAGTGAGGAA 1740
1681 AGAACACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAGAGATACAGTGAGGAA 1740
1741 CAAATGATCTCAGAGCAATTTTGTGAAGACAGACACCTGGAATTTACACGATGAG 1800
1741 CAAATGATCTCAGAGCAATTTTGTGAAGACAGACACCTGGAATTTACACGATGAG 1800
1801 ATTCTGATTCATGAAGAAAGCAGATAGAGAGTGAATAATGAATCTGAGCTTTCT 1860
1801 ATTCTGATTCATGAAGAAAGCAGATAGAGAGTGAATAATGAATCTGAGCTTTCT 1860
1861 ATTCTGATTCATGAAGAAAGCAGATAGAGAGTGAATAATGAATCTGAGCTTTCT 1860
1861 ATTCTGATTCATGAAGAAAGCAGATAGAGAGTGAATAATGAATCTGAGCTTTCT 1860
1921 GCCATGCTAAGCTGAGGTAGACCAATGAAGAAACATCAGAGCAGCTTAAAAA 1980
1921 GCCATGCTAAGCTGAGGTAGACCAATGAAGAAACATCAGAGCAGCTTAAAAA 1980
1981 AAAAAAAAAAAAAAAAAA 2000
1981 AAAAAAAAAAAAAAAAAA 2000

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RESULT 26
US-09-822-827-374
: Sequence 374, Application US/09822827
: GENERAL INFORMATION:

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: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.534C1
: CURRENT APPLICATION NUMBER: US/09/822,827
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374

Query Match      100.0%; Score 2000; DB 31; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTCGTTGAGGTGATTCATGCCGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
1 ATGTCGTTGAGGTGATTCATGCCGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
61 AGGAGCAATGAGGCAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
61 AGGAGCAATGAGGCAAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
121 AGCAACGTGGGCACTTCTGAGACACGACGACTGCTATGAAAGCACTCAGAGCAAG 180
121 AGCAACGTGGGCACTTCTGAGACACGACGACTGCTATGAAAGCACTCAGAGCAAG 180
181 ATGGGCAATGCTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
181 ATGGGCAATGCTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
241 GGGGCTTGGAGACACGACGACTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
241 GGGGCTTGGAGACACGACGACTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
301 TGGTGTGCTGAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
301 TGGTGTGCTGAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
361 GGAAGCTACGATGACAGTCCCTTCAATGAGAGCCAGTACACGCTCCGTGGAGAGATCTG 420
361 GGAAGCTACGATGACAGTCCCTTCAATGAGAGCCAGTACACGCTCCGTGGAGAGATCTG 420
421 GAAAGCTCAGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
421 GAAAGCTCAGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
481 CTCAGGAGACCTGACCTGTAACAAAGAGCAAGCAAAAGAGCACTCTACATCTGGCC 540
481 CTCAGGAGACCTGACCTGTAACAAAGAGCAAGCAAAAGAGCACTCTACATCTGGCC 540
541 TCTGCCAATGGAATTCAGAGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 TCTGCCAATGGAATTCAGAGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
601 GTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 720
601 GTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 720
721 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 780
721 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 780
781 TATGCTGCTGATATGCAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 TATGCTGCTGATATGCAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 CATGACCAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
841 CATGACCAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
901 CTGAGATGATATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 CTGAGATGATATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

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|||||
Db 661 TGTGGTTAATGTCTGTGGAACATGGCACTGATCCAAATATCTCAGATGATGGAAT 720
Qy 721 ACCACTGCGACTAGCGTATCTATATAGAGTAATTAATGAGCCCAACACTGCTCTTA 780
Db 721 ACCACTGCGACTAGCGTATCTATATAGAGTAATTAATGAGCCCAACACTGCTCTTA 780
Qy 781 TATGGTGTGATATGAAATCAAAAAACAAGCATGGCCCTCACACACTGTACTGGTGA 840
Db 781 TATGGTGTGATATGAAATCAAAAAACAAGCATGGCCCTCACACACTGTACTGGTGA 840
Qy 841 CATGAGCAAAAAACACCAAGTGTGAAATTTTATTCAGAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACACCAAGTGTGAAATTTTATTCAGAAAAAAGCGAATTTAAATGA 900
Qy 901 CTGGATATGATGGAAGAGCTGCTCATACCTGTGTATGTGGATGATCAGCAAGTATA 960
Db 901 CTGGATATGATGGAAGAGCTGCTCATACCTGTGTATGTGGATGATCAGCAAGTATA 960
Qy 961 GTACAGCTCTCTACTTGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGC 1020
Db 961 GTACAGCTCTCTACTTGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAAAAACATGCTTAAATCTCTTCTGAAACAGCAATCCAGAACAAAGCTTAAAG 1140
Db 1081 AAGAAAAACATGCTTAAATCTCTTCTGAAACAGCAATCCAGAACAAAGCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGGAGTGAAGAAATPCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGGAGTGAAGAAATPCCAGCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATAGAGAGTTGAGAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATAGAGAGTTGAGAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Qy 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 CCTGACAAACGAAAGTGAAGATATCAGAAATTTGGAAATTAAGTTCTGACTACAAAG 1440
Db 1381 CCTGACAAACGAAAGTGAAGATATCAGAAATTTGGAAATTAAGTTCTGACTACAAAG 1440
Qy 1441 AAGAGATGCCAAATATCTCTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAGAGATGCCAAATATCTCTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGAGCAGTGAAGATGGCCAGCAGAGAGAGAG 1560
Db 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGAGCAGTGAAGATGGCCAGCAGAGAGAGAG 1560
Qy 1561 TTTATGCTATGCTGAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TTTATGCTATGCTGAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Qy 1621 CTGACTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1621 CTGACTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Qy 1681 AGAAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AGAAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 CAAAATGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 CAAAATGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
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Db 1741 CAAAATGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Qy 1801 ATTTCATATCATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 ATTTCATATCATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 CTATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CTATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 28
US-09-852-911-374
; Sequence 374, Application US/09852911
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yashir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C25
; CURRENT APPLICATION NUMBER: US/09/852,911
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-852-911-374

Query Match 100.0%; Score 2000; DB 32; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226; Indels 0; Gaps 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCTGAGGTGATTCATGCGGCTGCTCTTGTGGAAGAGCAATTTGGCTTC 60
Db 1 ATGTGCTGAGGTGATTCATGCGGCTGCTCTTGTGGAAGAGCAATTTGGCTTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTGCTTCCCTGCTGCAAGAGAGAGAGAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTGCTTCCCTGCTGCAAGAGAGAGAGAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAG 240
```


APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.5342
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-374

Query Match 100.0%; Score 2000; DB 33; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGAGTGTGATTCATGCGGCTGCTCTTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGGGTGAGTGTGATTCATGCGGCTGCTCTTGTGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAGATGSGCAAGTGTGCTGCCGTTCCTCCCTGCGCAGGAGAGCGCAAG 120
DB 61 AGGAGCAGATGSGCAAGTGTGCTGCCGTTCCTCCCTGCGCAGGAGAGCGCAAG 120
QY 121 ACCAAGTGGGCACTTCTGGAAGCAGCAGACCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 ACCAAGTGGGCACTTCTGGAAGCAGCAGACCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAATGTCGCCGCTGCTCCCTGCTGAGGGGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAATGTCGCCGCTGCTCCCTGCTGAGGGGGAGTGGCAAGCAAGCTG 240
QY 241 GCGGCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTCCCTGCTGAGGGGGAGCGGCAAGAGAGTGGGCGCTTG 360
DB 301 TGGTGTGCTGCTGCTCCCTGCTGAGGGGGAGCGGCAAGAGAGTGGGCGCTTG 360
QY 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACGTCGCTGAGAGAGTCTG 420
DB 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACGTCGCTGAGAGAGTCTG 420
QY 421 GACAAAGCTCAGAGAGCTGCTGTTGGGTTAAAGTCCCGAAGAAAGATGTCATGCTATG 480
DB 421 GACAAAGCTCAGAGAGCTGCTGTTGGGTTAAAGTCCCGAAGAAAGATGTCATGCTATG 480
QY 481 CTCAGGAGACCTGACGCTGTAACAAAGAGGACAAAGAGGACTCTCTACATCTGGCC 540
DB 481 CTCAGGAGACCTGACGCTGTAACAAAGAGGACAAAGAGGACTCTCTACATCTGGCC 540
QY 541 TGTGCAATGGAATTCAGAAAGTAAAGTCTCTGCTGAGAGAGAGATGCACTTAAT 600
DB 541 TGTGCAATGGAATTCAGAAAGTAAAGTCTCTGCTGAGAGAGAGATGCACTTAAT 600
QY 601 GTCTCTTGACAAAG 660
DB 601 GTCTCTTGACAAAG 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTCTGACAGCTATCTATATTAAGATTAATTAATGAGAGAGAGAGAGAG 780
DB 721 ACCACTCTGACAGCTATCTATATTAAGATTAATTAATGAGAGAGAGAGAGAG 780

QY 781 TATGTGCTGATATCGAATCAAAAAACAGCATGCGCTACACCACTGTTACTGGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAAACAGCATGCGCTACACCACTGTTACTGGTGA 840
QY 841 CATGACAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAACGAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAACGAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 CTGATAGATATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATATCTTCTCAAGATCATCTGAGACAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATATCTTCTCAAGATCATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCCAGTTACTTTTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCCAGTTACTTTTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTGGAAGACAGCAATCCAGAACAGCTTAAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTGGAAGACAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAG 1200
DB 1141 CTGACATCAG 1200
QY 1201 ATGCTCAAGACACAGAAATTAATTAAGATGCTATGAGAGAGTTGAAGAAATGAG 1260
DB 1201 ATGCTCAAGACACAGAAATTAATTAAGATGCTATGAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAAGTATATGAGGATATCTGAAAGACCTGATGATAGTGCATGCTGGC 1320
DB 1261 AAGCATGAAAGTATATGAGGATATCTGAAAGACCTGATGATAGTGCATGCTGGC 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCGTCAAG 1440
DB 1381 CCGTCAAG 1440
QY 1441 AAGCATGCGCAAAATACCTTCTGAAAGACAGAACCCAGAACAGCTTAAAGCTGACA 1500
DB 1441 AAGCATGCGCAAAATACCTTCTGAAAGACAGAACCCAGAACAGCTTAAAGCTGACA 1500
QY 1501 TCAG 1560
DB 1501 TCAG 1560
QY 1561 TTTATGCTATGCAAGAAATGAAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 TTTATGCTATGCAAGAAATGAAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTGACATATGCTGCACTGCTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 CTGACATATGCTGCACTGCTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 AGAAGACCTGAAAG 1740
DB 1681 AGAAGACCTGAAAG 1740
QY 1741 CAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 CAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 ATTCTGATTCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1801 ATTCTGATTCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 CTAGATTGTAAAGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920

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|||||
Db 1861 CTTAGTTGTAAGAAAGAAAAAGACATCTTCATGAAAAATAGTACGTCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAGACGTGAGCTGACACAAATGAATACAGACCAGCTTAAATAAAAA 1980
Db 1921 GCCATGCTAGACGTGAGCTGACACAAATGAATACAGACCAGCTTAAATAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 30
US-09-895-814-374
; Sequence 374, Application US/09895814
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Meng, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-374

Query Match 100.0%; Score 2000; DB 33; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6, 6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 GCGCTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGGAACAGATGGCAAG 300
Qy 301 TGTGCTGCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAATCTG 420
Qy 421 GACAACTCCACAGAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAATCTG 480
Db 421 GACAACTCCACAGAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAATCTG 480
Qy 481 CTCAGGGACACTGACGTGAACAGAGGACAGCAAGAAAGAGAGCTCTCATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAGAGGACAGCAAGAAAGAGAGCTCTCATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACAGATGCAACTTAAT 600
Qy 601 GTCCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCCGTACAAATGCCAGGAAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCCGTACAAATGCCAGGAAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGTAACATGACGACATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGTAACATGACGACATGATCCAAATATTCAGATGATGAAAT 720
Qy 721 AACACTGTGACACTACGCTATCTATATGAAGATTAATGATGATGATGATGATGATGATGAT 780
Db 721 AACACTGTGACACTACGCTATCTATATGAAGATTAATGATGATGATGATGATGATGATGAT 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAGATGATGATGATGATGATGATGATGATGATGAT 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAGATGATGATGATGATGATGATGATGATGATGAT 840
Qy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCATACCTGATGATGATGATGATGATGATGATGATGAT 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATACCTGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 GTCAGCTTCTACTTGAACAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 GTCAGCTTCTACTTGAACAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1021 GCGAGAGATATGCTGTTTATGATCATCATGATTAATTTCCAGTTCCTTCTGACTAC 1080
Db 1021 GCGAGAGATATGCTGTTTATGATCATCATGATTAATTTCCAGTTCCTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAAACAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAAACAAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGCAAGTGA AAAATAGCACCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGCAAGTGA AAAATAGCACCCAGAGAAA 1200
Qy 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTATAGAGAGTGTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTATAGAGAGTGTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 AAGCATGAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Qy 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGACAGACACTGAAATACAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGACAGACACTGAAATACAGCAATTT 1380
```

QY	1381	CCACAGCAAGAAAGTAAGAGTATCCACAATTTGCGAATTAGTTTCTGACTACTCAAGAA	1440
Db	1381	CTTGACACAGAAAGTAAGAGTATCCACAATTTGCGAATTAGTTTCTGACTACTCAAGAA	1440
QY	1441	AAACAGATGCCAAAATACTCTTCTGAAAAACACCAACCAGAACACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATACTCTTCTGAAAAACACCAACCAGAACACAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAGAGAGTTCACAAAGGCTTTGAGGCGAGTGAAAATGGCCAGCCAGAGCTAGAAAAT	1560
Db	1501	TCAGAGGAGAGAGTTCACAAAGGCTTTGAGGCGAGTGAAAATGGCCAGCCAGAGCTAGAAAAT	1560
QY	1561	TTTATGGCTTTCAGAGAAATGAAAGACGACGGAGACTCATGTGCGAATTTCCCGAANAAC	1620
Db	1561	TTTATGGCTTTCAGAGAAATGAAAGACGACGGAGACTCATGTGCGAATTTCCCGAANAAC	1620
QY	1621	CTGACTAATGATGCCACTGCTGGCAATGGTGTGATGTGATTTAATTCCTCCCAAGCAAGAGC	1680
Db	1621	CTGACTAATGATGCCACTGCTGGCAATGGTGTGATGTGATTTAATTCCTCCCAAGCAAGAGC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAAGAGTATCACAGTACGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAAGAGTATCACAGTACGAA	1740
QY	1741	CAAAATGATCTCAGAAAGCAATTTTGTGAAGAACGACACGGAATTTACACAGATAG	1800
Db	1741	CAAAATGATCTCAGAAAGCAATTTTGTGAAGAACGACACGGAATTTACACAGATAG	1800
QY	1801	ATTCTGATTCATGAGCAAAAAGCAGATAGAGAGTGTTGAAAAAATGAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAGCAAAAAGCAGATAGAGAGTGTTGAAAAAATGAATTCGAGCTTCT	1860
QY	1861	CTTAGTGTGAAGAAAAAGACATCTTGCAATGAATATAGTACCTTGCGGGAAGAAATTT	1920
Db	1861	CTTAGTGTGAAGAAAAAGACATCTTGCAATGAATATAGTACCTTGCGGGAAGAAATTT	1920
QY	1921	GCCATGCTAGAGCTGAGCTAGACACAAATGAAGAAATCAGAGCCACTAAAAA	1980
Db	1921	GCCATGCTAGAGCTGAGCTAGACACAAATGAAGAAATCAGAGCCACTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

```

RESULT 31
US-09-924-400-302
? Sequence 302, Application US/09924400
? GENERAL INFORMATION:
? APPLICANT: Frudakis, Tony N.
? APPLICANT: Reed, Steven G.
? APPLICANT: Smith, John M.
? APPLICANT: Mishner, Lynda E.
? APPLICANT: Dillon, Davin C.
? APPLICANT: Retter, Marc W.
? APPLICANT: Wang, Aljun
? APPLICANT: Skeiky, Yasir A. W.
? APPLICANT: Harlocker, Susan L.
? APPLICANT: Day, Craig H.
? APPLICANT: Li, Samuel X.
? APPLICANT: Deng, Ta
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
? FILE REFERENCE: 210121,419612
? CURRENT APPLICATION NUMBER: US/09/924,400
? CURRENT FILING DATE: 2001-08-07
? NUMBER OF SEQ ID NOS: 340
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 302
? LENGTH: 2000
? TYPE: DNA
? ORGANISM: Homo sapiens

```

US-09-924-400-302

Query Match	100.0%;	Score 2000;	DB 34;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 6.6e-226;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATATGGTGTAGGGTAAATTTCATGACCCGGCGCCCTCTTGTGAAGAAGCATTTGGTGC	60
Db	1	ATGGGGTGTAGGGTATTCATGATCCGGCGGCTCTTCTGTGAAGAAGCATTTGGTGC	60
OY	61	AGGAGCAGAATGGGCAAGTGGTGGTCCGCTGGCTTCCCTGGTCAGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGGTGGTCCGCTGGCTTCCCTGGTCAGGAGAGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTTGGAGACACAGACGATCTGCTATGAAGACACTTCAGGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTTGGAGACACAGACGATCTGCTATGAAGACACTTCAGGAGCAAG	180
OY	181	ATGAGGCAAGTGGTCCCGCCCACTGCTTCCCTGGTCAGGAGGAGTGGCAAGCAACGTG	240
Db	181	ATGAGGCAAGTGGTGGCGCCCACTGCTTCCCTGGTCAGGAGGAGTGGCAAGCAACGTG	240
OY	241	GGCGCCTTCTGGAGACACACAGACACTGCTATGAACACTACAGAAACAATGGGCAAG	300
Db	241	GGCGCCTTCTGGAGACACACAGACACTGCTATGAACACTACAGAAACAATGGGCAAG	300
OY	301	TGGTGTGCGCCACTCTTCCCTGGTCGAGGGGAGGGAGCAAGCAAGTGGGCGCTTGG	360
Db	301	TGGTGTGCGCCACTCTTCCCTGGTCGAGGGGAGGGAGCAAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTGGCTTCTATGAGAGCCAGTACCAAGTCCGTGGAGAGATCTG	420
Db	361	GGAGACTACGATGACAGTGGCTTCTATGAGAGCCAGTACCAAGTCCGTGGAGAGATCTG	420
OY	421	GACAAGCTCCACAAGCTGGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATCTGCATG	480
Db	421	GACAAGCTCCACAAGCTGGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATCTGCATG	480
OY	481	CTCAGGCACTGACGTGAACACAGAAAGACACCAAAAGACATGCTTACATCTGGCC	540
Db	481	CTCAGGCACTGACGTGAACACAGAAAGACACCAAAAGACATGCTTACATCTGGCC	540
OY	541	TCTGCCAATGGGAATTGAGAAAGTAGTAAACTCTGCTGGACAGACGATGCAACTTAAAT	600
Db	541	TCTGCCAATGGGAATTGAGAAAGTAGTAAACTCTGCTGGACAGACGATGCAACTTAAAT	600
OY	601	GTCCTTGACACAAAAGAGAGACGCTCTGATTAAGGGCCGTACATGCCAGAGATGAA	660
Db	601	GTCCTTGACACAAAAGAGAGACGCTCTGATTAAGGGCCGTACATGCCAGAGATGAA	660
OY	661	TGTGGCTTAATGTTGCGTGAACATGGGACTGATCCAAATATTCCAGATCAGTATGGAAT	720
Db	661	TGTGGCTTAATGTTGCGTGAACATGGGACTGATCCAAATATTCCAGATCAGTATGGAAT	720
OY	721	ACCACTGTGCACTACGCTATCTATATGAAGATAAATTATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGTGCACTACGCTATCTATATGAAGATAAATTATGGCCAAAGCACTGCTCTTA	780
OY	781	TATGGTGTGATATCGAATCAAAAACACAGATGGGCTCACACCACTGTACTTGGTGA	840
Db	781	TATGGTGTGATATCGAATCAAAAACACAGATGGGCTCACACCACTGTACTTGGTGA	840
OY	841	CATGAGCAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAAGCGAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTCATACCTGCTGATGTTGTGGATCACAAGTTATA	960
Db	901	CTGATATGATATGGAAGAGCTGCTCATACCTGCTGATGTTGTGGATCACAAGTTATA	960
OY	961	GTCAGCCTTCTACTTGTGAGCAAAATATTGATGTATCTTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGTGAGCAAAATATTGATGTATCTTCAAGATCTATCTGGACAGAG	1020

```

QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
    |||||
Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCATCCAGAAACAGACTTAAAG 1140
    |||||
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGTCTCAAAAGGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
    |||||
Db 1141 CTGACATCAGAGAAAGTCTCAAAAGGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
QY 1201 ATGTCCTCAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
    |||||
Db 1201 ATGTCCTCAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATGTAATTAATGTTGGGATTAATAGAAAAACCTGACTAATGCTGACTGCGC 1320
    |||||
Db 1261 AAGCATGAAATGTAATTAATGTTGGGATTAATAGAAAAACCTGACTAATGCTGACTGCGC 1320
QY 1321 AATGGTGTAATGATTAATCTCTCAAGAAAGACAGAACACCTGAATAATCAGCAATTT 1380
    |||||
Db 1321 AATGGTGTAATGATTAATCTCTCAAGAAAGACAGAACACCTGAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAGTGAAGACTATTCACGAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
    |||||
Db 1381 CCTGACAAACGAAGTGAAGACTATTCACGAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTGAAAGACGAAACCCAGAAACAAAGACTTAAAGCTGACA 1500
    |||||
Db 1441 AAACAGATGCCAAATATCTCTGAAAGACGAAACCCAGAAACAAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT 1560
    |||||
Db 1501 TCAGAGGAAAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGACGGAAGTACTCATGTCGGATTCAGAGAAAAAC 1620
    |||||
Db 1561 TTTATGGCTATCGAAGAAATGAAGACGGAAGTACTCATGTCGGATTCAGAGAAAAAC 1620
QY 1621 CTGACTAATGTCGCACTGCTGCGCAATGCTGATGATGATTAATTTCCCTCCAGAGAAAGC 1680
    |||||
Db 1621 CTGACTAATGTCGCACTGCTGCGCAATGCTGATGATGATTAATTTCCCTCCAGAGAAAGC 1680
QY 1681 AGAACACCTGAAGCCAGCAATTTCTCTGACACTGAGATGAAGATATCAGAGTACGAA 1740
    |||||
Db 1681 AGAACACCTGAAGCCAGCAATTTCTCTGACACTGAGATGAAGATATCAGAGTACGAA 1740
QY 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATAG 1800
    |||||
Db 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATAG 1800
QY 1801 ATTCTGATTCATGAAGAAACAGATAGAAATGTTGTAATAATCAATTCGAGCTTTCT 1860
    |||||
Db 1801 ATTCTGATTCATGAAGAAACAGATAGAAATGTTGTAATAATCAATTCGAGCTTTCT 1860
QY 1861 CTTAGTTGTAGAAAGAAAGACATCTTGATGATAATTAATAGTTGCGGGAAGAAAT 1920
    |||||
Db 1861 CTTAGTTGTAGAAAGAAAGACATCTTGATGATAATTAATAGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAGAGCTGAGACTAGACAAATGAACATCAGAGCCAGCTTAAAAA 1980
    |||||
Db 1921 GCCATGCTAGAGCTGAGACTAGACAAATGAACATCAGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000

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RESULT 32
US-10-006-920-374
; Sequence 374, Application US/10006920

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: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Devin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Derrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghcon, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fander, Gary R.
: APPLICANT: Mantanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/006,920
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-006-920-374

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Query Match 100.0%; Score 2000; DB 38; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGCTCTC 60
    |||||
Db 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGCTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGTCCGCTGCTCCCTGCTCAGGAGAGGGGCAAG 120
    |||||
Db 61 AGAGCAAGATGGGCAAGTGGTGGTCCGCTGCTCCCTGCTCAGGAGAGGGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
    |||||
Db 121 AGCAAGTGGGCACTTCTGAGACCACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
    |||||
Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCTTGTGAGACACAGAGACTCTGATGAAGACACTCAGAGCAAGATGGGCAAG 300
    |||||
Db 241 GGGCTTGTGAGACACAGAGACTCTGATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCTTGGCGCTTGG 360
    |||||
Db 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCTTGGCGCTTGG 360
QY 361 GGAGACTRACATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGCTGGAGAGATCTG 420
    |||||
Db 361 GGAGACTRACATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGCTGGAGAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATTCATGCTCATG 480
    |||||
Db 421 GACAAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATTCATGCTCATG 480

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OY 481 CTCAGGACACTGAGCTGAACAAGAGCACAAGAGGAGCTGCTACATCGGCC 540
DB 481 CTCAGGACACTGAGCTGAACAAGAGCACAAGAGGAGCTGCTACATCGGCC 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTACTTAAACTCTGCTGGACAGAGATGTCACCTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTACTTAAACTCTGCTGGACAGAGATGTCACCTTAAT 600
OY 601 GTCTCTTGACACAAAAGAGCAGCTGATTAAGGCCGTCAATGCCAGAGATGAA 660
DB 601 GTCTCTTGACACAAAAGAGCAGCTGATTAAGGCCGTCAATGCCAGAGATGAA 660
OY 661 TGTGGCTTAATGTGTGGAACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
DB 661 TGTGGCTTAATGTGTGGAACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
OY 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
OY 781 TATGTGCTGATATGCAATCAAAAACAAGCATGGCCTCACACCACTGTACTTGCTTA 840
DB 781 TATGTGCTGATATGCAATCAAAAACAAGCATGGCCTCACACCACTGTACTTGCTTA 840
OY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
OY 901 CTGATAGATATGAAGAGCACTGCTCTCATCTGCTATGTTGATGATCAGCAAGTATA 960
DB 901 CTGATAGATATGAAGAGCACTGCTCTCATCTGCTATGTTGATGATCAGCAAGTATA 960
OY 961 GTACACCTCTCTCTGAGCAAAAATATGATGATCTTCCAAAGATCTATCTGACAGAG 1020
DB 961 GTACACCTCTCTCTGAGCAAAAATATGATGATCTTCCAAAGATCTATCTGACAGAG 1020
OY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGATTAATTTGCAAGTACTTTCTGCTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTATGATCATCATGATTAATTTGCAAGTACTTTCTGCTAC 1080
OY 1081 AAAAGAAAAACAGATCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAAAGAAAAACAGATCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
OY 1141 CTGACATCAGAGAGAGTCAACAAAGCTTCAAGAGCATGAAATATGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAAGCTTCAAGAGCATGAAATATGCCAGCAGAGAA 1200
OY 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGATGATGAGAGGTTCAAGAAATGAG 1260
DB 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGATGATGAGAGGTTCAAGAAATGAG 1260
OY 1261 AAGCATGAAGATTAATATGCTGGATTAATGAGAAACCTGACTAATGCTGCTGAGC 1320
DB 1261 AAGCATGAAGATTAATATGCTGGATTAATGAGAAACCTGACTAATGCTGCTGAGC 1320
OY 1321 AATGTGATATGATTAATTTCTCAAGAGAGCAGACACCTGAAAATACGCAATTT 1380
DB 1321 AATGTGATATGATTAATTTCTCAAGAGAGCAGACACCTGAAAATACGCAATTT 1380
OY 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGATTTGTTCTGACATCAAGAA 1440
DB 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGATTTGTTCTGACATCAAGAA 1440
OY 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
OY 1501 TTAGAGAGAGATGACAAAGGCTTGAAGGCACTGAAATGCGCAGCAGAGCTAGAAAAT 1560
DB 1501 TTAGAGAGAGATGACAAAGGCTTGAAGGCACTGAAATGCGCAGCAGAGCTAGAAAAT 1560

```

```

OY 1561 TTTATGCTATGAGAAATGAAGAAGCAGGAGATGATGCTGATTTCCAGAAAAAC 1620
DB 1561 TTTATGCTATGAGAAATGAAGAAGCAGGAGATGATGCTGATTTCCAGAAAAAC 1620
OY 1621 CTGACTAATGTCGCCACTGCTGGCAATGGTATGATGATTAATTTCTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTCGCCACTGCTGGCAATGGTATGATGATTAATTTCTCAAGAAAGAC 1680
OY 1681 AGAACACCTGAAAGCAGCAATTTCTGACACTGAGAAATGAAGATATACAGTACGAA 1740
DB 1681 AGAACACCTGAAAGCAGCAATTTCTGACACTGAGAAATGAAGATATACAGTACGAA 1740
OY 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAAGAACACTGGAATATTACAGTGA 1800
DB 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAAGAACACTGGAATATTACAGTGA 1800
OY 1801 ATCTGATTCATGAAGAAAGCAGATGAAGTGTGGAAGAAATGAATTTCTGAGCTTCT 1860
DB 1801 ATCTGATTCATGAAGAAAGCAGATGAAGTGTGGAAGAAATGAATTTCTGAGCTTCT 1860
OY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATGCTGCGGAGAAATTT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATGCTGCGGAGAAATTT 1920
OY 1921 GCCATGCTAAGACTGAGCTAGACACAATGAACATCAGAGCAGCTTAAGAAAAA 1980
DB 1921 GCCATGCTAAGACTGAGCTAGACACAATGAACATCAGAGCAGCTTAAGAAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

```

```

RESULT 33
US-10-010-940-374
; Sequence 374, Application US/10010940
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuyun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retler, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010.940
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-010-940-374

```

```

Query Match 100.0%; Score 2000; DB 38; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6; fe-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGGTGGTTGAGGTGATTCATAGCGGCTGCTCTTCTGTAAGAAAGCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATAGCGGCTGCTCTTCTGTAAGAAAGCATTTGGTCTC 60
OY 61 AGGAGCAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 AGGAGCAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

```

QY 121 AGCAGCTGGGCACTTTGGAGACCAGACACTCTCTATGAAGACACTCAGGACAG 180
 Db 121 AGCAACCTGGGCACTTTGGAGACCAGACACTCTCTATGAAGACACTCAGGACAG 180
 QY 181 ATGGGCAAGTGGTGGCGCCACTGGTCCCGCTGCAAGGGGAGTGGCAAGAGAGTGG 240
 Db 181 ATGGGCAAGTGGTGGCGCCACTGGTCCCGCTGCAAGGGGAGTGGCAAGAGAGTGG 240
 QY 241 GGGCCTTCTGGAGACAGACGACTCTGCTATGAAGACACTCAGGACAGAGTGGGAG 300
 Db 241 GGGCCTTCTGGAGACAGACGACTCTGCTATGAAGACACTCAGGACAGAGTGGGAG 300
 QY 301 TGGTGGTGGCACTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
 Db 301 TGGTGGTGGCACTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
 QY 361 GGAGACTACGATGACACTGCTCTATGAGGCCAGGTACACGCTCCGCGGAGAGTCTG 420
 Db 361 GGAGACTACGATGACACTGCTCTATGAGGCCAGGTACACGCTCCGCGGAGAGTCTG 420
 QY 421 GACAGCTCCACAGAGCTGCTGGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATG 480
 Db 421 GACAGCTCCACAGAGCTGCTGGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATG 480
 QY 481 CTCAGGACACTGACGTGAACAGAGACAGCAAGAGAGAGTCTCTACATCTGACC 540
 Db 481 CTCAGGACACTGACGTGAACAGAGACAGCAAGAGAGAGTCTCTACATCTGACC 540
 QY 541 TCTGCAATGGGAATTCAGAAATGCTAAACTCTGCTGACACAGCATCTCACTTAAT 600
 Db 541 TCTGCAATGGGAATTCAGAAATGCTAAACTCTGCTGACACAGCATCTCACTTAAT 600
 QY 601 GTCCCTGACAAACAAAGAGAGAGCTCTGATTAAGCCGTCATCAATCCAGAGATGAA 660
 Db 601 GTCCCTGACAAACAAAGAGAGAGCTCTGATTAAGCCGTCATCAATCCAGAGATGAA 660
 QY 661 TGTGCTTAATGTTGCTGGAACATGSCACTGATCCAAATATTCAGATGATGAAAT 720
 Db 661 TGTGCTTAATGTTGCTGGAACATGSCACTGATCCAAATATTCAGATGATGAAAT 720
 QY 721 ACCACTGTGACACTGCTATCTATGAAGATTAATGAAGCAAGCACTGCTCTTA 780
 Db 721 ACCACTGTGACACTGCTATCTATGAAGATTAATGAAGCAAGCACTGCTCTTA 780
 QY 781 TATGCTCTGATATGCAATCAAAAACAGCATGGCTCACACACGTTACTTGCTGA 840
 Db 781 TATGCTCTGATATGCAATCAAAAACAGCATGGCTCACACACGTTACTTGCTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 QY 901 CTGATAGATATGAGAGAGACTGCTCTCATCTGCTATGTTGAGTGCAGCAATGATA 960
 Db 901 CTGATAGATATGAGAGAGACTGCTCTCATCTGCTATGTTGAGTGCAGCAATGATA 960
 QY 961 GTGACCTTCTACTTGAAGCAAAATATGATATCTCTCAAGATCTATCTGACAGAGC 1020
 Db 961 GTGACCTTCTACTTGAAGCAAAATATGATATCTCTCAAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAAGATGCTAAATAATCTCTTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
 Db 1081 AAAGAAAAAGATGCTAAATAATCTCTTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAATAATACCCAGCCAGAGAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAATAATACCCAGCCAGAGAA 1200
 QY 1201 ATGCTCAAGAACCAAGAAATTAATTAAGAGTGTGATAGAGAGTTGAAGAAAGTAAG 1260

Db 1201 ATGCTCAAGAACCAAGAAATTAATTAAGAGTGTGATAGAGAGTTGAAGAAAGTAAG 1260
 QY 1261 AAGCATGAAGATTAATGTTGGATTTACTAGAAAACCTGACTAATGTTGCTGCTGGC 1320
 Db 1261 AAGCATGAAGATTAATGTTGGATTTACTAGAAAACCTGACTAATGTTGCTGCTGGC 1320
 QY 1321 AATGCTAATAATGATTAATTTCTCTCAAGAGAGCAAGAACCTGAAATTCAGCAATTT 1380
 Db 1321 AATGCTAATAATGATTAATTTCTCTCAAGAGAGCAAGAACCTGAAATTCAGCAATTT 1380
 QY 1381 CCTGACAAACGAAGTGAAGATATCACGAATTTGCCAATTAATTTGACTCAAAAGAA 1440
 Db 1381 CCTGACAAACGAAGTGAAGATATCACGAATTTGCCAATTAATTTGACTCAAAAGAA 1440
 QY 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 Db 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCAAGTGAATAATGAGCCAGCAGAGCTAGAAAT 1560
 Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCAAGTGAATAATGAGCCAGCAGAGCTAGAAAT 1560
 QY 1561 TTTATGCTATCGAAGAAATGAGAGACAGGAAATCTCATGTCGATTTCCAGAAAC 1620
 Db 1561 TTTATGCTATCGAAGAAATGAGAGACAGGAAATCTCATGTCGATTTCCAGAAAC 1620
 QY 1621 CTGACTAATGTTGCTGCACTGGCTGGCAATGTTGATGATGATTAATTTCTCCAGAGAGAGC 1680
 Db 1621 CTGACTAATGTTGCTGCACTGGCTGGCAATGTTGATGATGATTAATTTCTCCAGAGAGAGC 1680
 QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTACAGAA 1740
 Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTACAGAA 1740
 QY 1741 CAAATATATCTCGAAGCAATTTTGTGAAGACAGACACTGGAATTTACAGAGAGAG 1800
 Db 1741 CAAATATATCTCGAAGCAATTTTGTGAAGACAGACACTGGAATTTACAGAGAGAG 1800
 QY 1801 ATTCTGATTCATGAAGAAAGCAGATGAAAGTGGTTGAAAATTAATTTCTGACACTTCT 1860
 Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAAAGTGGTTGAAAATTAATTTCTGACACTTCT 1860
 QY 1861 CTTAGTTGAAGAAAGAAAGACATCTTGCATGAATAATGATGTTGCGGGAAGAAATTT 1920
 Db 1861 CTTAGTTGAAGAAAGAAAGACATCTTGCATGAATAATGATGTTGCGGGAAGAAATTT 1920
 QY 1921 GCCATGCTAAGACTGAGCTAGACAAATGAATCAGAGCCAGCTAAAGAAAAA 1980
 Db 1921 GCCATGCTAAGACTGAGCTAGACAAATGAATCAGAGCCAGCTAAAGAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 34
 US-10-012-896-374
 : Sequence 374, Application US/10012896
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, Devin C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yugu
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: Ketter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Carter, Darick
 : APPLICANT: Li, Samuel X.
 : APPLICANT: Wang, Aljun

Db 1741 CAAATATATCTCAGAACATTTTGTGAAGACAGAACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAAAGTGGTGAATAAATGAAATTCGACTTTC 1860
Db 1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAAAGTGGTGAATAAATGAAATTCGACTTTC 1860
Qy 1861 CTTAGATTGTAAAGAAAAAGACATCTTGCATGAAAAATAGTACGTTGCCGGAAGAAAT 1920
Db 1861 CTTAGATTGTAAAGAAAAAGACATCTTGCATGAAAAATAGTACGTTGCCGGAAGAAAT 1920
Qy 1921 GCCATGCTAGACGAGCTGACACATGAAATGAAATGAGCCGCTAAATAAATAAATAA 1980
Db 1921 GCCATGCTAGACGAGCTGACACATGAAATGAAATGAGCCGCTAAATAAATAAATAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 35
US-10-079-137B-302
; Sequence 302, Application us/10079137B
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Lynda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C13
; CURRENT APPLICATION NUMBER: US/10/079.137B
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-137B-302

Query Match 100.0%; Score 2000; DB 39; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGTTGATTCATCCGCTGCTCTCTCTGTAAGAACATTTGGTCTC 60
Db 1 ATGCTGTTGAGTTGATTCATCCGCTGCTCTCTCTGTAAGAACATTTGGTCTC 60
Qy 61 AGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTCTGTCAGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTCTGTCAGAGAGCGGCAAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGACACAGAGACCTCTGTATGAAGACACTGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGAGACCTCTGTATGAAGACACTGAGCAAG 180
Qy 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCCTTCTGGAGACACGAGACTGTCTATGAAGACACTCAGAGCAAGATGGCAAG 300
Db 241 GGGCCTTCTGGAGACACGAGACTGTCTATGAAGACACTCAGAGCAAGATGGCAAG 300
Qy 301 TGGTGTGCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360

Db 301 TGGTGTGCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGAGCTTCTATGAGAGCCGAGTACACAGCTGCGGAGAGATCTG 420
Db 361 GGAAGCTACGATGACAGAGCTTCTATGAGAGCCGAGTACACAGCTGCGGAGAGATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGCTGGGATTAAGTCCCGAGAAAGATCTCATGCTATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGGGATTAAGTCCCGAGAAAGATCTCATGCTATG 480
Qy 481 CTCAGGACACTGACGTGACACAGAGACACAGCAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGACACAGAGACACAGCAAGAGAGACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCCTGCTGGACAGAGTGCATCTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCCTGCTGGACAGAGTGCATCTTAAT 600
Qy 601 GTCCCTGACAAACAAAAGAGAGACGCTCTGTAAAGCCGCTACAAATGCCAGGAAGATGA 660
Db 601 GTCCCTGACAAACAAAAGAGAGACGCTCTGTAAAGCCGCTACAAATGCCAGGAAGATGA 660
Qy 661 TGTGCTTAAATGTTGCTGGAACATGCGACTGATCCAAATATCCAGATGAGTGAAT 720
Db 661 TGTGCTTAAATGTTGCTGGAACATGCGACTGATCCAAATATCCAGATGAGTGAAT 720
Qy 721 ACCACTGACACTGAGTATCTATATGAAGATTAATTAATGAGCAAGCAAGCTCTTGA 780
Db 721 ACCACTGACACTGAGTATCTATATGAAGATTAATTAATGAGCAAGCAAGCTCTTGA 780
Qy 781 TATGCTCTGATATGATGATCAAAAAACAGACAGCCCTCACACCACTGTTACTGTGTA 840
Db 781 TATGCTCTGATATGATGATCAAAAAACAGACAGCCCTCACACCACTGTTACTGTGTA 840
Qy 841 CATGAGCAAAAAACGCAAGTCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACGCAAGTCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATGATATGAGAGAGAGCTGCTCATATCTGCTATATGTTGATGATGACAGCAATGA 960
Db 901 CTGATGATATGAGAGAGAGCTGCTCATATCTGCTATATGTTGATGATGACAGCAATGA 960
Qy 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
Qy 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGTAAATAATCTCTTCTGAAACAGCAATCCAGAAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGTAAATAATCTCTTCTGAAACAGCAATCCAGAAAGACTTAAAG 1140
Qy 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAAAGCAAGTGAATAATGACCCAGAGAAA 1200
Db 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAAAGCAAGTGAATAATGACCCAGAGAAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGCTGATGACAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGCTGATGACAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAATATGTTGGGATTTCTGTAAGAAACCTGACTAATGCTGCTGCTG 1320
Db 1261 AAGCATGAAGTAATATGTTGGGATTTCTGTAAGAAACCTGACTAATGCTGCTGCTG 1320
Qy 1321 AATGCTAATATGATTAATTTCTCAAGAGAGAGCAAGCAACCTGTAATAATCAGCAATTT 1380
Db 1321 AATGCTAATATGATTAATTTCTCAAGAGAGAGCAAGCAACCTGTAATAATCAGCAATTT 1380
Qy 1381 CTTGACAAAGAAATGAAAGATATCAAGAAATTTGCCAATTAATGTTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAATGAAAGATATCAAGAAATTTGCCAATTAATGTTTCTGACTACAAAGAA 1440

Db	1381	CCTGACACGAAAGTGAAGGATTCACAGAAATTTGGGAATTAGTTCTTGACATACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTTTTGTGAAAACAGCACACCCAGAACAAAGACTTAAAGTGACA	1500
Db	1441	AAACGATGCCAAATATCTTTCTTGAAAAACAGCAACCCGAAACAAGACTTAAAGCTGACA	1500
Qy	1501	TCACAGAACAGTCCACAAAGGCGTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTGAAAT	1560
Db	1501	TCACAGAACAGTCCACAAAGGCGTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTGAAAT	1560
Qy	1561	TTTATGGCTTCCGAAAGAAATGAAGAAGCACAGAACTCATGTGGATTTCCACAGAAAC	1620
Db	1561	TTTATGGCTTCCGAAAGAAATGAAGAAGCACAGAACTCATGTGGATTTCCACAGAAAC	1620
Qy	1621	CTGACTAATGAGTGCCACTGCTGSCAAATGGTATGATGATTAATTCCTCCAGAAAGAC	1680
Db	1621	CTGACTAATGAGTGCCACTGCTGSCAAATGGTATGATGATTAATTCCTCCAGAAAGAC	1680
Qy	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGATATCACAGTGACGA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGATATCACAGTGACGA	1740
Qy	1741	CAAAATGATACTCAGAGCAATTTTGTGAAAACAGAACACATCGAATAATTACACATGAG	1800
Db	1741	CAAAATGATACTCAGAGCAATTTTGTGAAAACAGAACACATCGAATAATTACACATGAG	1800
Qy	1801	ATTCGTATTCATGAGAAAGACAGATAGAGTGTTGAAAAAATGAATTCGTGAGCTTCT	1860
Db	1801	ATTCGTATTCATGAGAAAGACAGATAGAGTGTTGAAAAAATGAATTCGTGAGCTTCT	1860
Qy	1861	CTTAGTGTGAAGAAAGAAAGCAGATCTTGATGAAATATGATGTTGGGGAGAAATT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGCAGATCTTGATGAAATATGATGTTGGGGAGAAATT	1920
Qy	1921	GCCATGCTAAGACTGAGACTGAGACACATGAATGAACATCAGAGCCACTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGACTGAGACACATGAATGAACATCAGAGCCACTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 36			
US-10-144-678A-374			
: Sequence 374, Application US/10144678A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jiang, Yugu			
: APPLICANT: Henderson, Robert A.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retter, Marc W.			
: APPLICANT: Stolk, John A.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Vedvick, Thomas S.			
: APPLICANT: Carter, Darrick			
: APPLICANT: Li, Samuel X.			
: APPLICANT: Wang, Aijun			
: APPLICANT: Skelky, Yasir A. W.			
: APPLICANT: Hepler, William T.			
: APPLICANT: Hurrel, John			
: APPLICANT: McNeill, Patricia D.			
: APPLICANT: Houghton, Raymond L.			
: APPLICANT: Vinals y de Bassols, Carlota			
: APPLICANT: Foy, Teresa M.			
: APPLICANT: Matanabe, Yoshihiro			
: APPLICANT: Deng, Ta			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			

```

FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-678A-374

Query Match      100.0%   Score 2000:   DB 40:   Length 2000:
Best Local Similarity   100.0%:   Pred. No. 6.6e-226;
Matches 2000:   Conservative   0:   Mismatches   0:   Indels   0:   Gaps   0:

QY      1  ATGTGTGTTGAGGTTGATTCATGCGCGGCTGCGCTTCTTGTAAGAACGCAATTTGGTCTC 60
DB      1  ATGGGTGTTGAGGTTGATTCATGCGCGGCTGCGCTTCTTGTAAGAACGCAATTTGGTCTC 60

QY      61  AGGACCAAGATGGGCAAGTGTGTGCGCTTCCCTGCTCCCTGCTGCAAGGAGCGGCAAG 120
DB      61  AGGACCAAGATGGGCAAGTGTGTGCGCTTCCCTGCTCCCTGCTGCAAGGAGCGGCAAG 120

QY      121  ACCAACGTGGGACATCTTCGAGACCAACGACACTCTGCTATGAAGCACTCGAGGACAG 180
DB      121  ACCAACGTGGGACATCTTCGAGACCAACGACACTCTGCTATGAAGCACTCGAGGACAG 180

QY      181  ATGGGCAAGTGTGCGCGGACATGCTTCCCTGCTGCAAGGGGAGTGGCAAGAGCAACGTG 240
DB      181  ATGGGCAAGTGTGCGCGGACATGCTTCCCTGCTGCAAGGGGAGTGGCAAGAGCAACGTG 240

QY      241  GGCAGCTTCTGAGAGCACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300
DB      241  GGCAGCTTCTGAGAGCACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300

QY      301  TGTGTCTGCTCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360
DB      301  TGTGTCTGCTCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360

QY      361  GGAGACTACGATGACAGTACCTTCATGTGAGCCAGGTACGACGTCGCTGGAGAAATCTG 420
DB      361  GGAGACTACGATGACAGTACCTTCATGTGAGCCAGGTACGACGTCGCTGGAGAAATCTG 420

QY      421  GACAAGCTTCACAGAGCTGCTGTGTGGGTAAAGTCCCCAGAAAGGATCTCATCTGTCATG 480
DB      421  GACAAGCTTCACAGAGCTGCTGTGTGGGTAAAGTCCCCAGAAAGGATCTCATCTGTCATG 480

QY      481  CTCAGGGACACTGACGTGAACAAGAGCAACAGCAAGAGAGACTGCTTACATCTGGCC 540
DB      481  CTCAGGGACACTGACGTGAACAAGAGCAACAGCAAGAGAGACTGCTTACATCTGGCC 540

QY      541  TCTGGCAATGGGAATTCCAGAACTAGTAAACCTCTGCTGACAGACGATGTCACCTTAT 600
DB      541  TCTGGCAATGGGAATTCCAGAACTAGTAAACCTCTGCTGACAGACGATGTCACCTTAT 600

QY      601  GTCTCTGACAAACAAAAGAGGACAGCTCTGATTAAGGCCGTACAATGGCCAGGAAGATGAA 660
DB      601  GTCTCTGACAAACAAAAGAGGACAGCTCTGATTAAGGCCGTACAATGGCCAGGAAGATGAA 660

QY      661  TGTGGCTTAATGTGCTGAGACATGGGACACTGATCCAAATATTTCCAGAGTATGGAAAT 720
DB      661  TGTGGCTTAATGTGCTGAGACATGGGACACTGATCCAAATATTTCCAGAGTATGGAAAT 720

QY      721  ACCACTCTGCACTAGGCTTCTATTAATGAAGTAAATTAATGGCCAAAGCACTGCTCTTA 780
DB      721  ACCACTCTGCACTAGGCTTCTATTAATGAAGTAAATTAATGGCCAAAGCACTGCTCTTA 780

QY      781  TATGTGTGCTGATATGCAATCAAAAAACAAGCATGGGCTTCACACCACTGTACTTGGTGA 840
DB      781  TATGTGTGCTGATATGCAATCAAAAAACAAGCATGGGCTTCACACCACTGTACTTGGTGA 840

QY      841  CATGAGCAAAAAACGCAAGCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB      841  CATGAGCAAAAAACGCAAGCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900

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Db 841 CATGACAAAAACGCAAGTCGTAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY CTGATAGATATGAGAGAGACTGCTCTCATACTGCTGATGTGTGATCAGCAAGTATA 960
Db 901 CTGATAGATATGAGAGAGAGACTGCTCTCATACTGCTGATGTGTGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTGTGAGCAAAATATGTGATATCTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAGCCTTCTACTGTGAGCAAAATATGTGATATCTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATAATCTCTCTGAAACAGCAATCCAGAAACAGACTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATAATCTCTCTGAAACAGCAATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAGCAGTGAATAATAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAGCAGTGAATAATAGCCAGCAGAGAAA 1200
QY 1201 ATGCTCAGAGAACGAAATTAATAGAGTGTGATAGAGGCTTGAAGAAGAAATGAG 1260
Db 1201 ATGCTCAGAGAACGAAATTAATAGAGTGTGATAGAGGCTTGAAGAAGAAATGAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACCTGACTATGTGCTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACCTGACTATGTGCTGCTGGC 1320
QY 1321 AATGGTATATGATTAATTTCTCAAGAGAGAGAGACAGACCTGAAATACAGCAATTT 1380
Db 1321 AATGGTATATGATTAATTTCTCAAGAGAGAGAGAGACAGACCTGAAATACAGCAATTT 1380
QY 1381 CCTGACACGAAATGAGAGAGTATCAGAGATTTGCCAATTAATGTTTCTGATACAAAGAA 1440
Db 1381 CCTGACACGAAATGAGAGAGTATCAGAGATTTGCCAATTAATGTTTCTGATACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCACAGAGAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTGAAAT 1560
Db 1501 TCACAGAGAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAGAGAGAGAGAGTACTCATGTCGGATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAGAGAGAGAGAGTACTCATGTCGGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGCTGACAGTGTGCAATGTGATGATGATTAATTCCTCCAGAGAGAGC 1680
Db 1621 CTGACTAATGCTGACAGTGTGCAATGTGATGATGATTAATTCCTCCAGAGAGAGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAGATACAGAGAGAGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAGATACAGAGAGAGAA 1740
QY 1741 CAAATATATCTCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATAATACAGAGAG 1800
Db 1741 CAAATATATCTCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATAATACAGAGAG 1800
QY 1801 ATTCTGATATGAGAGAGAGAGAGTGAAGTGTGTAATAATAATGAAATTTCTGACTTCT 1860
Db 1801 ATTCTGATATGAGAGAGAGAGAGTGAAGTGTGTAATAATAATGAAATTTCTGACTTCT 1860
QY 1861 CTTAGTTGTAGAGAGAGAGAGAGTGTGATGAAATATGTAATGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAGAGAGAGAGAGAGTGTGATGAAATATGTAATGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAGAGAGTGGAGCTAGACCAATGAACATCAGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAGAGAGTGGAGCTAGACCAATGAACATCAGAGCCAGCTTAAAAA 1980

QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 37
US-10-212-679-302
; Sequence 302, Application US/10212679
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ. ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-302

Query Match 100.0%; Score 2000; DB 42; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTGGAGTGGTGAATTCATGCGCGGCTCTCTGTGAAGAGCAATTTGTC 60
Db 1 ATGTGGTGGAGTGGTGAATTCATGCGCGGCTCTCTGTGAAGAGCAATTTGTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTGCTTCCCTGCTCAGAGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTGCTTCCCTGCTCAGAGAGAGCGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACAGAGACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTGTGAGACACAGAGACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGGTGGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
QY 241 GGGCTTCTGAGAGACAGAGACTGCTATGAAGACACTCAGAGCAAGAGATGGCAAG 300
Db 241 GGGCTTCTGAGAGACAGAGACTGCTATGAAGACACTCAGAGCAAGAGATGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGACTAGTACATGATGCTTATGAGAGCCAGAGTACACAGTCCCTGGAAGAGACTG 420
Db 361 GGAAGACTAGTACATGATGCTTATGAGAGCCAGAGTACACAGTCCCTGGAAGAGACTG 420
QY 421 GACAAGTCCACAGAGTGGCTGGTGAAGTCCCGAGAAAGATCTCATGTCATG 480
Db 421 GACAAGTCCACAGAGTGGCTGGTGAAGTCCCGAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGAGACTGACGTGAACAGAGAGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
Db 481 CTCAGGAGACTGACGTGAACAGAGAGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGAGACAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGAGACAGATGCAACTTAAT 600

QY 601 GTCTTGAACAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAAGATGAA 660
 DB 601 GTCTTGAACAAAAGAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGAA 660
 QY 661 TGTGGCTTAATGTTCTGTGAACATGGCACTGATCCAAATATTTCCAGATGATGAAAT 720
 DB 661 TGTGGCTTAATGTTCTGTGAACATGGCACTGATCCAAATATTTCCAGATGATGAAAT 720
 QY 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
 DB 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
 QY 781 TATGGTGTGATATGATCAAAAACAGCATGGCCCTACACCACTGTTACTGGTGA 840
 DB 781 TATGGTGTGATATGATCAAAAACAGCATGGCCCTACACCACTGTTACTGGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
 DB 841 CATGAGCAAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGCTGCTCATACCTGCTGATGTTGATGATCAGCAAGTATA 960
 DB 901 CTGGATAGATATGGAAGAGCTGCTCATACCTGCTGATGTTGATGATCAGCAAGTATA 960
 QY 961 GTGACGCTCTCTAGAGCAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
 DB 961 GTGACGCTCTCTAGAGCAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
 QY 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGATTAATTTGCCAGTTACTTTCTGACTAC 1080
 DB 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGATTAATTTGCCAGTTACTTTCTGACTAC 1080
 QY 1081 AAGAAAAACATATGCTTAATAATCTCTTGAAACAGCAATCCAGAACAGACTTAAAG 1140
 DB 1081 AAGAAAAACATATGCTTAATAATCTCTTGAAACAGCAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTACCAAAAGGTTCAAAAGCAGTGAATTTGCCAGCAGAGAA 1200
 DB 1141 CTGACATCAGAGAGAGTACCAAAAGGTTCAAAAGCAGTGAATTTGCCAGCAGAGAA 1200
 QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAAGAAATGAAG 1260
 DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATATGTTGGATTACTAGAAAACCTGAAATGTTGCTGCTGGC 1320
 DB 1261 AAGCATGAAAGTAAATATGTTGGATTACTAGAAAACCTGAAATGTTGCTGCTGGC 1320
 QY 1321 AATGGTGAATATGATTAATCTCTCAAAAGAGAGAGCAACCTGAAATGAGCAATTT 1380
 DB 1321 AATGGTGAATATGATTAATCTCTCAAAAGAGAGAGCAACCTGAAATGAGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGGGAATTTAGTTCTGACTACAAAGAA 1440
 DB 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGGGAATTTAGTTCTGACTACAAAGAA 1440
 QY 1441 AAGAGATGCCAAATATCTCTCTGAAAACAGCAACCCGAAACAGACTTAAAGCTGACA 1500
 DB 1441 AAGAGATGCCAAATATCTCTCTGAAAACAGCAACCCGAAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGAGAGTATCAAAAGGCTTGAGGAGCTGAAAATGGCCAGCAGAGCTAGAAAAT 1560
 DB 1501 TCAGAGAGAGTATCAAAAGGCTTGAGGAGCTGAAAATGGCCAGCAGAGCTAGAAAAT 1560
 QY 1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGAGTACTATGTCGATTTCCAGAAAAC 1620
 DB 1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGAGTACTATGTCGATTTCCAGAAAAC 1620
 QY 1621 CTGACTAATATGTTGCTGCTGCTGCAATGTTGATGATTAATTTCTTCCAAAGAAAGAG 1680
 DB 1621 CTGACTAATATGTTGCTGCTGCTGCAATGTTGATGATTAATTTCTTCCAAAGAAAGAG 1680

QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCAGATGACGAA 1740
 DB 1681 AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCAGATGACGAA 1740
 QY 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATATTACACGATGAG 1800
 DB 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATATTACACGATGAG 1800
 QY 1801 ATTTCGATTCATGAAGAAAGAGATGAGATGAGTGTGAAGAAATGAATTTCTGCTTCT 1860
 DB 1801 ATTTCGATTCATGAAGAAAGAGATGAGATGAGTGTGAAGAAATGAATTTCTGCTTCT 1860
 QY 1861 CTAGTGTATGAAGAAAGAAAGACATCTTGATGAATATGATGATTTGGCGGAAGAAAT 1920
 DB 1861 CTAGTGTATGAAGAAAGAAAGACATCTTGATGAATATGATGATTTGGCGGAAGAAAT 1920
 QY 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAA 1980
 DB 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 38
 PCT-US02-24917-303
 ; Sequence 303, Application PC/TUS0224917

; GENERAL INFORMATION:
 ; APPLICANT: Corixa Corporation
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Hirst, Shannon Kathleen
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Foy, Teresa M.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.41931PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/24917
 ; CURRENT FILING DATE: 2002-08-05
 ; NUMBER OF SEQ ID NOS: 428
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 303
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 PCT-US02-24917-303

Query Match 77.5%; Score 1551; DB 1: Length 2040;
 Best Local Similarity 100.0%; Pred. No. 1.9e-173;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTGATTCATGCCGGCTGCTCTTGTGAAGAAAGCATTTGGCTTC 60
 DB 1 ATGGTGTGAGGTGATTCATGCCGGCTGCTCTTGTGAAGAAAGCATTTGGCTTC 60
 QY 61 AGAGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGCGCAAG 120
 DB 61 AGAGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGCGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGGAGACACAGACACTGCTATGAAGACTCAGAGCAAG 180
 DB 121 AGCAAGTGGGCACTTCTGGAGACACAGACACTGCTATGAAGACTCAGAGCAAG 180
 QY 181 ATGGGCAATGAGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACAGTG 240
 DB 181 ATGGGCAATGAGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACAGTG 240
 QY 241 GGGGCTTCTGGAGACACAGCACTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
 DB 241 GGGGCTTCTGGAGACACAGCACTGCTATGAAGACACTCAGAAAGATGGGCAAG 300

[illegible]

QY	481	CTCAGGGAACCTGACGTAACGAAACGAAGAGCAAGCAAAAAGAGACTGCTCATATCTGGCC	540
Db	481	CTCAGGGAACCTGACGTAACGAAACGAAGAGCAAGCAAAAAGAGACTGCTCATATCTGGCC	540
QY	481	CTCAGGGAACCTGACGTAACGAAACGAAGAGCAAGCAAAAAGAGACTGCTCATATCTGGCC	540
Db	481	CTCAGGGAACCTGACGTAACGAAACGAAGAGCAAGCAAAAAGAGACTGCTCATATCTGGCC	540
QY	541	TCCTGCCAATGGGAATTCAGAAATAGTAAAACTCTGCTGGACAGACGATGTCACCTTAAT	600
Db	541	TCCTGCCAATGGGAATTCAGAAATAGTAAAACTCTGCTGGACAGACGATGTCACCTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGGCCGTCAATATGCCAGGAACATGA	660
Db	601	GTCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGGCCGTCAATATGCCAGGAACATGA	660
QY	661	TGTCGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
Db	661	TGTCGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
QY	721	ACCACTCTGCATACCTATCTAATTAAGAAATTAATTAAGCCAAAAGCACTGCTCTTA	780
Db	721	ACCACTCTGCATACCTATCTAATTAAGAAATTAATTAAGCCAAAAGCACTGCTCTTA	780
QY	781	TATGTCCTGATATTCGAATCAATAAAAAACAAGCAATGGCCCTCACACACTGTACTTGCTGA	840
Db	781	TATGTCCTGATATTCGAATCAATAAAAAACAAGCAATGGCCCTCACACACTGTACTTGCTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGAGTATGATATGGAAGGAATGCTCTCATATCTGGCTATGTTGGAATCAGACAGATTA	960
Db	901	CTGAGTATGATATGGAAGGAATGCTCTCATATCTGGCTATGTTGGAATCAGACAGATTA	960
QY	961	GTCAGCCTTACTTGAGCAAAAAATATTGATGTATCTTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTACTTGAGCAAAAAATATTGATGTATCTTCAAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATGCTGTTTCTACTCATCATCATATTTGGCACTTAATCTTCTGACATAC	1080
Db	1021	GCCAGAGATGCTGTTTCTACTCATCATCATATTTGGCACTTAATCTTCTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAAATCTCTTCGAAAACAGCAATCCAGAAACAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAAATCTCTTCGAAAACAGCAATCCAGAAACAGACTTAAG	1140
QY	1141	CTGCAATCAGAGGAAGATCACAAGGTTCAAAAGGCAAGTGAATAATAGCCAGCAGAGAA	1200
Db	1141	CTGCAATCAGAGGAAGATCACAAGGTTCAAAAGGCAAGTGAATAATAGCCAGCAGAGAA	1200
QY	1201	ATGCTCTAAGACACAGAAAATTAATTAAGAGTGGGATGATAGAGAGTTGAAGAAATTAAG	1260
Db	1201	ATGCTCTAAGACACAGAAAATTAATTAAGAGTGGGATGATAGAGAGTTGAAGAAATTAAG	1260
QY	1261	AAGCATGAAAGTAAATATGAGGATTAAGTGAAGAAACCTGACTAATGATGCTCACTGCTGGC	1320
Db	1261	AAGCATGAAAGTAAATATGAGGATTAAGTGAAGAAACCTGACTAATGATGCTCACTGCTGGC	1320
QY	1321	AATGCTGATATATGATTAATTTCTCAAAGGAAGAGAGCAACCTCGAAAATTCAGCAATTT	1380
Db	1321	AATGCTGATATATGATTAATTTCTCAAAGGAAGAGAGCAACCTCGAAAATTCAGCAATTT	1380

Qy	1381	CCACACAAAGAAATGAAAGGTTCCACAGAAATTTGGATTGTTTGACATACAAANA	1440
Db	1381	CCTGACCAACGAAGTGAAGAGTATCCACAGATTTGGCAATTGTCTTGACTACCAANA	1440
Qy	1441	AAACAGATGCCAAAATCTCTTCTGCAAAACAGCAACCCAGAACACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATCTCTTCTGCAAAACAGCAACCCAGAACACTTAAAGCTGACA	1500
Qy	1501	TCACAGGAAGAGTCCACAAAGCTTTGAGGGCAGTGAANAATGGCCACGCCACAG	1551
Db	1501	TCACAGGAAGAGTCCACAAAGCTTTGAGGGCAGTGAANAATGGCCACGCCACAG	1551

DB	Query Match	Best Local Similarity	Matches 1551;	Conservative	Score 1551;	DB 16;	Length 2040;	Pred. No. 1.9e-173;	Mismatches 0;	Indels 0;	Gaps 0;
39	US-09-288-946-375	77.5%;	100.0%;	0;	0;	0;	0;	0;	0;	0;	0;
375	Sequence 375, Application US/09288946										
GENERAL INFORMATION:											
APPLICANT:	Xu, Jiangchun										
APPLICANT:	Dillon, Davin C.										
APPLICANT:	Mitcham, Jennifer Lynn										
TITLE OF INVENTION:	COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS										
FILE REFERENCE:	210121.427C7										
CURRENT APPLICATION NUMBER:	US/09/288,946										
CURRENT FILING DATE:	1999-04-09										
NUMBER OF SEQ ID NOS:	381										
SOFTWARE:	FastSeq for Windows Version 3.0										
SEQ ID NO 375											
LENGTH:	2040										
TYPE:	DNA										
ORGANISM:	Homo sapien										
US-09-288-946-375											
Query Match											
Best Local Similarity											
Matches 1551;											
Conservative											
Score 1551;											
DB 16;											
Length 2040;											
Pred. No. 1.9e-173;											
Mismatches 0;											
Indels 0;											
Gaps 0;											
1	ATGTTGGTTGAGGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAAGCCATTGGCTTC										
1	ATGGTGGTTGAAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAAGCCATTGGCTTC										
61	AGGACCAAGATGGGCAAGTGTCGTCGCTTCCCTGCTGCAAGGAGACGGCAAG										
61	AGGACCAAGATGGGCAAGTGTCGTCGCTTCCCTGCTGCAAGGAGACGGCAAG										
121	AGCAACGTTGGGCACTTCTTGAGAGCCACGACGACTCTGTATGAAGACACTCAGAGCAAG										
121	AGCAACGTTGGGCACTTCTTGAGAGCCACGACGACTCTGTATGAAGACACTCAGAGCAAG										
121	AGCAACGTTGGGCACTTCTTGAGAGCCACGACGACTCTGTATGAAGACACTCAGAGCAAG										
181	ATGGGCAAGTGGTGGCGGCACGTCCTCCCTGCTCAGAGGGAGATGGCAAGCAAGTG										
181	ATGGGCAAGTGGTGGCGGCACGTCCTCCCTGCTCAGAGGGAGATGGCAAGCAAGTG										
181	ATGGGCAAGTGGTGGCGGCACGTCCTCCCTGCTCAGAGGGAGATGGCAAGCAAGTG										
241	GGCGGTTCTGAGACACGACGACACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG										
241	GGCGGTTCTGAGACACGACGACACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG										
241	GGCGGTTCTGAGACACGACGACACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG										
241	GGCGGTTCTGAGACACGACGACACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG										
301	TGTTCTGTCACACTGCTTCCCTGCTGTCAGAGGGAGCGGCAAGCAAGTGGGCGCTTGG										
301	TGTTCTGTCACACTGCTTCCCTGCTGTCAGAGGGAGCGGCAAGCAAGTGGGCGCTTGG										
301	TGTTCTGTCACACTGCTTCCCTGCTGTCAGAGGGAGCGGCAAGCAAGTGGGCGCTTGG										
301	TGTTCTGTCACACTGCTTCCCTGCTGTCAGAGGGAGCGGCAAGCAAGTGGGCGCTTGG										
361	GGAGACTAGAGTGAAGAGTCCCTCATGTGAGAGCCAGGTATCAGCTCCGTTGGAAGATCTG										
361	GGAGACTAGAGTGAAGAGTCCCTCATGTGAGAGCCAGGTATCAGCTCCGTTGGAAGATCTG										
361	GGAGACTAGAGTGAAGAGTCCCTCATGTGAGAGCCAGGTATCAGCTCCGTTGGAAGATCTG										
361	GGAGACTAGAGTGAAGAGTCCCTCATGTGAGAGCCAGGTATCAGCTCCGTTGGAAGATCTG										
421	GACAAAGCTTCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG										
421	GACAAAGCTTCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG										

541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGCTGAGACAGATGCTCACTTAAT 600
|||||
541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGCTGAGACAGATGCTCACTTAAT 600
QY 601 GTCCCTTGACACAAAAAAGGACAGCTCTGATTAAGCCGCTACATGCCAGCAATGAA 660
|||||
Db 601 GTCCCTTGACACAAAAAAGGACAGCTCTGATTAAGCCGCTACATGCCAGCAATGAA 660
QY 661 TGTGGCTTAATGTTGCTGGAAACATGGCACTGATCCAAATATTCCAGATAGTATGAAAT 720
|||||
Db 661 TGTGGCTTAATGTTGCTGGAAACATGGCACTGATCCAAATATTCCAGATAGTATGAAAT 720
QY 721 ACCACTCTGCACTAGCCCTATCTATATGAAGATTAATTAATGAGCCCAACACTGCTCTTA 780
|||||
Db 721 ACCACTCTGCACTAGCCCTATCTATATGAAGATTAATTAATGAGCCCAACACTGCTCTTA 780
QY 781 TATGGTGGCTGATATGCAATCAAAAAACAAGCATGGCCCTACACACTGTTACTTGGTGA 840
|||||
Db 781 TATGGTGGCTGATATGCAATCAAAAAACAAGCATGGCCCTACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTCTGAAAAATTTTAAATCAAAAAAAGCGAATTTAAATGCA 900
|||||
Db 841 CATGAGCAAAAAACAGCAAGTCTGAAAAATTTTAAATCAAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATAGATATGGAAGACTGCTCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
|||||
Db 901 CTGATATAGATATGGAAGACTGCTCTCATACTTGTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTACAGCTTCTACTTGAGCAAAAAATATGATATCTTCTCAAGATCTATCTGACAGAG 1020
|||||
Db 961 GTACAGCTTCTACTTGAGCAAAAAATATGATATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTATGTCATCATATGTAATTTGGCAGTACTTCTGCTCTAC 1080
|||||
Db 1021 GCCAGAGATATGCTGTTCTATGTCATCATATGTAATTTGGCAGTACTTCTGCTCTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
|||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCGAGAGAGAGATGACAAAAAGTTCAAAAGGATGAAATATGCCAGCCAGAGAA 1200
|||||
Db 1141 CTGACATCGAGAGAGAGATGACAAAAAGTTCAAAAGGATGAAATATGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATGAAG 1260
|||||
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTGGATTAATAGAAAACTGACTAATGTCTCACTGCTGGC 1320
|||||
Db 1261 AAGCATGAAAGTAAATATGTGGATTAATAGAAAACTGACTAATGTCTCACTGCTGGC 1320
QY 1321 AATGTGATATATGATTAATCTCTCAAGGAAGAGCAGAACCTGAAAAATCAGCAATTT 1380
|||||
Db 1321 AATGTGATATATGATTAATCTCTCAAGGAAGAGCAGAACCTGAAAAATCAGCAATTT 1380
QY 1381 CCTGCAACGAAGTGAAGATGATCAAGAAATTTGGCAATTTGTTCTGACTACAAAGAA 1440
|||||
Db 1381 CCTGCAACGAAGTGAAGATGATCAAGAAATTTGGCAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTCTGAAAAACAGCAACCCAGAACAGACTTAAGAGTGACA 1500
|||||
Db 1441 AAACAGATGCCAAATTAATCTCTGAAAAACAGCAACCCAGAACAGACTTAAGAGTGACA 1500
QY 1501 TTAGAGAGAGAGATGACAAAGGCTTGAGGGCAGTGAAGAAATGGCCAGCCAGAG 1551
|||||
Db 1501 TTAGAGAGAGAGATGACAAAGGCTTGAGGGCAGTGAAGAAATGGCCAGCCAGAG 1551

RESULT 40
US-09-289-198-303
; Sequence 303, Application US/09289198
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-303

Query Match 77.5%; Score 1551; DB 16; Length 2040;
Best Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTATATTCATGCGCGCTGCTTCTTGTGAAAGACATTTGGTCTC 60
|||||
Db 1 ATGGTGTGAGGTATATTCATGCGCGCTGCTTCTTGTGAAAGACATTTGGTCTC 60
QY 61 AGGAGCAAGTGGGCAAGTGTGCTGCGCTTCTCCCTGCGCAAGGAGAGCGGCAAG 120
|||||
Db 61 AGGAGCAAGTGGGCAAGTGTGCTGCGCTTCTCCCTGCGCAAGGAGAGCGGCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
|||||
Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAATGTGTGCGCCCACTCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
|||||
Db 181 ATGGGCAATGTGTGCGCCCACTCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
QY 241 GGGCTTCTGGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGCAAG 300
|||||
Db 241 GGGCTTCTGGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGCGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGCGCTTGG 360
|||||
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGTGCTTCAATGAGCCAGGTATCACCTCCGTGAGAAATCTG 420
|||||
Db 361 GGAGACTAGATGACAGTGTGCTTCAATGAGCCAGGTATCACCTCCGTGAGAAATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGGGGTAAAGTCCCCGAAAGATCATGCTCAT 480
|||||
Db 421 GACAACTCCACAGAGCTGCTGGGGTAAAGTCCCCGAAAGATCATGCTCAT 480
QY 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAGGAGCTCTACATCTGGCC 540
|||||
Db 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAGGAGCTCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGCTGAGACAGATGCTCAACTTAAT 600
|||||
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGCTGAGACAGATGCTCAACTTAAT 600


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QY 601 GTCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCCGTACCAATGCCAGGAAGATGAA 660
Db 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCCGTACCAATGCCAGGAAGATGAA 660
QY 661 TGTGGTTAATGTGTGGTAACATGGCAGCTGATCCAAATATTTCCAGATGATGGAAT 720
Db 661 TGTGGTTAATGTGTGGTAACATGGCAGCTGATCCAAATATTTCCAGATGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATTAATGAATTAATATGGCCAAAGCACTGCTTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGAATTAATATGGCCAAAGCACTGCTTTA 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTGGTGA 840
Db 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY 901 CTGATATATATGAGAGAGCTGCTCTACTACTGTGATGTTGGATCGACAGATTA 960
Db 901 CTGATATATATGAGAGAGAGCTGCTCTACTACTGTGATGTTGGATCGACAGATTA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTTACATCATCATGTAATTTGCCAGTTACTTTGACATAC 1080
Db 1021 GCCAGAGATATGCTGTTCTTACATCATCATGTAATTTGCCAGTTACTTTGACATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATATCTTCTGAAAAACAGCAATCCAGCAAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATATCTTCTGAAAAACAGCAATCCAGCAAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGCTCAAAAGTTCAAAGGCACTGAAATATAGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGCTCAAAAGTTCAAAGGCACTGAAATATAGCCAGCCAGAGAA 1200
QY 1201 ATGCTCTAGAGAAACAGAAATTAATTAAGGATGATGATGAGAGGTTGAAGAAATGAG 1260
Db 1201 ATGCTCTAGAGAAACAGAAATTAATTAAGGATGATGATGAGAGGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAATTAATTAATGTGGATTAAGTAAAGAACTGACTAATGTGCTACTGCTGC 1320
Db 1261 AAGCATGAAATTAATTAATGTGGATTAAGTAAAGAACTGACTAATGTGCTACTGCTGC 1320
QY 1321 AATGGTATTAATGATTAATCTCTCAAGAGAGAGAGACAGACCTGAATATCAGCAATTT 1380
Db 1321 AATGGTATTAATGATTAATCTCTCAAGAGAGAGAGACAGACCTGAATATCAGCAATTT 1380
QY 1381 CCTGACAAAGAGAGAGAGAGTATCAGAGATTTGCCAATTAATTTCTGATACAGAAAG 1440
Db 1381 CCTGACAAAGAGAGAGAGAGTATCAGAGATTTGCCAATTAATTTCTGATACAGAAAG 1440
QY 1441 AAACAGATGCCAAATACTCTTGAAGAAACAGCAACCCAGAAAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTGAAGAAACAGCAACCCAGAAAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGAGAGAGAGCTTGAAGGAGAGTGAATTTGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGAGAGAGAGAGCTTGAAGGAGAGTGAATTTGCCAGCCAGAG 1551

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RESULT 41
US-09-429-755-303

; Sequence 303, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda

```

; APPLICANT: Reller, Marc W.  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.419C6  
; CURRENT APPLICATION NUMBER: US/09/429,755A  
; CURRENT FILING DATE: 1999-10-28  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 303  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-429-755-303  
  
Query Match 77.5%; Score 1551; DB 18; Length 2040;  
Best Local Similarity 100.0%; Pctd. No. 1,9e-173;  
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGGGTGTTGAGGTGATTCATGCGCGCTGCTCTCTCTGTGAAGAACCAATTTGCTC 60  
Db 1 ATGGGTGTTGAGGTGATTCATGCGCGCTGCTCTCTCTGTGAAGAACCAATTTGCTC 60  
QY 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTCTGCGAGGAGCGGCAAG 120  
Db 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTCTGCGAGGAGCGGCAAG 120  
QY 121 AGCAACGTGGCACTTCTGGAGACACAGACAGACGCTGTATGAAGACACTGAGAGCAAG 180  
Db 121 AGCAACGTGGCACTTCTGGAGACACAGACAGACGCTGTATGAAGACACTGAGAGCAAG 180  
QY 181 ATGGCAAGTGTGGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240  
Db 181 ATGGCAAGTGTGGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240  
QY 241 GGCGCTTGTGAGACACAGACGACTCTGCTATGAAGACCTCAGAGACAGATGGCAAG 300  
Db 241 GGCGCTTGTGAGACACAGACGACTCTGCTATGAAGACCTCAGAGACAGATGGCAAG 300  
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGTGGGCTTGG 360  
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGTGGGCTTGG 360  
QY 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420  
Db 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420  
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480  
Db 421 GACAAAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480  
QY 481 CTCAGGGACACTGACGTGAACAGAGAGCAAGCAAGAAAGAGAGCTGCTCATCTGACC 540  
Db 481 CTCAGGGACACTGACGTGAACAGAGAGCAAGCAAGAAAGAGAGCTGCTCATCTGACC 540  
QY 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGACAGACGATGTCAACTTAAT 600  
Db 541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGACAGACGATGTCAACTTAAT 600  
QY 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCGCTTCAATGACAGAAAGATGAA 660  
Db 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCGCTTCAATGACAGAAAGATGAA 660  
QY 661 TGTGGTTAATGTGTGGTAACATGGCAGCTGATCCAAATATTTCCAGATGATGGAAT 720  
Db 661 TGTGGTTAATGTGTGGTAACATGGCAGCTGATCCAAATATTTCCAGATGATGGAAT 720  
QY 721 ACCACTGCACTACGCTATCTATTAATGAATTAATATGGCCAAAGCACTGCTTTA 780  
Db 721 ACCACTGCACTACGCTATCTATTAATGAATTAATATGGCCAAAGCACTGCTTTA 780  
QY 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTGGTGA 840  
Db 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTGGTGA 840

```



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Db 781 TATGTCGTGATATGCAATCAAAAAACAAGCATGGCTTCACACCACTGTACTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Oy 901 CTGATAGATATGGAAGAGCTGCTCTACTACTTCTGTATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCTACTACTTCTGTATGTTGTGGATCAGCAAGTATA 960
Oy 961 CTCAGACCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGACAGACG 1020
Db 961 CTCAGACCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGACAGACG 1020
Oy 1021 GCCAGAGATATGTTTCTATGATCATCATGTAATTTGCAAGTACTTCTGACACTAC 1080
Db 1021 GCCAGAGATATGTTTCTATGATCATCATGTAATTTGCAAGTACTTCTGACACTAC 1080
Oy 1081 AAAGAAAAACAGATCTTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Oy 1141 CTGATATCAGAGGAAGAGTCAACAAAGTTCAAGGCACTGAAATATGCCAGCAGAGAAA 1200
Db 1141 CTGATATCAGAGGAAGAGTCAACAAAGTTCAAGGCACTGAAATATGCCAGCAGAGAAA 1200
Oy 1201 ATGTCTCAAGAACAGAAATATAATAGGATGATAGAGAGTGAAGAAAGAAATAGAA 1260
Db 1201 ATGTCTCAAGAACAGAAATATAATAGGATGATAGAGAGTGAAGAAAGAAATAGAA 1260
Oy 1261 AAGCATGAAAGTAATATGTTGGGATTAAGGATGATAGAGAGTGAAGAAAGAAATAGAA 1320
Db 1261 AAGCATGAAAGTAATATGTTGGGATTAAGGATGATAGAGAGTGAAGAAAGAAATAGAA 1320
Oy 1321 AATGTTGATTAATGATTAATCTCTCAAGAGAGACAGAACCTGGAATATGATCACTG 1380
Db 1321 AATGTTGATTAATGATTAATCTCTCAAGAGAGACAGAACCTGGAATATGATCACTG 1380
Oy 1381 CCTGACAAAGAAAGAGATATCAGAAATTTGCAATTTGTTCTGACTACCAAGAA 1440
Db 1381 CCTGACAAAGAAAGAGATATCAGAAATTTGCAATTTGTTCTGACTACCAAGAA 1440
Oy 1441 AAACGATGCCAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAAGCTTGAAGGCACTGAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAAGCTTGAAGGCACTGAAATGGCCAGCCAGAG 1551
```

```
RESULT 42
US-09-443-686-375
; Sequence 375, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Hatlocke, Susan Louise
; APPLICANT: Jlang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Soik, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443.686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-375

Query Match          77.5%; Score 1551; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTGTTGAGTGTGATTCATGCCGCTCTCTTGTGAAGAACCAATTTGGTCTC 60
Db 1 ATGTGTTGAGTGTGATTCATGCCGCTCTCTTGTGAAGAACCAATTTGGTCTC 60
Oy 61 AGAGCAATATGGCAAGTGTGCTGCTTCTTCTTCTGCTGCGAGAGAGCGGCAAG 120
Db 61 AGAGCAATATGGCAAGTGTGCTGCTTCTTCTTCTGCTGCGAGAGAGCGGCAAG 120
Oy 121 AGCAAGTGGGCACTTCTGAGAACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Oy 241 GGGGCTTCTGGAGACAGACAGACTCTGCTATGAAGACACTGAGAAACAAGATGGGCAAG 300
Db 241 GGGGCTTCTGGAGACAGACAGACTCTGCTATGAAGACACTGAGAAACAAGATGGGCAAG 300
Oy 301 TGGTGTGCACTGCTCCCTGCTGCAAGGGGAGCGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTCCCTGCTGCAAGGGGAGCGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGTCCCTTCAAGAGCCAGGATACAGCTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCAAGAGCCAGGATACAGCTCCGTGGAGAAATCTG 420
Oy 421 GCAAGCTCCAGAGAGCTGCTGGGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
Db 421 GCAAGCTCCAGAGAGCTGCTGGGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
Oy 481 CTCAGGAGACCTGAGCTGGAACAAGAGCAAGCAAGAAAGAGACTCTTACATCTGGCC 540
Db 481 CTCAGGAGACCTGAGCTGGAACAAGAGCAAGCAAGAAAGAGACTCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAATGTAATAATCTCTGACAGACGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATAATCTCTGACAGACGATGTCAACTTAAT 600
Oy 601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATTAAGGCGCTACATGCCAGAAATGTA 660
Db 601 GTCTTTGACAAACAAAAAGAGAGAGCTCTGATTAAGGCGCTACAAAGCCAGAGAAATGTA 660
Oy 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTATGGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTATGGAAT 720
Oy 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Oy 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCTTCAACACACTGTTACTGTTGA 840
Db 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCTTCAACACACTGTTACTGTTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Oy 901 CTGATAGATATGGAAGAGCTGCTCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA 960
```

Qy	961	GTGACGCTTCTACTTGGACAAATATTGATGTATCTTCCAAAGATCTATCTGGACAGCG	1020
Db	961	GTGACGCTTCTACTTGGACAAATATTGATGTATCTTCCAAAGATCTATCTGGACAGCG	1020
Qy	1021	GCCAGAGATATGCTGTTTCTTACATCATCATGTATTTGGCAGTTCTCTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTTACATCATCATGTATTTGGCAGTTCTCTTCTGACTAC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAATCTTCTTGAAACAGACATTCGAAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTTCTTGAAACAGACATTCGAAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGAAAGAGTCCACAAAGGTTCCAAAGCAGTGAATAATAGCCAGCAGAAA	1200
Db	1141	CTGACATCAGAGAAAGAGTCCACAAAGGTTCCAAAGCAGTGAATAATAGCCAGCAGAAA	1200
Qy	1201	ATGTCTCAAGAACCCAGAAATTAATAAGATGGTATGATAGAGAGTTGAAGAAATAATGAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATTAATAAGATGGTATGATAGAGAGTTGAAGAAATAATGAG	1260
Qy	1261	AAGCATGAAGTAAATATATGTGGGATTAATCTAGAAACCTGACTAATGTGTCTACGTGCG	1320
Db	1261	AAGCATGAAGTAAATATATGTGGGATTAATCTAGAAACCTGACTAATGTGTCTACGTGCG	1320
Qy	1321	AATGTATATATGATTAATTTCTCTCAAGGAGAGCAGAAACCTGAAATACAGCAATTT	1380
Db	1321	AATGTATATATGATTAATTTCTCTCAAGGAGAGCAGAAACCTGAAATACAGCAATTT	1380
Qy	1381	CTGACACAGAAAGTGAAGAGTATCAGCAATTTGCGAATTTAGTTCTGACTACAAAGAA	1440
Db	1381	CTGACACAGAAAGTGAAGAGTATCAGCAATTTGCGAATTTAGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTCTTGTGAAAACAGCAACCCGAAACAGACTTAAAGTACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTGTGAAAACAGCAACCCGAAACAGACTTAAAGTACA	1500
Qy	1501	TCAGAGGAAAGATGCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1561
Db	1501	TCAGAGGAAAGATGCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1561
RESULT 43			
: US-09-483-672A-375			
: Sequence 375, Application US/09483672A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan Louise			
: APPLICANT: Jiang Yugu			
: APPLICANT: Reed, Steven G.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retter, Marc W.			
: APPLICANT: Solk, John A.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Wang, Aljun			
: APPLICANT: Meagher, Madeleine			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
: FILE REFERENCE: 210121.42711C11			
: CURRENT APPLICATION NUMBER: US/09/483,672A			
: CURRENT FILING DATE: 2000-01-14			
: NUMBER OF SEQ ID NOS: 590			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 375			
: LENGTH: 2040			
: TYPE: DNA			
: ORGANISM: Homo sapien			
: US-09-483-672A-375			

Query Match Similarity		77.5%;	Score 1551;	DB 18;	Length 2040;
Best Local		Similarity 100.0%;	Pred. No. 1, 9e-173;		
Matches 1551;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	ATGTGTTGAGTGTGATTCATGCGCGCTGCCTCTTCTGTGAAAGAACCATTTGGTCTC	60		
Db	1	ATGGTGTGTGAGTGTGATTCATGCGCGCTGCCTCTTCTGTGAAGAACCATTTGGTCTC	60		
OY	61	AGGACCAAGATGGGCAAGTGGTGGCGGTTGCTTCCCTCCTGTGAGGAGACAGGGGCAAG	120		
Db	61	AGGACCAAGATGGGCAAGTGGTGGCGGTTGCTTCCCTCCTGTGAGGAGACAGGGGCAAG	120		
OY	121	AGCAACGTGGGCACTTCTGGAAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG	180		
Db	121	AGCAACGTGGGCACTTCTGGAAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG	180		
OY	181	ATGGGCAAGTGTGGCGGCACTGCTTCCCTCCTGTGAGGAGTGGGCAAGACAGCTG	240		
Db	181	ATGGGCAAGTGTGGCGGCACTGCTTCCCTCCTGTGAGGAGTGGGCAAGACAGCTG	240		
OY	241	GCGCGTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGGACAAATATGGGCAAG	300		
Db	241	GCGCGTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGGACAAATATGGGCAAG	300		
OY	301	TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360		
Db	301	TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360		
OY	361	GGAGACTCGAGTGAAGAGTGGCGCTTCAATGGAAGCCAGAGTACACGTCGCCGAGGAAGATCTG	420		
Db	361	GGAGACTCGAGTGAAGAGTGGCGCTTCAATGGAAGCCAGAGTACACGTCGCCGAGGAAGATCTG	420		
OY	421	GACAAAGCTCCACAGAGCTGCCTGTGGGGTAAAGTCCCCAGAAAGATCTCATGTCATG	480		
Db	421	GACAAAGCTCCACAGAGCTGCCTGTGGGGTAAAGTCCCCAGAAAGATCTCATGTCATG	480		
OY	481	CTCAGGAGCACTGACGTGAACAAGAAAGGACAAAGCAAGAGACGCTCTACATCTGGCC	540		
Db	481	CTCAGGAGCACTGACGTGAACAAGAAAGGACAAAGCAAGAGACGCTCTACATCTGGCC	540		
OY	541	TCTGCGCAATGGGAATTCAGAAAGTAGTAATAACCTCCTGCTGGAGACAGACGATGTCAACTTAAT	600		
Db	541	TCTGCGCAATGGGAATTCAGAAAGTAGTAATAACCTCCTGCTGGAGACAGACGATGTCAACTTAAT	600		
OY	601	GTCCTTGACACAAAAAAGAGACAGCTCTGTATAAAGCCGTACAAATGGCAGAGAAATGAA	660		
Db	601	GTCCTTGACACAAAAAAGAGACAGCTCTGTATAAAGCCGTACAAATGGCAGAGAAATGAA	660		
OY	661	TGTGCGTAAATGTTGCTGGACATGAGGACACTATATTCAGATATTCAGATGATATGAAAT	720		
Db	661	TGTGCGTAAATGTTGCTGGACATGAGGACACTATATTCAGATATTCAGATGATATGAAAT	720		
OY	721	ACCACTCTGCACATACGCTATCTATATGAGATTAATTAATGCGCAAGCACTGCTCTTA	780		
Db	721	ACCACTCTGCACATACGCTATCTATATGAGATTAATTAATGCGCAAGCACTGCTCTTA	780		
OY	781	TATGTGCTGTGATTCGATTCGATCAAAAAACAAGATGGCCCTCACACCACTGTTACTTGGTGTGA	840		
Db	781	TATGTGCTGTGATTCGATTCGATCAAAAAACAAGATGGCCCTCACACCACTGTTACTTGGTGTGA	840		
OY	841	CATGAGCAAAAAACAGCAAGTGTGTAATTTTAAATTCAGAAAGAAAGCAATTTAAATGCA	900		
Db	841	CATGAGCAAAAAACAGCAAGTGTGTAATTTTAAATTCAGAAAGAAAGCAATTTAAATGCA	900		
OY	901	CTGGATAGATATGGAAGAGACTGCTCTCATCTTGTGTATTTGTGTGATGACGCAAGTATA	960		
Db	901	CTGGATAGATATGGAAGAGACTGCTCTCATCTTGTGTATTTGTGTGATGACGCAAGTATA	960		
OY	961	GTCAGCCTTCTACTTGAGCAAAATATTGATATCTATCTTCTCAAGATCTATCTGGACAGACG	1020		
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTGATATCTATCTTCTCAAGATCTATCTGGACAGACG	1020		
OY	1021	GCCAGAGATATGCTGTTTCTAGTATCATCATATGATTAATTTGCCAGATTACTTCTGACTAC	1080		

|||||
Db 1021 GCCAGAGATATGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Oy 1081 AAGAAAAACGATGCTAAATCTCTCTGAAAACAGAAATCCGAGAACAACTTAAAG 1140
Db 1081 AAGAAAAACGATGCTAAATCTCTCTGAAAACAGAAATCCGAGAACAACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGTAATATCTGGATTTACTAGAAAACCTGACTAAATGCTGCTGGC 1320
Db 1261 AAGCATGAAGTAATATCTGGATTTACTAGAAAACCTGACTAAATGCTGCTGGC 1320
Oy 1321 AATGGTGAATGATTAATCTCTCAAGAGAGAGCAGAAACCTGAAATAGCAATTT 1380
Db 1321 AATGGTGAATGATTAATCTCTCAAGAGAGAGCAGAAACCTGAAATAGCAATTT 1380
Oy 1381 CCTGACAAACGAAAGTGAAGATATCAGAAATTTGGAAATAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAACGAAAGTGAAGATATCAGAAATTTGGAAATAGTTCTGACTACAAAGAA 1440
Oy 1441 AAGCATGCTCAAAATCTCTCTGAAAACAGCAACCCGAGAACAACTTAAAGTGAACA 1500
Db 1441 AAGCATGCTCAAAATCTCTCTGAAAACAGCAACCCGAGAACAACTTAAAGTGAACA 1500
Oy 1501 TCAGAGAGAGTCAAAAGCTTGAGGAGTGAATAATGGCCAGCAGAG 1551
Db 1501 TCAGAGAGAGTCAAAAGCTTGAGGAGTGAATAATGGCCAGCAGAG 1551

RESULT 44

US-09-534-825A-303

Sequence 303, Application US/09534825A

GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Reed, Steven G.

APPLICANT: Misher, Lynda

APPLICANT: Reiter, Marc W.

APPLICANT: Dillon, David C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TREATMENT AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.419C7

CURRENT FILING DATE: US/09/534,825A

NUMBER OF SEQ ID NOS: 317

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 303

LENGTH: 2040

TYPE: DNA

ORGANISM: Homo sapien

US-09-534-825A-303

Query Match 77.5%; Score 1551; DB 20; Length 2040;
Best Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGGTGTTGAGTGTGATTCATGCCGCTGCTCTTCTGTGAAGAGCCATTTGGTCTC 60
Db 1 ATGGTGTTGAGTGTGATTCATGCCGCTGCTCTTCTGTGAAGAGCCATTTGGTCTC 60
Oy 61 AGGACAAAGATGGCAAGTGTGCTGCGTGTGCTCCCTGGTGGAGGAGCGGCAAG 120
Db 61 AGGACAAAGATGGCAAGTGTGCTGCGTGTGCTCCCTGGTGGAGGAGCGGCAAG 120
Oy 121 AGCAACGTGGGCACTTCTGGAGACCAAGCAGACTGCTATGAAGACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCAGACTGCTATGAAGACTCAGAGCAAG 180

Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCAGACTGCTATGAAGACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGGTGGCGGCACATGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
Db 181 ATGGGCAAGTGGTGGCGGCACATGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
Oy 241 GCGCTTCTGGAGACCAAGCAGACTGCTATGAAGAGCCTGAGAACAAAGTGGGCAAG 300
Db 241 GCGCTTCTGGAGACCAAGCAGACTGCTATGAAGAGCCTGAGAACAAAGTGGGCAAG 300
Oy 301 TGTGCTGCTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TGTGCTGCTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Oy 361 GGAGACTACGATGACAGTCTTCAATGAGCCAGGTACAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCTTCAATGAGCCAGGTACAGTCCGTGGAGAAATCTG 420
Oy 421 GACAAAGCTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GACAAAGCTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Oy 481 CTCAGGAGACCTGACGTGAACAAGAACGAAAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACCTGACGTGAACAAGAACGAAAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy 541 TCTGCCAATGGGAATTCAGAAATGATTAATCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATTAATCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Oy 601 GTTCCTTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTTCCTTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Oy 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
Oy 721 ACCACTCTGCTAGCTATCTATTAATGAAGATTAATGAGCCAAAGCAGTCTGCTTA 780
Db 721 ACCACTCTGCTAGCTATCTATTAATGAAGATTAATGAGCCAAAGCAGTCTGCTTA 780
Oy 781 TATGGTGTGATATCAATCAAAAAAACAAGCATGAGCTGCTGCTGCTGCTGCTGCT 840
Db 781 TATGGTGTGATATCAATCAAAAAAACAAGCATGAGCTGCTGCTGCTGCTGCTGCT 840
Oy 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTAATCAGAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTAATCAGAAAAAAGCGAATTTAAATGCA 900
Oy 901 CTGGATAGATGGAAG 960
Db 901 CTGGATAGATGGAAG 960
Oy 961 GTGAGCTTCTGCTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 GTGAGCTTCTGCTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATG 1020
Oy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Oy 1081 AAGAAAAACGATGCTAAATCTCTCTGAAAACAGAAATCCGAGAACAACTTAAAG 1140
Db 1081 AAGAAAAACGATGCTAAATCTCTCTGAAAACAGAAATCCGAGAACAACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGAGCAGTGAATAATAGCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAAGAAATGAAG 1260

QY	1261	AAGCATGAAGTATATATGAGGATCTACAGAAAACCTGACTAAATGGTGCATCGCTGGC	1320
Db	1261	AAGCATGAAGTATATATGAGGATCTACAGAAAACCTGACTAAATGGTGCATCGCTGGC	1320
QY	1321	AATGGTATTAATGATTAATCTCTCAAGGAAGAGCAGAACCTGAAATTCAGCAATTT	1380
Db	1321	AATGGTATTAATGATTAATCTCTCAAGGAAGAGCAGAACCTGAAATTCAGCAATTT	1380
QY	1381	CCTGACAAAGAAAGTGAAGAGTTCACAGAAATTTGGCAATTGTTCTGATACACAAAGAA	1440
Db	1381	CCTGACAAAGAAAGTGAAGAGTTCACAGAAATTTGGCAATTGTTCTGATACACAAAGAA	1440
QY	1441	AAACAGATGCCAAATTACTTCTTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATTACTTCTTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
QY	1501	TCACAGGAAGTACACAAAGGCGTTGAGGGCAGTGGAAAAATGGCCAGCCGAG	1551
Db	1501	TCACAGGAAGTACACAAAGGCGTTGAGGGCAGTGGAAAAATGGCCAGCCGAG	1551

```

RESULT 45
US-09-536-857-375
Sequence 375, Application US/09536857
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqul
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536,857
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 592
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-375

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[illegible]

Oy	301	TGAGCTCCACATCTGTCCTCCCTGCTGGAGGGGAGGGCAAGAGCAAGTGTGGCGCTGG	360
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Oy	361	GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGGTACACGCTCCGTGGAGAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGGTACACGCTCCGTGGAGAAGATCTG	420
Oy	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAATGCCCGAAGAAAGATCTCATCTGCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAATGCCCGAAGAAAGATCTCATCTGCATG	480
Oy	481	CTCAGGGACACTGCAGTGAACAAAGAGACAGCAAGAAAGAGAGACTGCTTCATCTGGCC	540
Db	481	CTCAGGGACACTGCAGTGAACAAAGAGAGACAGCAAGAAAGAGAGACTGCTTCATCTGGCC	540
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Db	541	TCTGCAATGGGAATTCAGAAATGTCTGCTGCTGAGACAGAGATCTCAACTTAAAT	600
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Db	601	GTCCTTGACACAAAGAGAGACAGCTCTGTAAAGCCGTAAACATCCAGGAAGATGA	660
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Db	661	TGTGCGTTAAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTCAGATGATGAAT	720
Oy	721	ACCACTGCGACTCGGCAATCTAATGAAGATTAATTAATGGCCAAAGCAGCTCTTA	780
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Db	781	TATGATGCTGATATCGAATCAAAAAGACATGGCCCTCAACACACTGTTACTTGGTGA	840
Oy	841	CATGAGCAAAAACAGCAAGTGTCAAAATTTTAAATCAAGAAAAAGGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTCAAAATTTTAAATCAAGAAAAAGGAATTTAAATGCA	900
Oy	901	CTGATAGATATGGAAGAGACTGCTCATACTTCTTAATGTTGGATCAGCAAGATTA	960
Db	901	CTGATAGATATGGAAGAGACTGCTCATACTTCTTAATGTTGGATCAGCAAGATTA	960
Oy	961	GTCAGCCTTCTACTTGAACAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGAGC	1020
Db	961	GTCAGCCTTCTACTTGAACAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGAGC	1020
Oy	1021	GCCAGAGATGTGCTGTTTCTAGTCAATCATCATATTAATTTGCCAGTACTTGTGACTAC	1080
Db	1021	GCCAGAGATGTGCTGTTTCTAGTCAATCATCATATTAATTTGCCAGTACTTGTGACTAC	1080
Oy	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAAAGCTTAAAG	1140
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Oy	1141	CTGACATATAGAGGAAGAGTCAACAAGGTTCAAAAGCAGTAAAAATACCCAGAGAAAA	1200
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Oy	1261	AAGCATGAAGTAATATGTGGATTCTAGAAAACTGCAATAGGTGTCACTGCTGGC	1320
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Oy	1321	AATGCTGATTAATGATTAATTTCTCAAGGAAGCAGAACACCTGAAAAATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGATTAATTTCTCAAGGAAGCAGAACACCTGAAAAATCAGCAATTT	1380

Qy	1021	GCACAGAGATGCGTGGTTTCAGTCAATCATTGTAATTTGGCAGTACTCTTGACTAC	108
Dp	1021	GCCAGAGAGTATGCGTGGTTTCAGTCAATCATTGTAATTTGGCAGTACTCTTGACTAC	108
Qy	1081	AAAGAAAACGAGATGCTAAAAATCTCTTGAAAAACGCAATCCAGAACAGCTTTAAAG	114
Dp	1081	AAAGAAAACGAGATGCTAAAAATCTCTTGAAAAACGCAATCCAGAACAGCTTTAAAG	114
Qy	1141	CTGACATCAGAGAGAGATGCACAAAGGTTTAAAGGCGATGAAATATAGCCACGAGAGAA	120
Dp	1141	CTGACATCAGAGAGAGATGCACAAAGGTTTAAAGGCGATGAAATATAGCCACGAGAGAA	120
Qy	1201	ATGTCCTCAAGAACCAAGAAATTAATTAAGGATGGTATGAAAGGTTGAAAGAAATTAAGG	126
Dp	1201	ATGTCCTCAAGAACCAAGAAATTAATTAAGGATGGTATGAAAGGTTGAAAGAAATTAAGG	126
Qy	1261	AAGCATGAAAGTAATTAATGTGGGATTAAGTGAAGAACCTGCATATGGTGTCACTGCTGGG	132
Dp	1261	AAGCATGAAAGTAATTAATGTGGGATTAAGTGAAGAACCTGCATATGGTGTCACTGCTGGG	132
Qy	1321	AATGGTGAATTAATGATTAATTTCTCCAAAGCAGACGAACACCTGAAAAATCAGCAATTT	138
Dp	1321	AATGGTGAATTAATGATTAATTTCTCCAAAGCAGACGAACACCTGAAAAATCAGCAATTT	138

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Search completed: November 8, 2002, 15:48:01
 Job time : 3957.07 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 02:07:38 : Search time 4020.92 Seconds
(without alignments)
12755.953 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atggttggtgagtgatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3	2040	100.0	2040	15	US-09-289-198-303
4	2040	100.0	2040	18	US-09-429-755-303
5	2040	100.0	2040	18	US-09-443-686-375
6	2040	100.0	2040	18	US-09-483-672A-375
7	2040	100.0	2040	20	US-09-534-825A-303
8	2040	100.0	2040	20	US-09-536-857-375
9	2040	100.0	2040	22	US-09-568-100A-375
10	2040	100.0	2040	22	US-09-577-505B-303
11	2040	100.0	2040	22	US-09-590-583-303
12	2040	100.0	2040	22	US-09-593-793A-375
13	2040	100.0	2040	23	US-09-636-215-375
14	2040	100.0	2040	24	US-09-636-215-375
15	2040	100.0	2040	25	US-09-651-236-375
16	2040	100.0	2040	25	US-09-657-279-375
17	2040	100.0	2040	26	US-09-679-272-375
18	2040	100.0	2040	26	US-09-679-426-375
19	2040	100.0	2040	27	US-09-685-166-375
20	2040	100.0	2040	27	US-09-685-166A-375
21	2040	100.0	2040	27	US-09-699-295-303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES


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23 2040 100.0 2040 29 US-09-759-143-375 Sequence 375, App
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25 2040 100.0 2040 31 US-09-810-936-303 Sequence 375, App
26 2040 100.0 2040 31 US-09-822-827-375 Sequence 375, App
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33 2040 100.0 2040 38 US-10-010-940-375 Sequence 375, App
34 2040 100.0 2040 38 US-10-012-896-375 Sequence 375, App
35 2040 100.0 2040 39 US-10-079-137B-303 Sequence 303, App
36 2040 100.0 2040 42 US-10-144-678A-375 Sequence 375, App
37 2040 100.0 2040 42 US-10-212-679-303 Sequence 303, App
38 1940 95.1 2000 16 PCT-US02-24917-302 Sequence 302, App
39 1940 95.1 2000 16 US-09-288-946-374 Sequence 374, App
40 1940 95.1 2000 16 US-09-288-198-302 Sequence 302, App
41 1940 95.1 2000 18 US-09-429-755-302 Sequence 302, App
42 1940 95.1 2000 18 US-09-443-686-374 Sequence 374, App
43 1940 95.1 2000 18 US-09-483-672A-374 Sequence 374, App
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45 1940 95.1 2000 20 US-09-536-857-374 Sequence 374, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-303
Sequence 303, Application PC/TUS0224917
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Fanger, Gary R.
APPLICANT: Hirst, Shannon Kathleen
APPLICANT: Dillon, Davin C.
APPLICANT: Foy, Teresa M.
APPLICANT: Houghton, Raymond L.
APPLICANT: Persing, David H.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: AND DIAGNOSTICS OF BREAST CANCER
CURRENT APPLICATION NUMBER: PCT/US02/24917
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 428
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-24917-303
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Query Match 100.0%, Score 2040, DB 1, Length 2040;
Best Local Similarity 100.0%, Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGGTGGTGGAGTATTCATGCGGGCTCTTGTGTAAGAACCATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGTGTCAGAGGAGCGCAAG 120
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DB 121 AGCAGCTGGGGCACTTGTGAGACACGAGACTGTGTATGAAGAACTCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCCACTGCTCCCTGTGTCAGAGGAGGAGTGGCAAGCAAGCTG 240
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Db 1381 CCTGCAACGAAGAGTGAAGAGTATCAGCAATTTGGCAATTAATGTTCTGACTACAAAGAA 1440
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Db 1441 AAACAGATGCCAAAATATCTCTTGAANAACAGCAACCCAGAACAAAGACTTAAAGCTGACA 1500
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Db 1501 TCAGAGAGAGAGTACAAAGAGCTTGAGGGCAGTGAATAATGGCCAGACAGAAAGATCT 1560
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Db 1561 CAAGAACCAAGAAATTAATTAAGAGTGTGATAGAGACTAGAAATTTTATGGCTATCGAA 1620
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Db 1621 GAATGGAAGAGACAGGAGATCTCATGTCCGATTTCCAGAAACCTGACTATATGTGCTC 1680
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Db 1861 GAAAGACGATAGAAAGTGTGAATAATGAAATTCGACTGCTTCTTGTGTAAGAA 1920
QY 1921 GAAAGACGATAGAAAGTGTGAATAATGAAATTCGACTGCTTCTTGTGTAAGAA 1980
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QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAA 2040
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Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAA 2040

RESULT 2

US-09-288-946-375
: Sequence 375, Application US/09288946
: GENERAL INFORMATION:
: APPLICANT: Xu, Jlangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C7
: CURRENT APPLICATION NUMBER: US/09/288, 946
: NUMBER OF SEQ ID NOS: 381
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-288-946-375

Query Match 100.0%; Score 2040; DB 16; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 GCGCGTTCTGGAGACACAGACACTCTCTATGAAGACACTCAGAACAGATGGGCAAG 300
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Db 241 GCGCGTTCTGGAGACACAGACACTCTCTATGAAGACACTCAGAACAGATGGGCAAG 300
QY 301 TGTGCTGCTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCTTGG 360
|||||
Db 301 TGTGCTGCTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTCAATGAGCCAGGTAACAGCTGCTGAGAGATCTG 420
|||||
Db 361 GGAGACTACGATGACAGTGGCTTCAATGAGCCAGGTAACAGCTGCTGAGAGATCTG 420
QY 421 GACAAAGCTCACAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
|||||
Db 421 GACAAAGCTCACAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAGAGCAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
|||||
Db 481 CTCAGGGACACTGACGTGAACAGAGCAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAATCCGCTGAGAGAGATGTCATTAAT 600
|||||
Db 541 TCTGCAATGGGAATTCAGAAAGTAAATCCGCTGAGAGAGATGTCATTAAT 600
QY 601 GTCTTTGCAACAAAAAAGAGACAGCTCTGATTAAGGCGCTTCAATGCGCAGGAAGATGA 660
|||||
Db 601 GTCTTTGCAACAAAAAAGAGAGACAGCTCTGATTAAGGCGCTTCAATGCGCAGGAAGATGA 660
QY 661 TGTGCTTAATGTTCTGGAACATGCACTGATCCAAATATTCAGATGATGTAAT 720
|||||
Db 661 TGTGCTTAATGTTCTGGAACATGCACTGATCCAAATATTCAGATGATGTAAT 720
QY 721 ACCACTGCACTAGCTATCTATATGAAGTAAATTAATGCGCAAGCACTGCTCTTA 780
|||||
Db 721 ACCACTGCACTAGCTATCTATATGAAGTAAATTAATGCGCAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAAAAGAGAGCTGCTCACACCACTTACTTGGTGA 840
|||||
Db 781 TATGCTGCTGATATGCAATCAAAAAAAGAGAGCTGCTCACACCACTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
|||||
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY 901 CTGATATATGGAAGAGAGCTGCTCACTGCTGATGATGTTGGAATCAGCAAGTATA 960
|||||
Db 901 CTGATATATGGAAGAGAGCTGCTCACTGCTGATGATGTTGGAATCAGCAAGTATA 960
QY 961 GTCAAGCTTCTACTTGAACAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020
|||||
Db 961 GTCAAGCTTCTACTTGAACAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020
QY 1021 GCGAGAGAGTATGCTGTTTCTAGTCATCATGTAATTTGGCACTTCTTCTGACTAC 1080
|||||
Db 1021 GCGAGAGAGTATGCTGTTTCTAGTCATCATGTAATTTGGCACTTCTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTTAAATATCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
|||||

Db	1081	AAAGAAAAACAGATGCTTAAATAATCTCTCTGAAACAGAAATCCAGAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGAAAGTCACAAAGGTTCAAAGCAGTGAATAATAGCACCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGTCACAAAGGTTCAAAGCAGTGAATAATAGCACCAGAGAAA	1200
Qy	1201	ATGCTCAAGAACCCAGAAATTAATAAGATGGGTAGAGAGTTGAGAGAAATGAG	1260
Db	1201	ATGCTCAAGAACCCAGAAATTAATAAGATGGGTAGAGAGTTGAGAGAAATGAG	1260
Qy	1261	AAGCATGAAAGTAATATATGCGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATATATGCGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC	1320
Qy	1321	AATGGTATATGATTAATCTCTCAAAGAGACAGAACCTGGAATAACACCAATTT	1380
Db	1321	AATGGTATATGATTAATCTCTCAAAGAGACAGAACCTGGAATAACACCAATTT	1380
Qy	1381	CTTGACAAAGAAAGTGAAGAGTATCCAGAAATTTGCAATTGTTCTGACTACAAAGAA	1440
Db	1381	CTTGACAAAGAAAGTGAAGAGTATCCAGAAATTTGCGAATTGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGAAAGTACCAAAAGGCTTGAGGCACTGAAATATGGCACCAGACAAAAAGACT	1560
Db	1501	TCAGAGAAAGTACCAAAAGGCTTGAGGCACTGAAATATGGCACCAGACAAAAAGACT	1560
Qy	1561	CAAGAACCAAGAAATTAATAAGATGGTGTAGAGAGCTAGAAAAATTTATGGCTATCGAA	1620
Db	1561	CAAGAACCAAGAAATTAATAAGATGGTGTAGAGAGCTAGAAAAATTTATGGCTATCGAA	1620
Qy	1621	GAAATGAAGAGACAGCGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATATGTTGCC	1680
Db	1621	GAAATGAAGAGACAGCGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATATGTTGCC	1680
Qy	1681	ACTGCTGCAATGATGATGATGATTAATTCCTCCAAAGGAAAGAGAGAAACCTGAAAGC	1740
Db	1681	ACTGCTGCAATGATGATGATGATTAATTCCTCCAAAGGAAAGAGAGAAACCTGAAAGC	1740
Qy	1741	CAGCAATTTCTGACACTGAGATGAAGAGTATCAAGTGAAGCAAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGACACTGAGATGAAGAGTATCAAGTGAAGCAAAATGATACTCAG	1800
Qy	1801	AAGCAATTTTGTGAGAAACAGAACTCGAATATTTACACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAGAAACAGAACTCGAATATTTACACAGATGAGATTTCTGATTCATGAA	1860
Qy	1861	GAAGAAGAGATGAAGGGTGTGAAAAAATGAATTCGACCTTCTCTTAGTTGTAAGAA	1920
Db	1861	GAAGAAGAGATGAAGGGTGTGAAAAAATGAATTTCTGACCTTCTCTTAGTTGTAAGAA	1920
Qy	1921	GAAAAAACATCTTGATGATAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
Db	1921	GAAAAAACATCTTGATGATAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
Qy	1981	GAGCTAGACCAATGAACATCTGAGGCGAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACCAATGAACATCTGAGGCGAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040

RESULT 3
US-09-289-198-303

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

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? TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
?
? FILE REFERENCE: 210121.419C5
?
? CURRENT APPLICATION NUMBER: US/09/289,198
?
? CURRENT FILING DATE: 1999-04-09
?
? EARLIER APPLICATION NUMBER: US 09/062,451
?
? EARLIER FILING DATE: 1998-04-17
?
? EARLIER APPLICATION NUMBER: US 08/991,789
?
? EARLIER FILING DATE: 1997-12-11
?
? EARLIER APPLICATION NUMBER: US 08/838,762
?
? EARLIER FILING DATE: 1997-04-09
?
? EARLIER APPLICATION NUMBER: PCT/US97/00485
?
? EARLIER FILING DATE: 1997-01-10
?
? EARLIER APPLICATION NUMBER: US 08/700,014
?
? EARLIER FILING DATE: 1996-08-20
?
? EARLIER APPLICATION NUMBER: US 08/585,392
?
? EARLIER FILING DATE: 1996-01-01
?
? NUMBER OF SEQ ID NOS: 312
?
? SOFTWARE: FastSeq for Windows Version 3.0
?
? SEQ ID NO 303
?
? LENGTH: 2040
?
? TYPE: DNA
?
? ORGANISM: Homo sapien
?
? US-09-289-198-303

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Query Match	100.0%	Score 2040:	DB 16;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2040; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	ATGCTGGTTGAGGTTGATTTCCATGCCCGGCGCCCTTTCTGTGAAGAAGCCATTTGGCTC	60
Db	1	ATGCTGGTTGAGGTTGATTTCCATGCCCGGCGCCCTTTCTGTGAAGAAGCCATTTGGCTC	60
QY	61	AGGAGCAAGATGGCAGTGGTGTGCTGCCGTTGCTTCCCTGCGTGCAGGGAGACGGCAAG	120
Db	61	AGGAGCAAGATGGCAGTGGTGTGCTGCCGTTGCTTCCCTGCGTGCAGGGAGACGGCAAG	120
QY	121	AGCAAGCTGGGCACTTCTTGAGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAAGCTGGGCACTTCTTGAGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG	180
QY	181	ATGCGGCAAGTGTGCTCCGCCACCTGCTTCCCTGCTGTCAGGGGGAGTGGCAAGACACGTG	240
Db	181	ATGCGGCAAGTGTGCTCCGCCACCTGCTTCCCTGCTGTCAGGGGGAGTGGCAAGACACGTG	240
QY	241	GGCGCTTCTGGAGACACAGACACTGTGCTATGAAGACACTCAGGAACAAGTGGGCAAG	300
Db	241	GGCGCTTCTGGAGACACAGACACTGTGCTATGAAGACACTCAGGAACAAGTGGGCAAG	300
QY	301	TGCTGTGCACTCTTCCCTGCTGTCAGGGGGAGCGCAGCAAGATGGCGCTTGG	360
Db	301	TGCTGTGCACTCTTCCCTGCTGTCAGGGGGAGCGCAGCAAGATGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGCCTTATGTGAGGCCAGGTCACACGTCCGTGGAGAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTATGTGAGGCCAGGTCACACGTCCGTGGAGAAGATCTG	420
QY	421	GACAGAGTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATCGTCATG	480
Db	421	GACAGAGTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATCGTCATG	480
QY	481	CTCAGGGACATGACGTGAACAAAGAGACAAAGCAAAAAGAGAGATGCTCTACATCTTGGCC	540
Db	481	CTCAGGGACATGACGTGAACAAAGAGACAAAGCAAAAAGAGAGATGCTCTACATCTTGGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAGTGTAAAACTCCTGCTGGACAGACATGTCAACTTAAT	600
Db	541	TCTGCCAATGGGAATTCAGAAGTGTAAAACTCCTGCTGGACAGACATGTCAACTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGAGACGCTCTGTATAAAGCCGTACAAATCCAGGAAGATGAA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACGCTCTGTATAAAGCCGTACAAATCCAGGAAGATGAA	660
QY	661	TGTGCGTTAATGTTGCTGGAACATGGACGTGATCCAAATATTCACAGTAGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACATGGACGTGATCCAAATATTCACAGTAGATGGAAT	720

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Db 661 TGTGGTTAAATGTTGCTGGAACTGACACTGATCCAAATATCTCCAGATGATGGAAT 720
Qy 721 ACCACTGCACTACGCTATCTATTAATGACATAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGACATAATTAATGAGCCAAAGCACTGCTTA 780
Qy 781 TATGGTGTGATATCGAATCAAAAAAACAAGCTGCTCACACGCTGTTACTTGCTGA 840
Db 781 TATGGTGTGATATCGAATCAAAAAAACAAGCTGCTCACACGCTGTTACTTGCTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGA 900
Qy 901 CTGATATATATGGAAGACGCTCTCATCTGCTGTATGTGTGATCAGCAAGTATA 960
Db 901 CTGATATATATGGAAGACGCTCTCATCTGCTGTATGTGTGATCAGCAAGTATA 960
Qy 961 GTCAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTCAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGTCTAAAAATCTCTCTGAAAACAGCAATCCGAAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGTCTAAAAATCTCTCTGAAAACAGCAATCCGAAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGACTCACAAGTTCAAGAGTCAAGAAATAGCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGACTCACAAGTTCAAGAGTCAAGAAATAGCAGCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGTGGGATTACTAGAAAACCTGACTAATGTGTCTGCTGCG 1320
Db 1261 AAGCATGAAAGTAAATATGTGGGATTACTAGAAAACCTGACTAATGTGTCTGCTGCG 1320
Qy 1321 AATGTTGATTAATGATTAATCTTCAAGAGAGACAGAACCTGAAAATAGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATCTTCAAGAGAGACAGAACCTGAAAATAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCAATTAATGTTCTGACTACAAAGA 1440
Db 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCAATTAATGTTCTGACTACAAAGA 1440
Qy 1441 AAACGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATTAATCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGTGCACAAAGCTTGAAGGCACTGAAAATGCGCAGCAGAGAAAAGATCT 1560
Db 1501 TCAGAGAGAGTGCACAAAGCTTGAAGGCACTGAAAATGCGCAGCAGAGAAAAGATCT 1560
Qy 1561 CAAGAACAGAAATTAATTAAGAGTGTATAGAGACTGAAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGAGTGTATAGAGACTGAAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGACAGAGAGTATCTATGCGATTCGCCAGAAAACCTGCTAATGCTGCC 1680
Db 1621 GAAATGAAGAGACAGAGAGTATCTATGCGATTCGCCAGAAAACCTGCTAATGCTGCC 1680
Qy 1681 ACTGCTGCAATGTGATGATGATTAATTTCTCCAGAGAAAGCAGAACACTGGAAGC 1740
Db 1681 ACTGCTGCAATGTGATGATGATTAATTTCTCCAGAGAAAGCAGAACACTGGAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAATGAGATCAAGTGAAGAACAAATGATACTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATCAAGTGAAGAACAAATGATACTCAG 1800

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Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAGTGAAGCAAAATGATACTAG 1800
Qy 1801 AAGCAATTTTGGAGAAACAGAACTGGAATATTACAGATGAGATTTCTGATCATGA 1860
Db 1801 AAGCAATTTTGGAGAAACAGAACTGGAATATTACAGATGAGATTTCTGATCATGA 1860
Qy 1861 GAAAGCAGATAGAAAGTGTGAAAATTAATGAAATTTCTGAGCTTTCTTATGTTAAGA 1920
Db 1861 GAAAGCAGATAGAAAGTGTGAAAATTAATGAAATTTCTGAGCTTTCTTATGTTAAGA 1920
Qy 1921 GAAAAAGACATCTTCATGAAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTCATGAAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAATACATGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040
Db 1981 GAGCTAGACACATGAATACATGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 4
US-09-429-755-303
; Sequence 303, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT FILING DATE: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTGAG 480
 DB 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTGAG 480
 QY 481 CTCAGGAGACTGACGTGAACAAGAGACAAGAGAGAGACTGCTTACATCTGGCC 540
 DB 481 CTCAGGAGACTGACGTGAACAAGAGACAAGAGAGAGACTGCTTACATCTGGCC 540
 QY 541 TCTGCCANTGGGAATTCAGAGTACTAAACCTCTGCTGGAGACAGATGTCACCTAAT 600
 DB 541 TCTGCCANTGGGAATTCAGAGTACTAAACCTCTGCTGGAGACAGATGTCACCTAAT 600
 QY 601 GTCTCTGACAAACAAAAGAGACAGCTCTGATTAAGGCGGTCAATGCGAGGAATGAA 660
 DB 601 GTCTCTGACAAACAAAAGAGACAGCTCTGATTAAGGCGGTCAATGCGAGGAATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAAATGGACACTGATCCAAATATTCAGATGATGGAAT 720
 DB 661 TGTGCGTTAATGTTGCTGGAAATGGACACTGATCCAAATATTCAGATGATGGAAT 720
 QY 721 ACCACTGCACTAGCTATCTATTAATGAAGTAAATTAATGCGCAAGACACTGCTCTTA 780
 DB 721 ACCACTGCACTAGCTATCTATTAATGAAGTAAATTAATGCGCAAGACACTGCTCTTA 780
 QY 781 TATGCTGCTGATTCGAATCAAAAAACAAGCATGGCTCACACCACTGTTACTTGGTGA 840
 DB 781 TATGCTGCTGATTCGAATCAAAAAACAAGCATGGCTCACACCACTGTTACTTGGTGA 840
 QY 841 CATAGCAAAAAACAAGCATGGCTGTAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
 DB 841 CATAGCAAAAAACAAGCATGGCTGTAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
 QY 901 CTGATGATGATGGAAGAGACTGCTCTACTTGTGCTGATGTTGATGATGCAAGATGA 960
 DB 901 CTGATGATGATGGAAGAGACTGCTCTACTTGTGCTGATGTTGATGATGCAAGATGA 960
 QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
 DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
 QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
 DB 1021 GCCAGAGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACTTAAG 1140
 DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACTTAAG 1140
 QY 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGCAGTGAATATCCAGCCAGAGAAA 1200
 DB 1141 CTGACATCAGAGAAAGTCAAAAAGTTCAAAAGCAGTGAATATCCAGCCAGAGAAA 1200
 QY 1201 ATGCTCTAGAACCAAGATTAATTAAGGATGCTGATAGAGAGTTGGAAGAAATGAAG 1260
 DB 1201 ATGCTCTAGAACCAAGATTAATTAAGGATGCTGATAGAGAGTTGGAAGAAATGAAG 1260
 QY 1261 AACGATGAAGTAATATGCGGATTCCTGAAAACTGCTAATGCTGCTGCTGCTG 1320
 DB 1261 AACGATGAAGTAATATGCGGATTCCTGAAAACTGCTAATGCTGCTGCTGCTGCTG 1320
 QY 1321 AATGCTGATGATGATTAATCTCTCAAAAAGAGAGAGACCTGAAATATCCAGCAAT 1380
 DB 1321 AATGCTGATGATGATTAATCTCTCAAAAAGAGAGAGACCTGAAATATCCAGCAAT 1380
 QY 1381 CCGACAAACGAAAGTGAAGATTCACAGAAATTTGGCAATTTCTGCTGCTGCTGCTG 1440
 DB 1381 CCGACAAACGAAAGTGAAGATTCACAGAAATTTGGCAATTTCTGCTGCTGCTGCTG 1440
 QY 1441 AAACGATGCTCAAAATATCTTCTGAAAAACGACCCAGCAAGCACTTAAGCTGACA 1500
 DB 1441 AAACGATGCTCAAAATATCTTCTGAAAAACGACCCAGCAAGCACTTAAGCTGACA 1500

QY 1501 TCAGAGAGAGAGTCCACAAAGCTTGAGGCACTGAAATATGCGCAGAGAGAAAGATCT 1560
 DB 1501 TCAGAGAGAGAGTCCACAAAGCTTGAGGCACTGAAATATGCGCAGAGAGAAAGATCT 1560
 QY 1561 CAAGAACCGAATTAATTAAGATGCTGATTAAGAGAGCTGAAATTTTGTGCTATGAA 1620
 DB 1561 CAAGAACCGAATTAATTAAGATGCTGATTAAGAGAGCTGAAATTTTGTGCTATGAA 1620
 QY 1621 GAAATGAAGAGACAGAGAGTACTATGCTGATTCGAGAAACCTGATTAATGCTG 1680
 DB 1621 GAAATGAAGAGACAGAGAGTACTATGCTGATTCGAGAAACCTGATTAATGCTG 1680
 QY 1681 ACTGCTGCAATGCTGATGATGATGATTAATCTCTCAAGAGAGAGAGACCTGAAAGC 1740
 DB 1681 ACTGCTGCAATGCTGATGATGATGATTAATCTCTCAAGAGAGAGAGACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTGACACAGAGAGATGATTAATGATCAAGAGAGAGAGAGAGAGAGAG 1800
 DB 1741 CAGCAATTTCTGACACAGAGAGATGATTAATGATCAAGAGAGAGAGAGAGAGAGAG 1800
 QY 1801 AAGCAATTTTGTGAAG 1860
 DB 1801 AAGCAATTTTGTGAAG 1860
 QY 1861 GAAAAAGCAGATGAG 1920
 DB 1861 GAAAAAGCAGATGAG 1920
 QY 1921 GAAAAAGCAGATGAG 1980
 DB 1921 GAAAAAGCAGATGAG 1980
 QY 1981 GAGCTAGACACATGAG 2040
 DB 1981 GAGCTAGACACATGAG 2040

RESULT 5

US-09-443-686-375
 ; Sequence 375, Application US/09443686

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocke, Susan Louise
 ; APPLICANT: Jiang Yugu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Reiter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 210121.427C9A
 ; CURRENT APPLICATION NUMBER: US/09/443,686
 ; NUMBER OF SEQ ID NOS: 551
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 375
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien

US-09-443-686-375

Query Match

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGATGAGTTGATTCATGCGGCTCTTCTGTAAGAGCAATTTGGCTC 60
 DB 1 ATGCTGATGAGTTGATTCATGCGGCTCTTCTGTAAGAGCAATTTGGCTC 60

APPLICANT: Solk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Wang, Ajun
APPLICANT: Meagher, Madeleine
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.4271ic11
CURRENT APPLICATION NUMBER: US/09/483.672A
NUMBER OF SEQ ID NOS: 390
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-483-672A-375

Query Match 100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATGCGGCTGCCCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGGTGGTTGAGTTGATTCATGCGGCTGCCCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAATGGTGGCTGGCTGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAATGGTGGCTGGCTGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAGACGACTCTGCTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACCAGACGACTCTGCTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCTGGCTGGCTTCCCTGCTGAGGAGAGTGGCAAGCAACGTG 240
Db 181 ATGGGCAAGTGGTGGCTGGCTGGCTTCCCTGCTGAGGAGAGTGGCAAGCAACGTG 240
QY 241 GGCCCTTCTGAGACACAGACGACTCTGCTATGAAGACACTGAGAGCAATGGGCAAG 300
Db 241 GGCCCTTCTGAGACACAGACGACTCTGCTATGAAGACACTGAGAGCAATGGGCAAG 300
QY 301 TGGTGGTGGCACTTCCCTGCTGAGGAGGAGCGGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGGTGGTGGCACTTCCCTGCTGAGGAGGAGCGGCAAGAGAGTGGGCGCTTGG 360
QY 361 GGAGACTACGATGACATGCTTCCCTGCTGAGGAGGAGCGGCAAGAGAGTGGGCGCTTGG 420
Db 361 GGAGACTACGATGACATGCTTCCCTGCTGAGGAGGAGCGGCAAGAGAGTGGGCGCTTGG 420
QY 421 GACAAAGTCCACAGAGCTGGCTGGGGAAGTCCCGCAAGAAAGATCTCATGCTATG 480
Db 421 GACAAAGTCCACAGAGCTGGCTGGGGAAGTCCCGCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGAGCAAGCAAGAAAGAGAGTCTCTACATCTGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAGAGAGCAAGCAAGAAAGAGAGTCTCTACATCTGCC 540
QY 541 TCTGCCAATGGGAATTTAGAAGTAGTAAATCTCGCTGAGACAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTTAGAAGTAGTAAATCTCGCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGGACAACAAAAGAGAGAGCTGTATAAAGGCGGTACAAATCCCGAAGAAAGTAA 660
Db 601 GTCTTGGACAACAAAAGAGAGAGCTGTATAAAGGCGGTACAAATCCCGAAGAAAGTAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCAAAATTTCCAGATGAGTAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCAAAATTTCCAGATGAGTAAAT 720
QY 721 ACCACTCTGACCTACGCTATCTATTAATGAAGATTAATTAAGGCCAAAGCACTGCTTTA 780
Db 721 ACCACTCTGACCTACGCTATCTATTAATGAAGATTAATTAAGGCCAAAGCACTGCTTTA 780

QY 781 TATGCTGCTGATATGCAATCAAAAAAAGACATGGCTTCACACCACTGTTACTGTGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAAAGACATGGCTTCACACCACTGTTACTGTGTGA 840
QY 841 CATGAGCAAAAACACCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACACCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATGAAGAGCTGCTCATACTTGGCTGATGTTGGATGACAGCAATTA 960
Db 901 CTGATATGATGAAGAGAGCTGCTCATACTTGGCTGATGTTGGATGACAGCAATTA 960
QY 961 GTACACCTTCTACTTGGACCAAAATTTATGATGATCTTCCAGATCTATTCGACAGAG 1020
Db 961 GTACACCTTCTACTTGGACCAAAATTTATGATGATCTTCCAGATCTATTCGACAGAG 1020
QY 1021 GCCAAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTAACTTTGACTAC 1080
Db 1021 GCCAAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTAACTTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAAGTGAATTAAGCCACAGAGAAA 1200
Db 1141 CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAAGTGAATTAAGCCACAGAGAAA 1200
QY 1201 ATGCTCAGAAACCAAGAAATTAATGAAGTGTATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAGAAACCAAGAAATTAATGAAGTGTATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGTTGGATTTACTAGAAAACCTGACTAATGGTCTGCTGCTGC 1320
Db 1261 AAGCATGAAGTAAATATGTTGGATTTACTAGAAAACCTGACTAATGGTCTGCTGCTGC 1320
QY 1321 AATGCTAATTAATGATTAATTTCTCAAGAGAGAGACACCTGAATTAAGCAATTT 1380
Db 1321 AATGCTAATTAATGATTAATTTCTCAAGAGAGAGACACCTGAATTAAGCAATTT 1380
QY 1381 CCTGCAACAGAAATGAAGAGTATCAGAAATTTGGCAATTAATGTTGCTGACTACAAAAG 1440
Db 1381 CCTGCAACAGAAATGAAGAGTATCAGAAATTTGGCAATTAATGTTGCTGACTACAAAAG 1440
QY 1441 AAACAGATGGCAAAATACTCTTCTGAAAACAGCAACCAAGCAAGCACTTAAGCTGACA 1500
Db 1441 AAACAGATGGCAAAATACTCTTCTGAAAACAGCAACCAAGCAAGCACTTAAGCTGACA 1500
QY 1501 TCGAGGAGAGAGTCACAAAAGCTTGGAGGCAAGTGAATAATGGCCAGCCAGAAAAAGTCT 1560
Db 1501 TCGAGGAGAGAGTCACAAAAGCTTGGAGGCAAGTGAATAATGGCCAGCCAGAAAAAGTCT 1560
QY 1561 CAAGAACCAAGAAATTAATGAAGAGTGTATGAGAGTATGAATAATTTTATGGCTATGAA 1620
Db 1561 CAAGAACCAAGAAATTAATGAAGAGTGTATGAGAGTATGAATAATTTTATGGCTATGAA 1620
QY 1621 GAAATGAAGAAGCAGGAAGTACTCATGTGGAATTTCCAGAAAAACCTGACTTAATGGTGC 1680
Db 1621 GAAATGAAGAAGCAGGAAGTACTCATGTGGAATTTCCAGAAAAACCTGACTTAATGGTGC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCAAGGAAGAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCAAGGAAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGGAATGAAGATATACAGATGAGATTAATGATGATGATGATG 1800
Db 1741 CAGCAATTTCTGACACTGGAATGAAGATATACAGATGAGATTAATGATGATGATGATG 1800
QY 1801 AAGCAATTTTGTGAAGAAGCAAGCACTGGAATTTACAGATGAGATTTGATTTCAATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAAGCAAGCACTGGAATTTACAGATGAGATTTGATTTCAATGAA 1860

Db 1561 CAAGACCAGAAATTAATAGAGTGTGATAGAGAGCTAGAAAATTTTATGCGTATTCGAA 1620
QY 1621 GAAATGAAAGACACGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC 1680
Db 1621 GAAATGAAAGACACGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGCC 1680
QY 1681 ACTGCTGGCAATGTGTGATGATGATTAATTCCTCCAGGAAGACAGAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGTGTGATGATGATTAATTCCTCCAGGAAGACAGAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGTATCAGAGTGCAGAAACAAATGATACACTAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGTATCAGAGTGCAGAAACAAATGATACACTAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAAGTGTGTTGAAAAATGAAATTCGACTTTCTTATGTTGTAAGAA 1920
Db 1861 GAAAAGCAGATGAAAGTGTGTTGAAAAATGAAATTCGACTTTCTTATGTTGTAAGAA 1920
QY 1921 GAAAAGCAGATTTGCAATGAAATAGTACGTTGGGGGGAAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAGCAGATTTGCAATGAAATAGTACGTTGGGGGGAAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAAATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACACAAATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040

RESULT 8
US-09-536-857-375
; Sequence 375, Application US/09536857
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuhui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42712C12
; CURRENT APPLICATION NUMBER: US/09/536, 857
; NUMBER OF SEQ ID NOS: 592
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-536-857-375

Query Match 100.0%; Score 2040; DB 20; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATCGCGCTGCTCTTCTGTGAGAAAGCCATTGGTCTC 60
Db 1 ATGGTGGTTGAGTTGATTCATCGCGCTGCTCTTCTGTGAGAAAGCCATTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTCAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTCAGGAGAGCGGCAAG 120
QY 121 AGCAGCTGGGCACTTGTGAGACCAAGACAGACACTCTGCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAGCTGGGCACTTGTGAGACCAAGACAGACACTCTGCTATGAAGACATCAGAGCAAG 180

Db 121 AGCAACGTGGGCACTTGTGAGACCAAGACAGACACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCGCACTGCTCCCTGTGTGACAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTCCGCGCACTGCTCCCTGTGTGACAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGTTCTGAGAACACACAGACACTGTGCTATGAAGACACTCAGGAACAGATGGCAAG 300
Db 241 GGGCGTTCTGAGAACACACAGACACTGTGCTATGAAGACACTCAGGAACAGATGGCAAG 300
QY 301 TGGTGTGCTCCACTGCTTCCCTGCTGCAAGGGGGAGCGGCAAGACAGTGGGGCTTGG 360
Db 301 TGGTGTGCTCCACTGCTTCCCTGCTGCAAGGGGGAGCGGCAAGACAGTGGGGCTTGG 360
QY 361 GGAGACTACATGACAGAGTCCCTTATGAGAGCCAGAGTACACAGTCCGCTGAGAGATCTG 420
Db 361 GGAGACTACATGACAGAGTCCCTTATGAGAGCCAGAGTACACAGTCCGCTGAGAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCCAGAAAGATCTCATGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCCAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGCACTGACGTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540
Db 481 CTCAGGGCACTGACGTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540
QY 541 TCTGCAATGGGAATTCAGAGTGAATAAATCTGCTGTGACAGACATGTCACATTAAT 600
Db 541 TCTGCAATGGGAATTCAGAGTGAATAAATCTGCTGTGACAGACATGTCACATTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGCAGCTCTGATTAAGGCCCTACATGACAGAAAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGCAGCTCTGATTAAGGCCCTACATGACAGAAAGATGAA 660
QY 661 TGTGCGTTAATGTGTGCGAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 720
Db 661 TGTGCGTTAATGTGTGCGAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 720
QY 721 ACCACTGTGACACTGATCTATATGATGAAGATTAATGAGCAAGCAAGCAAGCAAGCAAG 780
Db 721 ACCACTGTGACACTGATCTATATGATGAAGATTAATGAGCAAGCAAGCAAGCAAGCAAG 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAGATGAGCTCACACCACTGTACTGTGCTA 840
Db 781 TATGCTGTGATATGCAATCAAAAAACAGATGAGCTCACACCACTGTACTGTGCTA 840
QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTATTCAGAAAGAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAATTTTATTCAGAAAGAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCATATGCTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGACTGCTCATATGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGACGCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCGACAGACG 1020
Db 961 GTGACGCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTAATTTGCCAGTTATCTTGACACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTAATTTGCCAGTTATCTTGACACTAC 1080
QY 1081 AAGAAAAACAGATGTAAATAATCTCTTCTGAAACAGCAATCCAGAAACAGATTTAAAG 1140
Db 1081 AAGAAAAACAGATGTAAATAATCTCTTCTGAAACAGCAATCCAGAAACAGATTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGTGTCAAAAGGTCAAAAGCAAGTGAATAATAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAAAGTGTCAAAAGGTCAAAAGCAAGTGAATAATAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGTATGAGAGGTTGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGTATGAGAGGTTGAAAGAAATGAAG 1260

```
QY 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTC 1320
    |||||||
DB 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTC 1320
QY 1321 AATGTGATATATGATTAATTCCTCAAGGAAGACAGAACCTGAAAATCAGCAATTT 1380
    |||||||
DB 1321 AATGTGATATATGATTAATTCCTCAAGGAAGACAGAACCTGAAAATCAGCAATTT 1380
QY 1381 COTGACAAAGAAAGTAAGAGTATACACAGAAATTTGGTAATTTAGTTTCTACTACAAAGAA 1440
    |||||||
DB 1381 COTGACAAAGAAAGTAAGAGTATACACAGAAATTTGGTAATTTAGTTTCTACTACAAAGAA 1440
QY 1441 AAACGATGCCCCAAATACTCTCTGAAAACACAGAACCCAGAACAGACTTAAGAGTGACA 1500
    |||||||
DB 1441 AAACGATGCCCCAAATACTCTCTGAAAACACAGAACCCAGAACAGACTTAAGAGTGACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCACTGAAAATGGCCAGCAGAGAAAAGATCT 1560
    |||||||
DB 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCACTGAAAATGGCCAGCAGAGAAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGAGTGTGATAGAGACTAGAAAATTTTATGCTATCGAA 1620
    |||||||
DB 1561 CAAGAACCAAGAAATTAATAGAGTGTGATAGAGACTAGAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAAAGCAGGAAAGTCTCATGTGCGATTCCCGAAAACCTGACTAATGGTGC 1680
    |||||||
DB 1621 GAAATGAAGAAAGCAGGAAAGTCTCATGTGCGATTCCCGAAAACCTGACTAATGGTGC 1680
QY 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCCAGGAAGAGCAGAACACCTGAAAC 1740
    |||||||
DB 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCCAGGAAGAGCAGAACACCTGAAAC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGATGTCACAGTGCAGAACCAAAATGATCTCAG 1800
    |||||||
DB 1741 CAGCAATTTCTGACACTGAGATGAAGATGTCACAGTGCAGAACCAAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACTGGAATTTACAGATGAGATGCTGATTCATGAA 1860
    |||||||
DB 1801 AAGCAATTTTGTGAAGACAGAACTGGAATTTACAGATGAGATGCTGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGACCTTCTTCTAGTTGAAGAA 1920
    |||||||
DB 1861 GAAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGACCTTCTTCTAGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATGCGCATGTAAGACTG 1980
    |||||||
DB 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATGCGCATGTAAGACTG 1980
QY 1981 GAGCTAGACACAATGAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
    |||||||
DB 1981 GAGCTAGACACAATGAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
```

RESULT 9
US-09-568-100A-375
Sequence 375. Application US/09568100A

GENERAL INFORMATION:

APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun

APPLICANT: Skelky, Yashir A.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42713C13
CURRENT APPLICATION NUMBER: US/09/568,100A
NUMBER OF SEQ ID NOS: 701
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-568-100A-375

Query Match 100.0% Score 2040: DB 22: Length 2040:
Best Local Similarity 100.0% Pred. No. 0:
Matches 2040: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```
QY 1 ATGTGTGTGAGTGTGATTCATGCGCGCTGCTCTGTGAAGAACCATTTGGTCTC 60
    |||||||
DB 1 ATGTGTGTGAGTGTGATTCATGCGCGCTGCTCTGTGTGAAGAACCATTTGGTCTC 60
QY 61 AGAGAGCAAGATGGCAAGTGTGCTGCCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
    |||||||
DB 61 AGAGAGCAAGATGGCAAGTGTGCTGCCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 ACCAAGCTGGGCACTTCTGGAGACCAGCAGACTGCTATGAAACACTCAGAGCAAG 180
    |||||||
DB 121 ACCAAGCTGGGCACTTCTGGAGACCAGCAGACTGCTATGAAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGAGGAGTGGCAAGACGTG 240
    |||||||
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGAGGAGTGGCAAGACGTG 240
QY 241 GCGGCTTGTGAGACACAGCAGACTCTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300
    |||||||
DB 241 GCGGCTTGTGAGACACAGCAGACTCTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAGGAGGAGGCGCAAGCAAGTGGCGCTTGG 360
    |||||||
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCAGGAGGAGGCGCAAGCAAGTGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTCTCTCATGAGCCAGGATACAGTCCGCTGGAGAAATCTG 420
    |||||||
DB 361 GGAGACTAGATGACAGTCTCTCATGAGCCAGGATACAGTCCGCTGGAGAAATCTG 420
QY 421 GACAAAGCTTCACAGAGCTGCTGTGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
    |||||||
DB 421 GACAAAGCTTCACAGAGCTGCTGTGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAAACAAGAACCAAGCAAGAAAGAGCTCTTACATCTGGCC 540
    |||||||
DB 481 CTCAGGGACACTGACGTGAAACAAGAACCAAGCAAGAAAGAGCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGAAGTAAAGTCTGCTGCAGAGAGATGCAACTTAAT 600
    |||||||
DB 541 TCTGCCAATGGGAATTCAGAAATGAAGTAAAGTCTGCTGCAGAGAGATGCAACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGAAAGTGA 660
    |||||||
DB 601 GTCTCTTGACAAACAAAAGAGAGAGCTGTATAAAGCCGTACAAATGCCAGAAAGTGA 660
QY 661 TGTGCGTTATATGTGCTGGAACATGGCACTGATCCAAATATTCACAGATAGTGAAT 720
    |||||||
DB 661 TGTGCGTTATATGTGCTGGAACATGGCACTGATCCAAATATTCACAGATAGTGAAT 720
QY 721 ACCACTGCTACCTACGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGGCTTA 780
    |||||||
DB 721 ACCACTGCTACCTACGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGGCTTA 780
QY 781 TATGTGTGCTGATATGAATCAAAAAACAAGCATGGCGCTCACACACTGTACTGTGTA 840
    |||||||
DB 781 TATGTGTGCTGATATGAATCAAAAAACAAGCATGGCGCTCACACACTGTACTGTGTA 840
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QY 541 TCTGCAATGGGAATTCAGAAAGTAGTAAACCTCTGTGGACAGACGATGCACTTAAT 600
    |||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGTGGACAGACGATGCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGGAGACGCTCGATTAAGGCCGTACAAATGCCAGAAATGAA 660
    |||
Db 601 GTCCCTTGACAAACAAAAGAGGAGACGCTCGATTAAGGCCGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCTTAATGTGTGTGGACATGCGACTGATCCAAATTTCCAAATGATGTAAT 720
    |||
Db 661 TGTGCTTAATGTGTGTGGACATGCGACTGATCCAAATTTCCAAATGATGTAAT 720
QY 721 AACACCTGCACTAGCCTTCTATTAATGAAGATTAATTAATGGCAAGACGCTCTTA 780
    |||
Db 721 AACACCTGCACTAGCCTTCTATTAATGAAGATTAATTAATGGCAAGACGCTCTTA 780
QY 781 TATGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACACTGTACTTGTGTA 840
    |||
Db 781 TATGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACACTGTACTTGTGTA 840
QY 841 CATGACCAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
    |||
Db 841 CATGACCAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGTGATAGATATGGAAGAGACTGCTCATATCTTCTGTATGTGTGATGAGCAAGTATA 960
    |||
Db 901 CTGTGATAGATATGGAAGAGACTGCTCATATCTTCTGTATGTGTGATGAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
    |||
Db 961 GTGAGCCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTTTCTTCTATCATCATCATGTAATTTGCCAGTTACTTTGTGACTAC 1080
    |||
Db 1021 GCCAGAGATATGCTTTCTTCTATCATCATCATGTAATTTGCCAGTTACTTTGTGACTAC 1080
QY 1081 AAGGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
    |||
Db 1081 AAGGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCTAGAGAGAGATCTACAAAGGTTCAAGGCAAGTGAATAGCCAGCAGAGAAA 1200
    |||
Db 1141 CTGACATCTAGAGAGAGATCTACAAAGGTTCAAGGCAAGTGAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAA 1260
    |||
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAA 1260
QY 1261 AAGCATGAAGATTAATTAATGCGGATCTCTAAGAAACCTGACTAATGCTGCTGCG 1320
    |||
Db 1261 AAGCATGAAGATTAATTAATGCGGATCTCTAAGAAACCTGACTAATGCTGCTGCG 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
    |||
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTAGTTCTGACTCAAAAGAA 1440
    |||
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTAGTTCTGACTCAAAAGAA 1440
QY 1441 AAACATGATGCAAAATACCTTCTGAAAAACAGAACCCAGAACCAACTTAAGCTGACA 1500
    |||
Db 1441 AAACATGATGCAAAATACCTTCTGAAAAACAGAACCCAGAACCAACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGATCTACAAAGGCTTGAGGCGAGTGAATATGGCCAGCAGAGAAAGATCT 1560
    |||
Db 1501 TCAGAGAGAGATCTACAAAGGCTTGAGGCGAGTGAATATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620
    |||
Db 1561 CAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGCTAGAAAAATTTATGCTATCGAA 1620

```

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QY 1621 GAATGAAAGACGAGGAAAGTACTCATGTGCGATTCCTCAGAAAACTGATTAATGCTGCC 1680
    |||
Db 1621 GAATGAAAGACGAGGAAAGTACTCATGTGCGATTCCTCAGAAAACTGATTAATGCTGCC 1680
QY 1681 ACTGTGGCAATGTGATGATGATTAATTTCTCCAAAGAGACGAAACCTGAAAGC 1740
    |||
Db 1681 ACTGTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTTACACTGAGATGAAGATATCACAGTACAGCAACAAAAATGATACTGAC 1800
    |||
Db 1741 CAGCAATTTCTTACACTGAGATGAAGATATCACAGTACAGCAACAAAAATGATACTGAC 1800
QY 1801 AAGCAATTTTGTGAACACAGAACACTGGAATTTACAGATGATGATGATGATGAA 1860
    |||
Db 1801 AAGCAATTTTGTGAACACAGAACACTGGAATTTACAGATGATGATGATGATGAA 1860
QY 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTGAGGCTTCTTATGTTAAGAAA 1920
    |||
Db 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTGAGGCTTCTTATGTTAAGAAA 1920
QY 1921 GAAAAAGACATCTTGATGAAATTAATGATGCTTCCGGGAGAAATTTGCCATGCTAAGATC 1980
    |||
Db 1921 GAAAAAGACATCTTGATGAAATTAATGATGCTTCCGGGAGAAATTTGCCATGCTAAGATC 1980
QY 1981 GAGCTGACACATGAAACATCAGAGCCAGCTAAAAAATTTAAAAAATTTAAAAA 2040
    |||
Db 1981 GAGCTGACACATGAAACATCAGAGCCAGCTAAAAAATTTAAAAAATTTAAAAA 2040

```

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RESULT 11
US-09-583-303
; Sequence 303, Application US/09590583
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419c9
; CURRENT APPLICATION NUMBER: US/09/590,583
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-583-303

Query Match      100.0%: Score 2040: DB 22: Length 2040:
Best Local Similarity 100.0%: Pred No. 0:
Matches 2040: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 241 GGGCTTCTGGAGACACGACGACTCTGTATGAAGACACTCAGAACACAGATGGGCAAG 300
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Db 241 GGGCTTCTGGAGACACGACGACTCTGTATGAAGACACTCAGAACACAGATGGGCAAG 300
QY 301 TGGGTGCGCCACGCTGCTCCCTGCTGCAAGGGGAGCGGCAAGACAGAGTGGGCTTGG 360
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Db 301 TGGGTGCGCCACGCTGCTCCCTGCTGCAAGGGGAGCGGCAAGACAGAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACACGTCCTGGAGAAAGATGTG 420
|||||
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACACGTCCTGGAGAAAGATGTG 420
QY 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCCAGAAAGATCTCATGCTATG 480
|||||
Db 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCCAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGACACTGACGTGGAACAAGAAGACAAAGAGAGACTGCTCATCTGGCC 540
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Db 481 CTCAGGACACTGACGTGGAACAAGAAGACAAAGAGAGACTGCTCATCTGGCC 540
QY 541 TCTCCATGAGGATTCAGAGTGTAAACTCCTGCTGGACAGACGATGTCACCTTAAT 600
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Db 541 TCTCCATGAGGATTCAGAGTGTAAACTCCTGCTGGACAGACGATGTCACCTTAAT 600
QY 601 GTCTTGACAAACAAAG 660
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Db 601 GTCTTGACAAACAAAG 660
QY 661 TGTGCGCTTAATGTTGCTGGAGACATGGCAGCTATCCAAATATTCAGAGATGGAAT 720
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Db 661 TGTGCGCTTAATGTTGCTGGAGACATGGCAGCTATCCAAATATTCAGAGATGGAAT 720
QY 721 ACCACTGACACTACGCTATCTATATGAAGATTAATATGAGCAAGAGAGAGAGAGAG 780
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Db 721 ACCACTGACACTACGCTATCTATATGAAGATTAATATGAGCAAGAGAGAGAGAGAG 780
QY 781 TATGCTGCTGATATGCAATCAAAAAACAGCAGTGGCTCACACCACTGTACTTGGTGA 840
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Db 781 TATGCTGCTGATATGCAATCAAAAAACAGCAGTGGCTCACACCACTGTACTTGGTGA 840
QY 841 CATAGCAAAAAACAGCAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
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Db 841 CATAGCAAAAAACAGCAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY 901 CTGATAGATATGGAAGAGAGCTCTCATCTGCTGTATGTTGGATCAGCAAGTATA 960
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Db 901 CTGATAGATATGGAAGAGAGCTCTCATCTGCTGTATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG 1020
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Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTTCCAGTTACTTTCGACATC 1080
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Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTTCCAGTTACTTTCGACATC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGA AAAACAGCAATCCAGAACAGACTTAAAG 1140
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Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGA AAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGTGA AAAATAGCCAGCCAGAGAAA 1200
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Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGTGA AAAATAGCCAGCCAGAGAAA 1200
QY 1201 ATGCTCTCAAGAACAGAAATTAATAGAGTGTATAGAGAGGTTGAAGAAAGAAATGAG 1260
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Db 1201 ATGCTCTCAAGAACAGAAATTAATAGAGTGTATAGAGAGGTTGAAGAAAGAAATGAG 1260
QY 1261 AAGCATGAAATTAATATGTTGGATTAATAGAGAAACCTGACTAATGTTGCTACTGCTGC 1320
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Db 1261 AAGCATGAAATTAATATGTTGGATTAATAGAGAAACCTGACTAATGTTGCTACTGCTGC 1320

QY 1321 AATGCTAATATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
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Db 1321 AATGCTAATATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAGAGAGAGAGAGAGATATCACAGATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440
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Db 1381 CCTGACAGAGAGAGAGAGATATCACAGATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAAGAGATGCCAAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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Db 1441 AAAGAGATGCCAAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGCTTGAGGCGAGTGA AAAATGSCCAGAGAGAGAGAGATCT 1560
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Db 1501 TCAGAGAGAGAGTCAAAAGCTTGAGGCGAGTGA AAAATGSCCAGAGAGAGAGATCT 1560
QY 1561 CAAGAACCGAAATTAATTAAGAGATGATAGAGAGTGA AAAATTTATGCTATGCGAA 1620
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Db 1561 CAAGAACCGAAATTAATTAAGAGATGATAGAGAGTGA AAAATTTATGCTATGCGAA 1620
QY 1621 GAAATGAAGAGAGAGAGAGAGTATGCTGATTCGAGAAACCTGACTAATGCTGCC 1680
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Db 1621 GAAATGAAGAGAGAGAGAGAGTATGCTGATTCGAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCCAGAGAGAGAGAGAGAGAGAGAG 1740
|||||
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCCAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAGAGAGAGAGAGAGAG 1800
|||||
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAGAGAGAGAGAGAGAG 1800
QY 1801 AAGCAATTTTCTGAGAGAGAGAGAGAGAGTATATACAGATGAGATCTGATTCATGAA 1860
|||||
Db 1801 AAGCAATTTTCTGAGAGAGAGAGAGAGAGTATATACAGATGAGATCTGATTCATGAA 1860
QY 1861 GAAAAAGCAGATGAG 1920
|||||
Db 1861 GAAAAAGCAGATGAG 1920
QY 1921 GAAAAAGCAGATGAG 1980
|||||
Db 1921 GAAAAAGCAGATGAG 1980
QY 1981 GAGCTAGACAGATGAG 2040
|||||
Db 1981 GAGCTAGACAGATGAG 2040

RESULT 12
US-09-593-793A-375
Sequence 375, Application US/09593793A
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: L.I. Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helper, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42715C15

; CURRENT APPLICATION NUMBER: US/09/593,793A
; CURRENT FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-593-793A-375

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGTTGAGTGGATTCATGCGCGGCTGCTCTTGTAAGAGCAATTTGGTCTC 60
DB 1 ATGGTGGTTGAGTGGATTCATGCGCGGCTGCTCTTGTAAGAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTGCTATGAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTGCTATGAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGAGAGGAGGCAAGCAAG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGAGAGGAGGCAAGCAAG 240
QY 241 GCGGCTTCTGGAGACCAAGCACTGCTATGAGACACTCAGAGCAAGTGGGCAAG 300
DB 241 GCGGCTTCTGGAGACCAAGCACTGCTATGAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGTGTCTGCCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGCAAGTGGGCTTGG 360
DB 301 TGTGTCTGCCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGCAAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGTCCGTGGAGAGTCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGTCCGTGGAGAGTCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATTCATCGCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATTCATCGCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAAGTCCGTGGAGAGCATGCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAAGTCCGTGGAGAGCATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGGAATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGACAGCTGTATAAAGCCGTACAAATGCCAGGAATGAA 660
QY 661 TGTGCGTTAATGTGTGTGAGACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
DB 661 TGTGCGTTAATGTGTGTGAGACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
QY 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAATGGCCAAACACTGCTTAA 780
DB 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAATGGCCAAACACTGCTTAA 780
QY 781 TATGTTGCTGATATGAATCAAAAAACAAGCATGGCCCTACACACTGTTACTTGGTGA 840
DB 781 TATGTTGCTGATATGAATCAAAAAACAAGCATGGCCCTACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGA 900

QY 901 CTGGATGATATGAAGAGACTGCTCTCATACCTTGTGTATGTTGGATCAGCAAGTATA 960
DB 901 CTGGATGATATGAAGAGACTGCTCTCATACCTTGTGTATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGGAGCAAAATATGATGATATCTTCAAGATATCATGTGACAGAG 1020
DB 961 GTGAGCTTCTACTTGGAGCAAAATATGATGATATCTTCAAGATATCATGTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGTGTAATAATCTGTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
DB 1081 AAAAGAAAACAGATGTGTAATAATCTGTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAAGCTTCAAGGAGTGAATAATGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAAGCTTCAAGGAGTGAATAATGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGGTATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGGTATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGGGATTAAGTGAAGAAACCTGACTAATGGTGCATGCTGGC 1320
DB 1261 AAGCATGAAGTAAATATGGGATTAAGTGAAGAAACCTGACTAATGGTGCATGCTGGC 1320
QY 1321 AATGGTATATGATTAATTCCTCAAGAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
DB 1321 AATGGTATATGATTAATTCCTCAAGAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTTAGTTTCTGACTTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTTAGTTTCTGACTTCAAGAA 1440
QY 1441 AAAAGATGCCAAAATACCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCCAAAATACCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGTACACAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGAGAGTACACAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATTAAGATGGTATGAGAGACTTGAATAATTTATGGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATTAAGATGGTATGAGAGACTTGAATAATTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAGCAGGAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGGTGGC 1680
DB 1621 GAAATGAAGAGCAGGAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGGTGGC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTCCTCAAGAGAGAGCAACACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGGTATGATGATTAATTCCTCAAGAGAGAGCAACACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATACACAGTCAACAAATAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATACACAGTCAACAAATAATGATACTCAG 1800
QY 1801 AAGCAATTTTGAAGAAACAGAACTGGAATTTACAGATGAGATTCGATCTATGAA 1860
DB 1801 AAGCAATTTTGAAGAAACAGAACTGGAATTTACAGATGAGATTCGATCTATGAA 1860
QY 1861 GAAAGCAGATGAAGTGTGAAAAATGAATTCGACCTTCTCTTATGTTTAAAGAA 1920
DB 1861 GAAAGCAGATGAAGTGTGAAAAATGAATTCGACCTTCTCTTATGTTTAAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAAATGATACGTTGGGGAAGAAATTCATGCTTAAGCTG 1980
DB 1921 GAAAAAGACATCTTGATGAAAAATGATACGTTGGGGAAGAAATTCATGCTTAAGCTG 1980


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QY 1981 GAGCTAGACACAAATGAATCAGAGCCAGCTAAAAA 2040
|
Db 1981 GAGCTAGACACAAATGAATCAGAGCCAGCTAAAAA 2040
|
RESULT 13
US-09-605-783A-375
; Sequence 375, Application US/09605783A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605.783A
; NUMBER OF FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-783A-375

Query Match 100.0%; Score 2040; DB 23; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGTGTGATTCATCGCCGCTCTCTTGTGAAGAACATTTGGTCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATCGCCGCTCTCTTGTGAAGAACATTTGGTCTC 60
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QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCGCTTCCCTCCCTCCAGGAGGAGGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCGCTTCCCTCCCTCCAGGAGGAGGCGCAAG 120
|
QY 121 AGCAACGTGGGCACTTGTGAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTGTGAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
|
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGACGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGACGCTG 240
|
QY 241 GGGCTCTTGAGACACGAGACTGCTGTGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCTCTTGAGACACGAGACTGCTGTGAAGACACTCAGAGCAAGATGGGCAAG 300
|
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCGCTTGG 360
|
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACACGCTCCGTGAGAAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACACGCTCCGTGAGAAAGATCTG 420
|
QY 421 GACAACTCCACAGAGCTGCTGCTGGGTAAATGCCCAAAAGATCTATGCTATG 480
|
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Db 421 GACAACTCCACAGAGCTGCTGCTGGGTAAATGCCCAAAAGATCTATGCTATG 480
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QY 481 CTCAGGACACTGACGTGACCAAGAGACAAAGAGAGTGGTCTACATCTGCGCC 540
|
Db 481 CTCAGGACACTGACGTGACCAAGAGACAAAGAGAGTGGTCTACATCTGCGCC 540
|
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCCTGCTGACAGACATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCCTGCTGACAGACATGTCAACTTAAT 600
|
QY 601 GTCTTCGACAAACAAAAGAGACAGCTGCTGTAAGGCCGTCACATGCCAGGAAGATGAA 660
Db 601 GTCTTCGACAAACAAAAGAGACAGCTGCTGTAAGGCCGTCACATGCCAGGAAGATGAA 660
|
QY 661 TGTGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGAAAT 720
|
QY 721 ACCACTGTGCACTACGCTATCTAATGAGATTAATTAATGCGCAAGCACTGCTTTA 780
Db 721 ACCACTGTGCACTACGCTATCTAATGAGATTAATTAATGCGCAAGCACTGCTTTA 780
|
QY 781 TATGTCGTGATATCGAATCAAAAACAGATGCGCCACACACATGTTACTTGGTGA 840
Db 781 TATGTCGTGATATCGAATCAAAAACAGATGCGCCACACACATGTTACTTGGTGA 840
|
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
|
QY 901 CTGATGATGATGGAAGAGACTGCTCTCAATCTTCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATGATGATGGAAGAGACTGCTCTCAATCTTCTGATATGTTGGATCAGCAAGTATA 960
|
QY 961 GTCAAGCTTCTACCTGAGCAAAATTAATGATGATCTCTCAAGATCTATGCAAGACG 1020
Db 961 GTCAAGCTTCTACCTGAGCAAAATTAATGATGATCTCTCAAGATCTATGCAAGACG 1020
|
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCATGTAATTTGCCAGTTACTTGTGATAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCATGTAATTTGCCAGTTACTTGTGATAC 1080
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QY 1081 AAAGAAAAACAGATGCTTAATAATCTCTTCTGAAAACAGCAATCCAGAAACAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTTAATAATCTCTTCTGAAAACAGCAATCCAGAAACAGACTTAAG 1140
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QY 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAGGACAGTGAATTAAGCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAGGACAGTGAATTAAGCAGCAGAGAAA 1200
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QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGATGAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGATGAG 1260
|
QY 1261 AAGCATGAATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
Db 1261 AAGCATGAATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
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QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGACAGAACCTGAAATTAATTAATTAAT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGACAGAACCTGAAATTAATTAATTAAT 1380
|
QY 1381 CCTGACAAACGAAGATGAAGATATCACGAATTTGCCAATTAATTAATTAATTAATTAAT 1440
Db 1381 CCTGACAAACGAAGATGAAGATATCACGAATTTGCCAATTAATTAATTAATTAATTAAT 1440
|
QY 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACGCAACCAAGAAAGATTAATTAATTAATTAAT 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACGCAACCAAGAAAGATTAATTAATTAATTAAT 1500
|
QY 1501 TCAGAGGAAGAGTACAAAGGCTTGAGGGAGTGAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 1501 TCAGAGGAAGAGTACAAAGGCTTGAGGGAGTGAATTAATTAATTAATTAATTAATTAATTAAT 1560
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QY 1561 CAGAAGCAGAAATTAATAGATGATAGAGAGCTAGAAAATTTTATGCTATCGAA 1620
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Db 1561 CAGAAGCAGAAATTAATAGATGATAGAGAGCTAGAAAATTTTATGCTATCGAA 1620
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QY 1621 GAAATGAGAGCAGGAGAGTACTCATGTGCTGCCAGAAAACCTGACTAATGTGCC 1680
| | | | |
Db 1621 GAAATGAGAGCAGGAGAGTACTCATGTGCTGCCAGAAAACCTGACTAATGTGCC 1680
| | | | |
QY 1681 ACTGCGCAATGATGATGATTAATTCCTCCAGAGAGAGAGACACCTGAAAGC 1740
| | | | |
Db 1681 ACTGCGCAATGATGATGATTAATTCCTCCAGAGAGAGAGACACCTGAAAGC 1740
| | | | |
QY 1741 CAGCAATTCCTGACACTGAGATGAAAGATACAGATGACAGACAAAATGATCTAG 1800
| | | | |
Db 1741 CAGCAATTCCTGACACTGAGATGAAAGATACAGATGACAGACAAAATGATCTAG 1800
| | | | |
QY 1801 AAGCAATTTTGTGAGAGACAGAACTGGAATATACAGATGAGATTCGATTCATGAA 1860
| | | | |
Db 1801 AAGCAATTTTGTGAGAGACAGAACTGGAATATACAGATGAGATTCGATTCATGAA 1860
| | | | |
QY 1861 GAAAGCAGATGAGATGATGATTAATTCCTGAGCTTCTCTTACTTGTAGAAA 1920
| | | | |
Db 1861 GAAAGCAGATGAGATGATGATTAATTCCTGAGCTTCTCTTACTTGTAGAAA 1920
| | | | |
QY 1921 GAAAGCAGATGAGATGATGATTAATTCCTGAGCTTCTCTTACTTGTAGAAA 1980
| | | | |
Db 1921 GAAAGCAGATGAGATGATGATTAATTCCTGAGCTTCTCTTACTTGTAGAAA 1980
| | | | |
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTGCATGCTAAGACTG 2040
| | | | |
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTGCATGCTAAGACTG 2040
| | | | |

RESULT 14
US-09-636-215-375
; Sequence 375, Application US/09636215
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvyck, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636, 215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-375

Query Match 100.0%; Score 2040; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTTGAGGTGATTCATGCGGCTCTTCTGTGAAGAACATTTGTGCTC 60

Db 1 ATGGTGTTGAGGTGATTCATGCGGCTCTTCTGTGAAGAACATTTGTGCTC 60
| | | | |
QY 61 AGAGAGCAAGTGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGAGCCGCAAG 120
| | | | |
Db 61 AGAGAGCAAGTGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGAGCCGCAAG 120
| | | | |
QY 121 AGCAAGTGGGCACTTCTGAGAGACAGAGACTGCTATGAAAGACTCAGAGAGCAAG 180
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RESULT 15

US-09-651-236-375

; Sequence 375, Application US/09651236

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

; APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Patrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-651-236-375

Query Match 100.0%; Score 2040; DB 25; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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Search completed: November 8, 2002, 08:45:47
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 02:17:58 ; Search time 213.594 Seconds

1500.171 million cell updates/sec

Title: US-09-924-400-303

Sequence: 1 atgtgtgttgagttgattc.....aaaaaaaaaaaaaaaaaaaaa 2040

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Searched: 205966 seqs, 78536166 residues

Total number of hits satisfying chosen parameters: 411932

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	170.6	8.4	1041	6	US-10-131-813A-21	Sequence 21, App
3	170.6	8.4	1041	6	US-10-131-819A-21	Sequence 21, App
4	170.6	8.4	1041	6	US-10-131-823A-21	Sequence 21, App
5	170.6	8.4	1041	6	US-10-131-824A-21	Sequence 21, App
6	170.6	8.4	1041	6	US-10-131-826A-21	Sequence 21, App
7	170.6	8.4	1041	6	US-10-131-829A-21	Sequence 21, App
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27	170.6	8.4	1041.6	US-10-128-666A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

; Sequence 3605, Application US/09513999C

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Giordano, J.Y.

FILE REFERENCE: 59.US2.REG

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 30081
SOFTWARE: Patent.pm

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      SEQ ID NO 380
      LENGTH: 298

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TYPE: DNA
ORGANISM: Homo sapiens

FEATURE: NAME/REV. CDS

; LOCATION: 77..298

Query Match	10.18;	Score 205.4;	DB 5;	Length 298;
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OV 869 TTTTATCAAGAAAAAGCGAATTTAAATGCACCTGGATAGATATGGAAGGACTGCTCTCA 92E

Db 141 TTTTAAATCAAGAAAAAGCAATTTAAATGCACCTGGATAGATATGGAGAACTGCTCTCA 200

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RESULT 2

; Sequence 21, Application US/10131813A

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: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C139
: CURRENT FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
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: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
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: NUMBER OF SEQ ID NOS: 550
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: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-131-813A-21

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Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1,7e-32;
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QY 558 AGAAGTATAAAGTCTGCTGAGACGATGTCACTTAATGTCTTGAACAACAAAA 617
DB 477 GGAATGTGACATCTCGGTGTCAGAAAGATGTGAGCTTAACCTGCGACCGTAGAGA 536
QY 618 GAGACAGCTGTGAATAAGGCGGTACATGCGAAGAAATGAATGTGCTTAATGTCTCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACACTGAGGAGGAGGCTGTGTCAACTCTTCTGCT 596

```

```

QY 678 GGAACATGCGACATGATCCAAATATTCCAGATGATGAAATACCACTGCACTACGC 737
DB 597 GCAAAATGCGCGCATCCAAATATTACGATTTCTTGGAGAGCTGCTGCACTACGC 656
QY 738 TATCTATATGAGATTAATTAATGCGCAAGACATGCTCTTATATGCTGTGATATGGA 797
DB 657 TGTGTATATGAAATATCATCATCATGATGAAAAAACTTCTTACATGGTGTACAAATATTGA 716
QY 798 ATCAAAAAACAAG 810
DB 717 AGAATGCAAGCAAG 729

```

```

RESULT 3
US-10-131-819A-21
: Sequence 21, Application US/10131819A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C134
: CURRENT FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-131-819A-21

```

```

Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1,7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```

```

QY 378 TGCCTTCATGAGCCAGTACGATCCGTCGAGAAAGATCTGGCAAGCTCCACAGAGC 437

```



```
Db 300 TGGCTTCGGATTTCCCAATACCCATTAACCGTATCATCTGAAAGAGATCCACAGAGC 359
Oy 438 TGCCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCTGATCTGAGGACACTAGCT 497
Db 360 TGTCTTACATGGTAACTTAGAGAAACTGAA---GTACCTTCTGCTCAGCTATTTATGACGC 416
Oy 498 GAACAGAAGAGCAAGCAAAAGAGAGCTGCTACATCTGGGCTCTGCCAATGGGAATTC 557
Db 417 CATATAGAGAGACAGAGAGAAAGAGCCGCCCTACATTTGGCCTGTGCCACCGCAACC 476
Oy 558 AGAAGTAGTAAACTCTCTGCTGAGACAGATGTCACTTAAATGTCCTGACAAACAAA 617
Db 477 GGAATGTGACATCTCTGCTGTGCGAGAGATGTGAGCTTAACTCTGGACCGTAAGA 536
Oy 618 GAGGACAGCTCTGATTAAGGCGGTACATGCCAGAGATGAATGTCCTTAATGTTGCT 677
Db 537 CAGGACACCTCTGATCAAGAGCTGTACACTGAGGAGGAGGCTTGTCAACTCTTCTGCT 596
Oy 678 GGAACATGCGACTGATCCAAATATTCAGATGATGGAATACACCTCTGCACTAGCG 737
Db 597 GCAAAATGGCGCCATCCAAATATTTACGATTTCTTTGGAAGAGCTGCTCTGCACTAGCG 656
Oy 738 TATCTATTAATGAAGATTAATTAATGCGCAAGACACTGCTTATATATGCTGATATCA 797
Db 657 TGTGTATTAATGAAGATACATCATGATAGAAAAACTTTTTCACATGATGTAACAATTTGA 716
Oy 798 ATCAAAAACAAG 810
Db 717 AGAATGACAGCAAG 729
```

RESULT 4

US-10-131-823A-21

Sequence 21, Application US/10131823A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P333081C143

CURRENT APPLICATION NUMBER: US/10/131,823A

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

```
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 21
;; LENGTH: 1041
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-131-823A-21
```

Query Match

8.4%; Score 170.6; DB 6; Length 1041;

Best Local Similarity 63.7%; Pred. No. 1.7e-32;

Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```
Oy 378 TGCCTTCATGAGAGCCAGTACACGTCCTGTGAGAGATCTGAGACAGCTCCACAGAGC 437
Db 300 TGGCTTCGGATTTCCCAATACCCATTAACCGTATCATCTGAAAGAGATCCACAGAGC 359
Oy 438 TGCCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCTGATCTGAGGACACTAGCT 497
Db 360 TGTCTTACATGGTAACTTAGAGAAACTGAA---GTACCTTCTGCTCAGCTATTTATGACGC 416
Oy 498 GAACAGAAGAGCAAGCAAAAGAGAGCTGCTACATCTGGGCTCTGCCAATGGGAATTC 557
Db 417 CATATAGAGAGACAGAGAGAAAGAGCCGCCCTACATTTGGCCTGTGCCACCGCAACC 476
Oy 477 GGAATGTGACATCTCTGCTGTGCGAGAGATGTGAGCTTAACTCTGGACCGTAAGA 536
Oy 618 GAGGACAGCTCTGATTAAGGCGGTACATGCCAGAGATGAATGTCCTTAATGTTGCT 677
Db 537 CAGGACACCTCTGATCAAGAGCTGTACACTGAGGAGGAGGCTTGTCAACTCTTCTGCT 596
Oy 678 GGAACATGCGACTGATCCAAATATTCAGATGATGGAATACACCTCTGCACTAGCG 737
Db 597 GCAAAATGGCGCCATCCAAATATTTACGATTTCTTTGGAAGAGCTGCTCTGCACTAGCG 656
Oy 738 TATCTATTAATGAAGATTAATTAATGCGCAAGACACTGCTTATATATGCTGATATCA 797
Db 657 TGTGTATTAATGAAGATACATCATGATAGAAAAACTTTTTCACATGATGTAACAATTTGA 716
Oy 798 ATCAAAAACAAG 810
Db 717 AGAATGACAGCAAG 729
```

RESULT 5

US-10-131-824A-21

Sequence 21, Application US/10131824A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P333081C143

```
; FILE REFERENCE: P330R1C126
; CURRENT APPLICATION NUMBER: US/10/131, 824A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-824A-21
```

```
Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
QY 378 TGCCTTATGAGCCCGACGATCCAGTCCGTCGAGGAAGATCTGACAAAGCTCCACAGAC 437
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTGCATTTCCCAATTAACCCGATTAACCGTATCATCTGAAGAGATCCACAGAC 359
QY 438 TGCCTGATGAGTAAAGTCCCGACAGAGATCTGATGCTGATGCTGAGGACACTGACGT 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGTATTTATGACGC 416
QY 498 GAACAAAGAGACAAGAAAAGAGACTGCTCTACATCTGCGCTTCCCAATGGGAATTC 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 CAATTAAGAGAGACGAAGGAAGACCGCCCTACATTTGGCTGTGCGCACTGCCAAC 476
QY 558 AGAAGTGTAAACTCTGCTGAGACAGCATGTCAACTTAATCTCTTACAAACAAAA 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATGTGATCTCTGCTGAGTCCAGAAAGTGAAGTGAACCTTGCAGCGCTGAAGA 536
QY 618 GAGCAGACCTCTGATTAAGGCGGTACATGCGCAGGAAGATGATGTCGTTAATGTGCT 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACACCTCTGATCAAGGCTGTACACATGAGGACAGAGGCTTGTCAACTCTTCTGCT 596
QY 678 GGAACATGAGCATGATCCAAATATTTCCAGATGATGATGAATACCACTGTGACACTAGC 737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 597 GCAAAATGGGCGCCAAATCAATATTTACGATTTCTTGAAGGACGTGCTGTGCACTAGC 656
QY 738 TATCTATTAATGAATTAATTAATGAGCAAGCACTGCTTATTAATGTGCTGATATGCA 797
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 657 TGTGTATAAAGAAATCATTCATCCAGATGATGAAGAAAACCTTCTTACATGATGATCAATATATGA 716
QY 798 ATCAAAAAACAAG 810
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 717 AGAATGCAGCAAG 729
```

```
RESULT 6
US-10-131-826A-21
; Sequence 21, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-21
```

```
Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
QY 378 TGCCTTATGAGCCCGACGATCCAGTCCGTCGAGGAAGATCTGACAAAGCTCCACAGAC 437
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTGCATTTCCCAATTAACCCGATTAACCGTATCATCTGAAGAGATCCACAGAC 359
QY 438 TGCCTGATGAGTAAAGTCCCGACAGAGATCTGATGCTGATGCTGAGGACACTGACGT 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGTATTTATGACGC 416
QY 498 GAACAAAGAGACAAGAAAAGAGACTGCTCTACATCTGCGCTTCCCAATGGGAATTC 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 CAATTAAGAGAGACGAAGGAAGACCGCCCTACATTTGGCTGTGCGCACTGCCAAC 476
QY 558 AGAAGTGTAAACTCTGCTGAGACAGCATGTCAACTTAATCTCTTACAAACAAAA 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATGTGATCTCTGCTGAGTCCAGAAAGTGAAGTGAACCTTACATGATGATCAATATATGA 536
QY 618 GAGCAGACCTCTGATTAAGGCGGTACATGCGCAGGAAGATGATGTCGTTAATGTGCT 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACACCTCTGATCAAGGCTGTACACATGAGGACAGAGGCTTGTCAACTCTTCTGCT 596
```

QY	678	GGAACTGGACCTATCCAAATATCCAGATGATGGAAATACACACTGTGACATACGC	737
	1		
	11		
	111		
	1111		
	11111		
Db	597	GCAAAATGGGCCCAATCCAAATATTTACGGATTTCTTTGGAAAGCTGCTGTGCATPACGC	656
	1		
	11		
	111		
	1111		
	11111		
QY	738	TATCTATATGATGATAAATTAATGAGCAAGCACCTCTTATATGATGCTCATATCGA	797
	1		
	11		
	111		
	1111		
	11111		
Db	657	TGTGTATATATGATATCATTCATCATGATAGAAAACTTCTTCACATGGTACAAATATTTGA	716
	1		
	11		
	111		
	1111		
	11111		
QY	798	ATCAAAAAACAAAG	810
	1		
	11		
	111		
	1111		
	11111		
Db	717	AGAAATGCAGCAAG	729

RESULT 7
US-10-131-829A-21
; Sequence 21, Application US/10131829A
: GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: Deforge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Collin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C138
 CURRENT APPLICATION NUMBER: US/10/131,829A

```

? CURRENT FILING DATE: 2002-04-27
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 21
?
? LENGTH: 1041
?
? TYPE: DNA
?
? ORGANISM: Homo Sapien
US-10-131-829A-21

```

Query Match	8.4%	Score 170.6;	DB 6;	Length 1041;
Best Local Similarity	63.7%;	Pred. No. 1.7e-32;		
Matches 276;	Conservative 0;	Mismatches 154;	Indels 3;	Gaps

QY	378	TGCTTCATGAGCCCAAGTACCAACGTCGCGAGAAAGATGTGACACAGTCCACAGAGC	437

Db 300 TGGCTTGCATTTCGCCCAATACCCCATTTAAACGATCATCTGAAAGAGATCCACAGAGC 359

Qy 438 TGCCTGGGGGTAAAGTCCCCAGAAAGATCTTCATCTGATGCTCAAGGACACTGACGT 497

Db 360 TGTCTACATGATGTAATCATAGAGAAACTGAA---GTACCTCTCTGCTACGTAATTAATGACGC 416

Qy 498 GAACAAAGAGACAAAGCAAAAAGAGACATGCTCTACATCTTGGGCTCTGGCCAAATGGGAATTC 557

Db 417 CAATTAAGGAGACACAGGAAGGAAGGACCGGCTTACATTTGGCCTGTGTGCCACTGGCCAAAC 476

Qy 558 AGAAGTGTAAACTGCTGCTGAGACAGCATGTCACATTAATGTCTTGCATCAACAAAAA 617

Db 477 GGAATGGTATCATCTCTCGTGGTGTCCAAAGATGTGACCTTAACCTCTGGCAGCCGTGAAGA 536

Qy 618 GAGGACACCTCTGATTTAAAGGCCGCTACACATGGCAGAGATGAAATGTGCTTAAATGTTGCT 677

Db 537 CAGGACACCTCTGATTCAGAGCTGTACACACTGAGGACAGAGGCTTGTCCAACTTCTTGCT 596

Qy 678 GGAAACATGCGACATCCAAATATTTCCAGATGAGTATGAGAAATCCACTCTGGACATACGC 737

Db 597 GCAAAATGCGCCCAATCCAAATATTTACGAGATTTCTTTGGAAAGGACTCTCTGGACATACGC 656

Qy 738 TATCTATATGATGAGATTAATTAATGCGCAAAAGACACTGCTCTATATATGTCGTGATATGCA 797

Db 657 TGTGATATATGAAGATACATCCATGATAGAAAACCTTCTTACATGTGTCACAAATATTGA 716

Qy 798 ATCAAAAAAACAAG 810

Db 717 AGAATGACGACAAG 729

```

RESULT 8
US-10-125-926A-21
; Sequence 21, Application US/10125926A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C80
; CURRENT APPLICATION NUMBER: US/10/125,926A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18

```

```
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-926A-21

Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCTTCATGAGCCGACGATCCCTGCGAGAAAGATCTGACAAAGCTCCACAGAGC 437
DB 300 TGCTTCGATTTCCCAATACCCATTTAAACCGTATCATGTGAAGGATCCACAGAGC 359
QY 438 TGCTGTGGGCTAAAGTCCCGAGAAAGATCTCATGCTGTCAGAGCACTGACGT 497
DB 360 TGCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGCTATTATGACGC 416
QY 498 GAACAAAGAGACAGCAAAAGAGACTGCTTACATCTGGCTCTGCCAATGGGAATTC 557
DB 417 CAATTAAGAGAGACAGAGAAAGAGACCGCCCTACATTTGGCTGCTGCCAACC 476
QY 558 AGAAGTAGTAAACTCTGCTGACAGAGATGCAACTTAATGCTCTTACAAACAAA 617
DB 477 GGAATGATACATCTCTGCTGTCAGAAAGATGTGACCTTACCTGACACCGTGAAGA 536
QY 618 GAGGACAGCTCTGATTAAGCCCGTACAAATGCGAGAAAGATGAATGCTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACACCTGAGGAGGAGGAGCTTGTGCACTCTTCTGCT 596
QY 678 GGAACATGCGCTGATCCAAATATTCAGATGATGATGAATACCACTGTGCACTACGC 737
DB 597 GCAAAATGGGCGCAATCCAAATATTAAGGATTTCTTTGGAAGGACGCTCTGCACTACGC 656
QY 738 TATCTAATGAAGATAAATTAATGGCCAAAGACGCTCTTATGAGGCTGATATGCA 797
DB 657 TGCTTAATGAAGATACATCATGATAGAAAACCTTCTTACATGATGTAACAAATATTGA 716
QY 798 ATCAAAAACAG 810
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RESULT 9
US-10-127-829A-21
; Sequence 21, Application US/10127829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
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; CURRENT APPLICATION NUMBER: US/10/127, 829A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829A-21

Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCTTCATGAGCCGACGATCCCTGCGAGAAAGATCTGACAAAGCTCCACAGAGC 437
DB 300 TGCTTCGATTTCCCAATACCCATTTAAACCGTATCATGTGAAGGATCCACAGAGC 359
QY 438 TGCTGTGGGCTAAAGTCCCGAGAAAGATCTCATGCTGTCAGAGCACTGACGT 497
DB 360 TGCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGCTATTATGACGC 416
QY 498 GAACAAAGAGACAGCAAAAGAGACTGCTTACATCTGGCTCTGCCAATGGGAATTC 557
DB 417 CAATTAAGAGAGACAGAGAAAGAGACCGCCCTACATTTGGCTGCTGCCAACC 476
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DB 537 CAGGACACCTCTGATCAAGGCTGTACACCTGAGGAGGAGGAGCTTGTGCACTCTTCTGCT 596
QY 678 GGAACATGCGCTGATCCAAATATTCAGATGATGATGAATACCACTGTGCACTACGC 737
DB 597 GCAAAATGGGCGCAATCCAAATATTAAGGATTTCTTTGGAAGGACGCTCTGCACTACGC 656
QY 738 TATCTAATGAAGATAAATTAATGGCCAAAGACGCTCTTATGAGGCTGATATGCA 797
DB 657 TGCTTAATGAAGATACATCATGATAGAAAACCTTCTTACATGATGTAACAAATATTGA 716
QY 798 ATCAAAAACAG 810
DB 717 AGAATGACAGCAAG 729

RESULT 10
US-10-127-831A-21
; Sequence 21, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C107
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-831A-21

Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTCATGAGCCAGGACCGATCCGCTGGAGAGATCTGACAAAGCTCCACAGAGC 437
DB 300 TGGCTTCGATTTCCCAATACCCCATTAACCGTATCATCTGAGAGAGATCCACAGAGC 359
QY 438 TGGCTGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATGCTCCAGGAGACAGCTG 497
DB 360 TGTCTTCATGATGTATGTAGAGAAACTGAA--GTACCTTCCTCAGAGTATATAGAGC 416
QY 498 GAACAGAGAGAGCAAGCAAGAGAGCTGCTTACATCTGGCCCTGCGCAATGGGAATTC 557
DB 417 CAATAG 476
QY 558 AGAGTACTAAACTCTGCTGCTGAGAGAGAGATGTCACACTTAATGCTTGGACAAAGAA 617
DB 477 GGAATGTGATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
QY 618 GAGGACAGCTGATTAAGGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTG 677
DB 537 CAGGACAGCTGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
QY 678 GGAACATGGCACTGATCCCAATATATTCAGAGATGATGGAATATACACTCTGCACTAG 737

DB 597 GCAAAATGGCGCCCAATCCAAATATTAACGATTTCTTTGGAGAGACTGCTCTGCACAGC 656
QY 738 TATCTATATGAAGATTAATTAATGCGCAACAGACTGCTTATATGCTGATATGCA 797
DB 657 TGTGTATATGAAGATATCATCATGATGAAAACTTCTTCACATGTTACAAATATGCA 716
QY 798 ATCAAAAAACAG 810
DB 717 AGAATGACAGCAG 729

RESULT 11
US-10-127-835A-21
Sequence 21, Application US/10127835A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C102
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-835A-21

Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTCATGAGCCAGGACCGATCCGCTGGAGAGATCTGACAAAGCTCCACAGAGC 437
DB 300 TGGCTTCGATTTCCCAATACCCCATTAACCGTATCATCTGAGAGAGATCCACAGAGC 359

Db 597 GCAAAATGGCGCCAAATCCAAATATTACGATTTCTTTGGAAGGACCTCTCGACTACGC 656
QY 738 TATCTAATATGAAGATAAATTAATGCGCAAGACACTGCTCTATATGTCGCTGATATCGA 797
Db 657 TGTGTATATGAAGATACATCCATGATAGAAAACCTTCTTTCACATGTCATCAATATTGCA 716
QY 798 ATCAAAAACCAAG 810
Db 717 AGAATGCAGCAAG 729

RESULT 15

US-10-127-901A-21
; Sequence 21, Application US/10127901A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RJC86
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-901A-21

Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCTTCATGAGCGCCAGTACACGCTCGTGAGAAAGATCGGACAGCTCCACAGAGC 437
Db 300 TGCTTCGATTTCCCAATACCCCATTTAAACCGTATCATCTGAGAGGATCCACAGAGC 359

QY 438 TGCTGTGGGGTAAAGTCCCGCAAGAAAGATCTCATGCTGATGCTGAGGACACTGACGT 497
Db 360 TGCTTACATGATGAATCTAGAGAACTGAA--GTACCTTCTGCTCAGCATATTATGACGC 416
QY 498 GATCAAGAGGACACCAAGAAAGAGACTGCTGCTACATGCGCCCTGCGCAATGGGAATTC 557
Db 417 CAATTAAGAGAGACAGAGAGAAAGAGACCGCTTACATTTGGCTGTGCCCTGGCCCAAC 476
QY 558 AGAAGTAGTAAACCTCTGCTGAGACAGAGATGTCAACTTAATGCTTGCACAAACAAA 617
Db 477 GGAATGTGATCATCTCTGCTGTGTCAGAAAGATGTGACCTTAACCTGTGGACCGTGAAG 536
QY 618 GAGGACAGCTGTGATTAAGGCGCTACAAATGCCAGAAAGATGAATGTCGTTAATGTGCT 677
Db 537 CAGGACACCTGTGATCAAGGCTGTACAACTGAGAGGAGGAGGCTGTGCAACTCTCTGCT 596
QY 678 GGAACATGGCAGCTGATCCAAATATTCCAGATGATGATGAAATACCACTCTGACACTACGC 737
Db 597 GCAAAATGGCGCCAAATCCAAATATTACGGATTTCTTTGGAAAGGACCTCTGACACTACGC 656
QY 738 TATCTAATATGAAGATAAATTAATGCGCAAGACACTGCTCTTATATGTCGCTGATATCGA 797
Db 657 TGTGTATATGAAGATACATCCATGATAGAAAACCTTCTTTCACATGTCATCAATATTGCA 716
QY 798 ATCAAAAACCAAG 810
Db 717 AGAATGCAGCAAG 729

Search completed: November 8, 2002, 08:53:04
Job time : 219.594 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 05:05:38 ; Search time 410.891 Seconds
(without alignments)
1726.908 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atgtgtgtgtgtgtgtgttc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2000	100.0	2000	10	US-09-759-143-374
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4	2000	100.0	2000	10	US-09-810-936-302
5	2000	100.0	2000	10	US-09-822-827-314
6	2000	100.0	2000	10	US-09-429-755-302
7	1940	97.0	2040	10	US-09-825-301-7
8	1940	97.0	2040	10	US-09-759-143-375
9	1940	97.0	2040	10	US-09-780-669-375
10	1940	97.0	2040	10	US-09-810-936-303
11	1940	97.0	2040	10	US-09-822-827-315
12	1940	97.0	2040	10	US-09-429-755-303
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14	1147.6	57.4	1853	10	US-09-780-669-369
15	1147.6	57.4	1853	10	US-09-810-936-295
16	1147.6	57.4	1853	10	US-09-822-827-309
17	1147.6	57.4	1853	10	US-09-429-755-295
18	1131.6	56.6	1155	10	US-09-825-301-5
19	1131.6	56.6	1155	10	US-09-759-143-373

20	1131.6	56.6	1155	10	US-09-780-669-373	Sequence 373, App
21	1131.6	56.6	1155	10	US-09-810-936-301	Sequence 301, App
22	1131.6	56.6	1155	10	US-09-822-827-373	Sequence 373, App
23	1131.6	56.6	1155	10	US-09-429-755-301	Sequence 301, App
24	1129.6	56.3	1155	10	US-09-810-936-323	Sequence 323, App
25	1126.8	56.3	1155	10	US-09-810-936-328	Sequence 328, App
26	1016.4	50.8	1155	10	US-09-810-936-329	Sequence 329, App
27	1011.6	50.5	1155	10	US-09-810-936-325	Sequence 325, App
28	1010	50.5	1155	10	US-09-810-936-330	Sequence 330, App
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33	912.8	45.6	1852	10	US-09-822-827-530	Sequence 530, App
34	912.8	45.6	1852	10	US-09-429-755-313	Sequence 313, App
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36	900.8	45.0	1851	10	US-09-759-143-366	Sequence 366, App
37	900.8	45.0	1851	10	US-09-780-669-366	Sequence 366, App
38	900.8	45.0	1851	10	US-09-810-936-291	Sequence 291, App
39	900.8	45.0	1851	10	US-09-810-936-292	Sequence 291, App
40	900.8	45.0	1851	10	US-09-822-827-366	Sequence 366, App
41	900.8	45.0	1851	10	US-09-429-755-291	Sequence 291, App
42	900.8	45.0	1851	10	US-09-429-755-292	Sequence 291, App
43	888	44.4	2184	10	US-09-759-143-370	Sequence 370, App
44	888	44.4	2184	10	US-09-780-669-370	Sequence 370, App
45	888	44.4	2184	10	US-09-810-936-296	Sequence 296, App

ALIGNMENTS

RESULT 1
US-09-825-301-6
Sequence 6, Application US/09825301
Patent No. US20020009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jianshun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
OF INVENTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-825-301-6

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTGTTGAGTGTGATTCATCGCGGCTCTTGTGTAAGACATTTGTTTC 60
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QY 61 AGGAGCAAGTGGGCAAGTGGTGTCTCCGTTGCTTCCCTGTCAGGAGCGGCAAG 120
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DB 61 AGGAGCAAGTGGGCAAGTGGTGTCTCCGTTGCTTCCCTGTCAGGAGCGGCAAG 120
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QY 121 AGCAAGTGGGCACTTCTGGAAGCAGACGATCTGCTATGAAGACACTCAGAGCAAG 180
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DB 121 AGCAAGTGGGCACTTCTGGAAGCAGACGATCTGCTATGAAGACACTCAGAGCAAG 180
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QY 181 ATGGGCAAGTGGGCGGCACTCTCCCTGCTGAGGGGAGTGAGCAAGCAAGCTG 240
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Qy 601 GTCTTGAACCAAAAGAGAGAGAGAGTGTATTAAGGCGCTACATGCGAGAGATGAA 660
Db 601 GTCTTGAACCAAAAGAGAGAGAGAGTGTATTAAGGCGCTACATGCGAGAGATGAA 660
Qy 661 TGTGCTGTAATGTTGCTGAGACATGAGCGCTATCCAAATATTCCAGATGATGGAAT 720
Db 661 TGTGCTGTAATGTTGCTGAGACATGAGCGCTATCCAAATATTCCAGATGATGGAAT 720
Qy 721 ACCACTGCTGACACTGACATCTATATGAATGAATTAATGAGCAAGCACTGCTCTTA 780
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Qy 841 CATGAGCAAAAGAGAGAGTGTGTAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900
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Db 1141 CTGACATCAGAGAGAGTGTCAAAAGTTCAAGAGCAGTGAATAAGCCAGCCAGAGAA 1200
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Qy 1261 AAGCATGAAATTAATATGTTGATTAATAGAAAAAGTATGATGTTGCTGCTGCTG 1320
Db 1261 AAGCATGAAATTAATATGTTGATTAATAGAAAAAGTATGATGTTGCTGCTGCTG 1320

Qy 1321 AATGCTAATTAATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGCTAATTAATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
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Db 1501 TCAG 1560
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Db 1741 CAAATGATATCAG 1800
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Db 1861 CTTAGTGTGAAG 1920
Qy 1921 GCCATGCTAAG 1980
Db 1921 GCCATGCTAAG 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-759-143-374
Sequence 374, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jjiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedivick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTTATTCATGCCGGCTCTTCTGTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGGAGTTATTCATGCCGGCTCTTCTGTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGAGAGCAAGTGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
DB 61 AGAGAGCAAGTGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
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QY 181 ATGGGCAAGTGGTGGGCGCCACTGCTCCCTGCTGAGGGGGAGTGGCAAGCAACGTG 240
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QY 301 TGGTGGTGGCACTGCTCCCTGCTGACAGGGGGAGCGCAAGCAAGTGGGCGCTTG 360
DB 301 TGGTGGTGGCACTGCTCCCTGCTGACAGGGGGAGCGCAAGCAAGTGGGCGCTTG 360
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DB 361 GGAAGACTAGATGACAGTGGCTTCTCATGAGCCAGGTACACGCTCCGTGGAGAAATCTG 420
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DB 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGATGATGAGAGGTTGAGAAATGAAG 1260
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DB 1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGCAATTTCTGACTCAAAAGAA 1440
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DB 1561 TTTATGCTATCGAAGAAATGAAGAGCAAGCAAGTCAATGCTGATTTCCAGAAAA 1620
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DB 1621 CTGACTAATGCTGCCACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAG 1680
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Qy 1981 AAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-780-669-374
Sequence 374, Application us/09780669
Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Wang, Aljun
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yashir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghon, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 TGGTGTGCGCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGTGGGCGCTTGG 360

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Db 841 CATGAGCAAAACAGCAAGCTGTAATTTTAATCAAGAAAGCAATTTAAATGA 900
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Db 1321 AATGCTAATATGATTAATTTCTCAAAAGAGCAGAACACTGAAAACACCAATTT 1380
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OY 1861 CTTACTTGTAGAGAAAGAAAGACATCTTGCAATGAAATAGTACGTTGGGAGAAAT 1920
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Db 1921 GCCATGCTAGAGCTGAGCTAGACAAATGAAACATCAGAGCAGCTAAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-810-936-302
; Sequence 302, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-302

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACGACTTTGGTCTC 60

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Db 1 ATGTGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACGACTTTGGTCTC 60
OY 61 AGGACCAAGATGCGCAAGTGGTCTGCTTCTCCCTGCTGCAAGGAGCCGCAAG 120
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Db 1501 TCAGAGAGAGAGTCCAAAGGCTTGAGGCGAGTGAATGGCCAGCAGAGCTGAAAT 1560
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Db 1561 TTTATGGCTATCGAAGAAATGAGAGACACGGAAGTACTCATGTGCGAATTTCCAGAAAAC 1620
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Db 1621 CTGACTAATGCTGCTGCTGCTGCAATGGTATGATGATTAATCTCTCCAGAGAAAGGC 1680
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Qy 1801 ATTCTGATCTGAGAAAGCAAGCATAGTAGAGTGTGAAAAAATGAAATTCGACCTTCT 1860
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Qy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAGTACGTTGCGGAGAAATTT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAGTACGTTGCGGAGAAATTT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACAATGAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 5

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US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827

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; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374

Query Match      100.0%  Score 2000:  DB 10:  Length 2000:
Best Local Similarity 100.0%:  Pred. No. 0;
Matches 2000;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 1  ATGTGGTTGAGTTGATTCATGCGCGCTGCTCTCTGTGTGAAGAAAGCAATTTGCTC 60
Db 1  ATGTGGTTGAGTTGATTCATGCGCGCTGCTCTCTGTGTGAAGAAAGCAATTTGCTC 60
Qy 61  AGGACAAAGATGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61  AGGACAAAGATGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121  AGCAAGTGGGCACTTGTGGAGACACAGACACTGCTATGAAGACATCAGAGAGCAAG 180
Db 121  AGCAAGTGGGCACTTGTGGAGACACAGACACTGCTATGAAGACATCAGAGAGCAAG 180
Qy 181  ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
Db 181  ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
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Db 241  GCGCTTCTGAGACACACAGACACTGCTATGAAGACACTCAGAGAAAGATGGGCAAG 300
Qy 301  TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCGGCAAGAGCAAGTGGGCGTTGG 360
Db 301  TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCGGCAAGAGCAAGTGGGCGTTGG 360
Qy 361  GGAGACTACGATGACAGTGGCTTTCATGAGAGCCAGTACCAACGTCCGTTGGAAGATCTG 420
Db 361  GGAGACTACGATGACAGTGGCTTTCATGAGAGCCAGTACCAACGTCCGTTGGAAGATCTG 420
Qy 421  GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421  GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481  CTCAGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGAGTGTCTACATCTGGCC 540
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Db 541  TCTGCAATGGGAATTCAGAAATAGTAAACTCTGCTGCAAGAGATGCAACTTAAT 600
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Db 601  GTCTTGAACAACAAAAGAGAGACGCTGTGATTAAGGCGCTGACAAATCCAGGAAGATGAA 660
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Db 841  CATAGCAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCAATTTTAATGCA 900

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Qy	961	GTGAGCCTTACTCTGAGCAAAATATGATATGATCTTCGAAGATCTATCGAGACAGC	1020
Dp	961	GTGAGCCTTACTCTGAGCAAAATATGATATGATCTTCGAAGATCTATCGAGACAGC	1020
Qy	1021	GCCAGAGATATGCTGTTTCTTACTCATCATATGTAATTTGGCAATTACTTTCTGACTAC	1080
Dp	1021	GCCAGAGAGATATGCTGTTTCTTACTCATCATATGTAATTTGGCAATTACTTTCTGACTAC	1080
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Dp	1081	AAAGAAAACAGATGCTAAAAATCTTTTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGGAGAGTCACAAAGGTTCAAAAGGACAGTAAATATGACCCAGAGAA	1200
Dp	1141	CTGACATCAGAGGAGAGTCACAAAGGTTCAAAAGGACAGTAAATATGACCCAGAGAA	1200
Qy	1201	ATGCTCAGAACCCAGAAATAAATAAGATGGTGATAGAGAGTTGAAGAAGAAATGAG	1260
Dp	1201	ATGCTCAGAACCCAGAAATAAATAAGATGGTGATAGAGAGTTGAAGAAGAAATGAG	1260
Qy	1261	AAGCATTAAGCTAATTAATGTGGGATTACTAGAAAACCTGACTAATATGTTGCTACTGTCGC	1320
Dp	1261	AAGCATTAAGCTAATTAATGTGGGATTACTAGAAAACCTGACTAATATGTTGCTACTGTCGC	1320
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Dp	1321	AATGCTAATATGATTAATTCCTCAAGAGACAGAACCCAGAAATCAGCAATTT	1380
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Dp	1441	AAACAGATGCCAAATAATCTTCTTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
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Dp	1621	CTGACTAATGCTGCTGCTGCGCAATGGTATGATGATTAATTCCTCAAGAGAGC	1680
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Dp	1681	AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATCACAGTGAAGAA	1740
Qy	1741	CAAAATGATACTCAGAAACAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAG	1800
Dp	1741	CAAAATGATACTCAGAAACAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAG	1800
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Dp	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCT	1860
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Qy	1921	GCCATGCTAAGACTGAGACTGAGACAAATGAAGAAACATCAGAGCCACTAAAAAAGAAAAA	1980
Dp	1921	GCCATGCTAAGACTGAGACTGAGACAAATGAAGAAACATCAGAGCCACTAAAAAAGAAAAA	1980
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Db      1981 AAAAAAAAAAAAAAAAAA 2000

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US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Ketter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

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Query Match	100.0%	Score 2000;	DB 10;	Length 2000;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2000;	Conservative	0;	Mismatches	0;
			Indels	Gaps
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Db 1	ATGGTGTGTTGAGGTTGATTCATGCCGGTGCCTCTTCTGTAAAGACATTTGCTC	60		
QY 61	AGGAGCAAGATGGGCAAGTGTGCTGTGCCCTTTCCTCCCTGCTGCAAGGAGAGCGGCAAG	120		
Db 61	AGGAGCAAGATGGGCAAGTGTGCTGTGCCCTTTCCTCCCTGCTGCAAGGAGAGCGGCAAG	120		
QY 121	AGCAACGTGGGCACTTTGTGAGACCAACGACGACTCTGTATTAACACCTCGAGAGCAAG	180		
Db 121	ACCAACGTGGGCACTTTGTGAGACCAACGACGACTCTGTATTAACACCTCGAGAGCAAG	180		
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Db 241	GGCGCTTCTGAGAGCCACGACGACTCTGTATGAAGACACTAGGAACAATGGGCAAG	300		
QY 301	TGGTGTGTCACATGCTTCCCTGCTGTGCAAGGGGAGCGGCAAGCAAGGTGGGCTTTGG	360		
Db 301	TGGTGTGTCACATGCTTCCCTGCTGTGCAAGGGGAGCGGCAAGCAAGGTGGGCTTTGG	360		
QY 361	GGAGACTACGATGACAGCTGCTTCATGTGAGCCCGAGTACACGTCCTGTGGAAGATCTG	420		
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Db 421	GACAAGCTCCACAGAGCTCCTGTGGGGGTAAAGTCCCGAAGAAAGATCTCATGCTCATG	480		
QY 481	CTCAGGACACTGACGTGAGCAAGAGCAAGCAAAAGAGGACTGCTTCATCTGTGCC	540		
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Db 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGGAAGTATCTATGTCGATTTCCAGAAAG 1620
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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-825-301-7
; Sequence 7, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehntner, Barbara
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; NUMBER OF SEQ. ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-825-301-7

Query Match 97.0%; Score 1940; DB 10; Length 2040;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

Qy 1 ATGCTGTTGAGGTGATTCATGCGCGGCTGCTCTTCTGAAAGAGCCATTGGTCTC 60
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Db 1861 GAAAGCAGATAGAAAGTGTGAAAAATGAATTCAGACTTCTCTAGTTGTAAGAA 1920
Qy 1876 GAAAAAGACATCTTGCATGAAAAATAGTACTTGCAGGAGAAATTTCCATGCTAAGACAG 1935
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACTTGCAGGAGAAATTTCCATGCTAAGACAG 1980
Qy 1936 GAGCTAGACACATGAACATCAGAGCCAGCTGAAAAAAGAAAAAAGAAAAA 1995
Db 1981 GAGCTAGACACATGAACATCAGAGCCAGCTGAAAAAAGAAAAAAGAAAAA 2040

RESULT 8
US-09-759-143-375
: Sequence 375, Application US/09759143
: Patent No. US200202248A1
: GENERAL INFORMATION:
: APPLICANT: Xu, JIANGCHUN
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: JIANG, YUQU
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C23
: CURRENT APPLICATION NUMBER: US/09/759,143
: CURRENT FILING DATE: 2001-01-12
: NUMBER OF SEQ ID NOS: 934
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040

TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 97.0% Score 1940: DB 10: Length 2040:
Best Local Similarity 97.8% Pred. No. 0:
Matches 199; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 ATGAGTGGTTGAGTTGATTCATCCGCGCTCTCTCTGTGAGAAAGCCATTGGTCTC 60
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Db 361 GGAGACTACGATGACGAGTGCCTTTCATGAGGCCAGTACACGTCCTGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGGGCTTAACTCCCGAAGAGATCTCATGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGGGCTTAACTCCCGAAGAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAGAGTGCCTCATCTGATCTGGCC 540
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Db 1981 GAGCTAGACACATGAAGACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 2040

RESULT 9

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US-09-780-669-375
: Sequence 375, Application US/09780669
: Patent No. US20020051577A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Veolvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427024
: CURRENT APPLICATION NUMBER: US/09/780.669
: CURRENT FILING DATE: 2001-02-09
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-780-669-375

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Query Match	97.0%:	Score 1940:	DB 10:	Length 2040:
Best Local Similarity	97.8%:	Pred. No. 0:		
Matches 1995:	Conservative	0:	Mismatches	0:
			Indels	45:
			Gaps	1:
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Db 181	ATGGGCAAGTGTGGCCGACACTGCTTCCCTGCTGCAGGGGGAGTGGCAAGACAGTGG	240		
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Db 301	TGTGTCTCCACACTGCTTCCCTGCTGCAGGGGGAGCGGCAAGGAGTGGGCGCTTGG	360		
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Db	601	GTCCCTTGACAAACAAAAGAGAGACAGCTTGATTAAGGCCGTACCAATGCCAGGAAGATGA	660
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Db	841	CATGACGAAAAACAGCAAGCTGCTGAAATTTTAAATCAGAAAAAGCAATTTAAATGCA	900
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Db	901	CTGGATATGATATGGAAGGACTGCTCATACCTGATGCGTATGTTGGATACGCAAGTATA	960
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QY	1081	AAACAAAAACAGATGCTAAAAATCTCTTGAAAAACAGAAACCGAACAAGACTTAAAG	1140
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RESULT 10
US-09-810-936-303
; Sequence 303, Application us/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Smith, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-303

Query Match 97.08; Score 1940; DB 10; Length 2040;
Best Local Similarly 97.88; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 ATGTGTGATGAGTGAATTCATGCGGCTGCTCTCTGTGAAGAGCCATTGGTCTC 60
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Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCACAGTGAACAAATATGATCTCAG 1800
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QY 1876 GAAAGACATCTTCGATGAAATAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1935
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QY 1936 GAGCTAGACACATGAACATCAGAGCCGCTGAAAAAATGAAAAAATGAAAAAATGAAAAA 1995
Db 1981 GAGCTAGACACATGAACATCAGAGCCGCTGAAAAAATGAAAAAATGAAAAAATGAAAAA 2040

RESULT 11

US-09-822-827-375
; Sequence 375, Application US/09822827
; Patent No. US2002081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-375

Query Match 97.0%; Score 1940; DB 10; Length 2040;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;
QY 1 ATGTGCTTGAAGTGGATTCATGCGGCTGCTCTTCTGTGAAGAACGCAATTTGGTCTC 60
Db 1 ATGTGCTTGAAGTGGATTCATGCGGCTGCTCTTCTGTGAAGAACGCAATTTGGTCTC 60
QY 61 AAGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AAGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
QY 121 AAGCAAGTGGGCACTTCTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AAGCAAGTGGGCACTTCTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGGAGAGAGAGAGAGAGAGAG 240
QY 241 GGCGCTTCTGAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGCGCTTCTGAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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QY 361 GGAGACTAG 420
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QY 421 GACAGCTCCAG 480
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QY 481 CTCAGGAG 540
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QY 541 TCTGCCAATGGGAAATTCAGAAAGTAAATCTCTGCTGAGAGAGAGAGAGAGAGAG 600
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QY 601 GTCTTGGACACAAAAG 660
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QY 661 TGTGCTTAAATGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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QY 721 ACCACTGCTGACTAG 780
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QY 781 TATGCTGCTGATATGCAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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QY 841 CATGAGCAAAAAAG 900
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QY 901 CTGATAGATATGAG 960
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QY 961 GTGAGCTTCTGACTGAG 1020
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Db 721 ACCACTCTGCTACGCTCTATATAGAAAGATTAATTAATGATGCGCAAGACACTGCTCTTA 780
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Db 781 TATGTCGTGATATGAATCAAAAAAACAAGCATGGCTTACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAATCGTAATTTTAATCAAAAAAAGCAATTTAATGCA 900
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QY 901 CTGATAGATATGGAAGAGCTGCTCATATCTGCTATGTTGTTGATCAGCAATATA 960
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QY 961 GTCAGCTTCTACTTGAGCAAAAAATATGATGTAATCTTCAAGATCTATCTGAGACAGC 1020
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QY 1021 GCGAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
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QY 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAACAGCAATCCAGACAAGACTTAAAG 1140
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QY 1141 CTGACATCTAGAGAGAGCTCACAAAGGTTCAAGCAGTGAATAATGCCAGAGAAA 1200
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QY 1201 ATGCTCAGAAACCAAGAAATTAATAGATGGTGAATGAGAGGTTGAAGAAGAAATGAAG 1260
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QY 1261 AAGCATGAAGATTAATATGTTGGATTAATCTAGAAAACCTACTAATGTTGCTCACTGGC 1320
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QY 1381 CCGTACAGAGAAAGTGAAGATATCAAGATTTGCAATTTGTTCTGACTCAAGAA 1440
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QY 1501 TCAGAGAGAGAGTCAAGAGGCTTGAGGCGAGTGAATAATGCGCAGCC----- 1547
Db 1501 TCAGAGAGAGAGTCAAGAGGCTTGAGGCGAGTGAATAATGCGCAGAGAAATGCT 1560
QY 1548 -----AGAGCTGAAAATTTTAATGCTATGCA 1575
Db 1561 CAAGAACCAAGAAATTAATAGATGGTGAATAGAGAGCTGAAAAATTTTAAGGCTATGCA 1620
QY 1576 GAAATGAAAGAGACAGGAAGTACTCATGTCGATTTCCAGAAAACTGACTAATGTTGCC 1635
Db 1621 GAAATGAAAGAGACAGGAAGTACTCATGTCGATTTCCAGAAAACTGACTAATGTTGCC 1680
QY 1636 ACTGCTGGCAATGCTGATGATGATTAATTTCTTCCAGAGAGAGCAAGAACCTGGAAGC 1695
Db 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTTCCAGAGAGAGCAAGAACCTGGAAGC 1740
QY 1696 CAGCAATTTCTGACACTGGAATGAAGATACAGTGAAGCAAAAAATGATGATCTAG 1755
Db 1741 CAGCAATTTCTGACACTGGAATGAAGATACAGTGAAGCAAAAAATGATGATCTAG 1800
QY 1756 AAGCAATTTTGTGAAGAGAGAACTGGAATTTACAGAGTGAATGATGATCTAGATTCAGAA 1815
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Db 1801 AAGCAATTTTGTGAAGAGAGAACTGGAATTTACAGAGTGAATGATCTGATTCAGAA 1860
QY 1816 GAAAGCAGATAGAAATGTTGAAAAAATGAATTCAGACTTCTCTGATTTAGTGA 1875
Db 1861 GAAAGCAGATAGAAATGTTGAAAAAATGAATTCAGACTTCTCTGATTTAGTGA 1920
QY 1876 GAAAGCAGATTTGATGAAATTAATGATGTTGCGGAGAGAAATTCATGTAAGACTG 1935
Db 1921 GAAAGCAGATTTGATGAAATTAATGATGTTGCGGAGAGAAATTCATGTAAGACTG 1980
QY 1936 GAGCTGAGACAAATGAAGATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 1995
Db 1981 GAGCTGAGACAAATGAAGATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 2040

RESULT 13
US-09-759-143-369
; Sequence 369, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Wang, Aljun
; APPLICANT: L1, Samuel
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-369

Query Match 57.4%; Score 1147.6; DB 10; Length 1853;
Best Local Similarity 97.1%; Pred. No. 1,3e-256;
Matches 1163; Conservative 23; Mismatches 7; Indels 5; Gaps 2;

QY 1 ATGCTGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGGAAGAGCAATTTGGTCTC 60
Db 223 ATGCTGTTGAGTTGATTCATGCGCGGCTGCTCTTCTTCTGGAAGAGCAATTTGGTCTC 282
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCCTTCTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 283 AGGAGCAAGATGGGCAAGTGTGCTGCCCTTCTCCCTGCTGCAAGGAGAGCGGCAAG 342
QY 121 AGCAAGTGGGCACTTCTGGAAGACAGAGCACTGCTATGAAAGACACTCAGAGCAAG 180
Db 343 AGCAAGTGGGCACTTCTGGAAGACAGAGCACTGCTATGAAAGACACTCAGAGCAAG 402
QY 181 ATGGGCAAGTGTGCGCGCACTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db 403 ATGGGCAAGTGTGCGCGCACTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 462
QY 241 GGGCTTCTGGAGACCAAGCACTGCTATGAAAGCACTCAGAAACAAGATGGGCAAG 300
Db 463 GGGCTTCTGGAGACCAAGCACTGCTATGAAAGCACTCAGAAACAAGATGGGCAAG 522
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QY	301	TGTCGTCGCACTGCTTCCCTCGTGGAGGGGAGGCGGCAAGCAAGTGCGGCGCTTGG	360
Db	523	TGTCGTCGCACTGCTTCCCTCGTGGAGGGGAGGCGGCAAGCAAGTGCGGCGCTTGG	582
QY	361	GGAGACTACGATGACAGTGGCCCTTCATGGAGCCCGAGTACACGTCGCGTGAGAAATCTG	420
Db	583	GGAGACTACGATGACAGTGGCCCTTCATGGAGCCCGAGTACACGTCGCGTGAGAAATCTG	642
QY	421	GACAAAGCTCCACAGAGCTGCTGGTGGGCTTAAGTCCCGCAAAAAGATCTCATGCTCATG	480
Db	643	GACAAAGCTCCACAGAGCTGCTGGTGGGCTTAAGTCCCGCAAAAAGATCTCATGCTCATG	702
QY	481	CTCAGGGACACTGACGCTGTAACAAAGAGACAAAGCAAAAGAGGACGTGCTACATCTGCGC	540
Db	703	CTCAGGGACACTGACGCTGTAACAAAGAGACAAAGCAAAAGAGGACGTGCTACATCTGCGC	762
QY	541	TCTGCGCAATGGGAAATTCAGAAAGTATGATAAACTCCTGCTGACAGAGCATGTCAACTTAAT	600
Db	763	TCTGCGCAATGGGAAATTCAGAAAGTATGATAAACTCCTGCTGACAGAGCATGTCAACTTAAT	822
QY	601	GTCTCTGACAAACAAAAGAGGACAGCTCTGTATAAGCCGCTACAAATGCCAGGAATGAA	660
Db	823	GTCTCTGACAAACAAAAGAGGACAGCTCTGTATAAGCCGCTACAAATGCCAGGAATGAA	882
QY	661	TGTGCGTAATGGTTGTCGGGAACATGGGCACTGATCCAAATTTCCAGTATGGTATGGAAT	720
Db	883	TGTGCGTAATGGTTGTCGGGAACATGGGCACTGATCCAAATTTCCAGTATGGTATGGAAT	942
QY	721	ACCACTGTGCACACACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
Db	943	ACCACTGTGCACACACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	1000
QY	781	TATGTGCTGATATTCGAATCAAAAAACAACGATGGCTCAGACCACTGTTACTGTGTGA	840
Db	1003	TATGTGCTGATATTCGAATCAAAAAACAACGATGGCTCAGACCACTGTTACTGTGTGA	1060
QY	841	CATGAGCAAAAACGCAAGTGGTAATTTTATCAAGAAAAAGCGAATTT-AAATGC	899
Db	1063	CATGAGCAAAAACGCAAGTGGTAATTTTATCAAGAAAAAGCGAATTTAAATATGC	1122
QY	900	ACTGATATGATATGGAAGGACTGCTGCATACTCTGCTATGTTGTGGATCAGCAAGTAT	959
Db	1123	ACTGATATGATATGGAAGGACTGCTGCATACTCTGCTATGTTGTGGATCAGCAAGTAT	1188
QY	960	AGTAGCCTTACTGTTGCGCAAAATATGATNGTATCTTCCAGATCTATCGGAAAGAC	1011
Db	1183	AGTAGCCTTACTGTTGCGCAAAATATGATNGTATCTTCCAGATCTATCGGAAAGAC	1233
QY	1020	GGCCAGAGAGTATGCTGTTCTACTCATCATATGTAATTTGCCAGTACTTCTTGACTA	1071
Db	1239	GGCCAGAGAGTATGCTGTTCTACTCATCATATGTAATTTGCCAGTACTTCTTGACTA	1291
QY	1080	CAAAAGAAAAACAGTACTGTAATAATCTTCTGAAAAACAGCAATCCGAACAGACTTAA	1133
Db	1299	CAAAAGAAAAACAGTACTGTAATAATCTTCTGAAAAACAGCAATCCGAACAGACTTAA	1351
QY	1140	GCTGACATCAGAGGAGAGTACAAAGAGTTCAAAGGAGTGAATAAGCAGCGCAGAG	1197
Db	1359	GCTGACATCAGAGGAGAGTACAAAGAGTTCAAAGGAGTGAATAAGCAGCGCAGAG	1416
RESULT 14			
US-09-780-669-369			
Sequence 369, Application US/09780669			
Patent No. US20020051977A1			
GENERAL INFORMATION:			
APPLICANT: Xu, JIANGCHUN			
APPLICANT: DILLON, DAVID C.			
APPLICANT: MITCHELL, JENNIFER L.			
APPLICANT: HARLOCKER, SUSAN L.			
APPLICANT: JIANG, YUQU			
APPLICANT: HENDERSON, ROBERT A.			

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APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 369
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669--369

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Query Match	Score	DB	Length
57.48;	1147.6;	10;	1853;

Best Local Similarity 97.1%; Pred. No. 1.3e-256;
Matches 1163; Conservative 23; Mismatches 7; Indels 5; Gaps 2;

29 1 ATGGTGGTTGAGTTGATTCCATGCCGGCTGCCCTTCTGTGAAGAAGCCATTGGTCTC

Db 223 ATGGTGGTTGAGGTTGATTCATGCCGCGTGGTTCCTCTGTGAAGAGCCATTGTGCTC 28:

01 AGGAGGCACGATGGCCAAAGTGGTAGCCTCGTTTCCTGCTGTGCAAGTGGAAGAACCCTCAAG

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22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

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181 240

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241 GCGCTTCTGGAGACCACGACCTCTGCTATGAGACACTCAGGAACAAGATGGCAAG 300

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[illegible]

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Db 883 TGTGGCTAATAGTTGCTGGACATGGCACTGATCCAAATATCCGATGAGATGGAAT 942
Oy 721 ACCACTCTGCACCTACGCTATCTATTAATGAGATTAATTAATGAGCCAAAGCACTGCTTTA 780
Db 943 ACCACTCTGCACCTACGCTATCTATTAATGAGATTAATTAATGAGCCAAAGCACTGCTTTA 1002
Oy 781 TATGGTGTGATATGCAATCAAAAACAGCATGCGCTCACACCACTGTACTTGGTGA 840
Db 1003 TATGGTGTGATATGCAATCAAAAACAGCATGCGCTCACACCACTGTACTTGGTGA 1062
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Db 1063 CATGAGCAAAAACAGCATGCGTGAATTTTAAATTAAGAAAACCAATTTAAATGC 1122
Oy 900 ACTGATAGATATGGAAGAGCTGCTCATACTGCTGTATGTTGGATCAGCAAGTAT 959
Db 1123 RCTGGATGATATGGAAGAGCTGCTCATACTGCTGTATGTTGGATCAGCAAGTAT 1182
Oy 960 AGTCAGCTTCTACTTGTGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAC 1019
Db 1183 AGTCAGCTTCTACTTGTGCAAAATATGATGATCTTCTCAAG-ATCTGCAAGAC 1238
Oy 1020 GGGCAGAGATATGCTGTTCTAGTCATCATCATGATTAATGGCCGTTACTTCTGACTA 1079
Db 1239 GGGCAGAGATATGCTGTTCTAGTCATCATCATGATTAATGGCCGTTACTTCTGACTA 1298
Oy 1080 CAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAAAGACTTAA 1139
Db 1299 CAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAAAGACTTAA 1358
Oy 1140 GCTGACATCAAGAGAGAGTCAAAAGCTTCAAGGCGAGTAAATGAGCCAGAG 1197
Db 1359 GCTGACATCAAGAGAGAGTCAAAAGCTTAAAGGAGTAAAGCAGCCAGAG 1416

RESULT 15

US-09-810-936-295
Sequence 295, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Mishner, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810, 936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-295

Query Match 57.4%; Score 1147.6; DB 10; Length 1853;
Best Local Similarity 97.1%; Pred. No 1.3e-256;
Matches 1163; Conservative 23; Mismatches 7; Indels 5; Gaps 2;
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Oy 61 AGGACCAAGATGGGCAAGTGGTGGCTTCCCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 283 AGGACCAAGATGGGCAAGTGGTGGCTTCCCTTCCCTGCTGCAAGGAGCGGCAAG 342
Oy 121 AGCAACGTGGGCACTTCTGAGACACAGCAGCACTGCTGATGAACACTGAGGACAG 180
Db 343 AGCAACGTGGGCACTTCTGAGACACAGCAGCACTGCTGATGAACACTGAGGACAG 402
Oy 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGAACGTC 240
Db 403 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGAACGTC 462
Oy 241 GGGCTTCTGAGACACAGCAGCACTGCTGATGAACACTGAGGACAGTGGGCAAG 300
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Oy 421 GACAAAGCTTCCACAGAGCTGGTGGTGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
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Oy 481 CTCAGGACACTGAGCTGTAACAGAGGACAGCAAGAGAGAGTGTCTATCATCTGGCC 540
Db 703 CTCAGGACACTGAGCTGTAACAGAGGACAGCAAGAGAGAGTGTCTATCATCTGGCC 762
Oy 541 TCTGCCAATGGGAATTCAGAAATGATAAACTCTGCTGAGACAGATGTCACCTTAAT 600
Db 763 TCTGCCAATGGGAATTCAGAAATGATAAACTCTGCTGAGACAGATGTCACCTTAAT 822
Oy 601 GTCTTGACAAACAAAAGAGACACCTCTGATTAAGGCGCTTCAATGCCAGAAATGAA 660
Db 823 GTCTTGACAAACAAAAGAGAGACCTCTGATAAAGGCGCTTCAATGCCAGAAATGAA 882
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Oy 781 TATGGTGTGATATGCAATCAAAAACAGCATGCGCTCACACCACTGTACTTGGTGA 840
Db 1003 TATGGTGTGATATGCAATCAAAAACAGCATGCGCTCACACCACTGTACTTGGTGA 1062
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Db 1183 AGTCAGCTTCTACTTGTGCAAAATATGATGATCTTCTCAAG-ATCTGCAAGAC 1238
Oy 1020 GGGCAGAGATATGCTGTTCTAGTCATCATCATGATTAATGGCCGTTACTTCTGACTA 1079
Db 1239 GGGCAGAGATATGCTGTTCTAGTCATCATCATGATTAATGGCCGTTACTTCTGACTA 1298
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 02:07:38 ; Search time 3942.08 Seconds
(without alignments)
12755.953 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atggtgtgtgagtgatc.....aaaaaaaaaaaaaaaaa 2000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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No.	Score	Query Match	Length DB	ID	Description
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2	2000	100.0	2000	16	US-09-288-946-374 Sequence 374, App
3	2000	100.0	2000	16	US-09-289-198-302 Sequence 302, App
4	2000	100.0	2000	18	US-09-429-755-302 Sequence 302, App
5	2000	100.0	2000	18	US-09-443-686-374 Sequence 374, App
6	2000	100.0	2000	18	US-09-483-672A-374 Sequence 374, App
7	2000	100.0	2000	20	US-09-534-825A-302 Sequence 302, App
8	2000	100.0	2000	20	US-09-536-857-374 Sequence 374, App
9	2000	100.0	2000	22	US-09-568-100A-374 Sequence 374, App
10	2000	100.0	2000	22	US-09-577-505B-302 Sequence 302, App
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13	2000	100.0	2000	23	US-09-605-783A-374 Sequence 374, App
14	2000	100.0	2000	24	US-09-636-215-374 Sequence 374, App
15	2000	100.0	2000	25	US-09-651-236-374 Sequence 374, App
16	2000	100.0	2000	25	US-09-657-279-374 Sequence 374, App
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18	2000	100.0	2000	26	US-09-679-426-374 Sequence 374, App
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20	2000	100.0	2000	27	US-09-685-166A-374 Sequence 374, App
21	2000	100.0	2000	27	US-09-699-295-302 Sequence 302, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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26 2000 100.0 2000 31 US-09-822-827-374 Sequence 374, App
27 2000 100.0 2000 31 US-09-825-301-6 Sequence 6, Appl1
28 2000 100.0 2000 32 US-09-852-911-374 Sequence 374, App
29 2000 100.0 2000 33 US-09-895-793-374 Sequence 374, App
30 2000 100.0 2000 33 US-09-895-814-374 Sequence 374, App
31 2000 100.0 2000 34 US-09-924-400-302 Sequence 302, App
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35 2000 100.0 2000 39 US-10-079-137B-302 Sequence 302, App
36 2000 100.0 2000 40 US-10-144-678A-374 Sequence 374, App
37 2000 100.0 2000 42 US-10-212-679-302 Sequence 302, App
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39 1940 97.0 2040 16 PCT-US02-24917-303 Sequence 375, App
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41 1940 97.0 2040 18 US-09-289-198-303 Sequence 303, App
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ALIGNMENTS

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RESULT 1
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; Sequence 302, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Panger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-302
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Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGAGAGGGCAAG 120
QY 121 AGCAACGTGGGCACTTGTGAGACACAGAGACTCTCTATGAAGACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTGTGAGACACAGAGACTCTCTATGAAGACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGAGAGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGAGAGAGTGGCAAGCAACGTG 240
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DB 241 GGGCTTCTGAGACACAGAGACTCTCTATGAAGACTCAGAAACAAGATGGCAAG 300
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QY 361 GGAGACTACGATGACATGCTTCATGAGCCCAAGATCCACGCTCGTGAAGATCTG 420
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QY 421 GACAGCTCCACAGAGCTGCTGCTGAGGATTAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAGCTCCACAGAGCTGCTGCTGAGGATTAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGACAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGACAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TGTGCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGAGATGCAACTTAAT 600
DB 541 TGTGCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGACAGCTCTGATTAAGGCGCTACAAATCCAGAAATGAA 660
DB 601 GTCCCTTGACAAACAAAAGAGAGAGACAGCTCTGATTAAGGCGCTACAAATCCAGAAATGAA 660
QY 661 TGTGCTTAAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATAGATGGAAT 720
DB 661 TGTGCTTAAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATAGATGGAAT 720
QY 721 ACCACTGTGACATGCTATCTATTAATGAAGATTAATTAAGGCAAGCACTGCTTAA 780
DB 721 ACCACTGTGACATGCTATCTATTAATGAAGATTAATTAAGGCAAGCACTGCTTAA 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCCCTCACACCACTGTTAGTGTGTA 840
DB 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCCCTCACACCACTGTTAGTGTGTA 840
QY 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGAGAGAGACTGCTCATACCTGCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATGATATGAGAGAGACTGCTCATACCTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATGACAGAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCCAGTTACTTTCATCAG 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCCAGTTACTTTCATCAG 1080
QY 1081 AAAAGAAAAAGATGCTAAATAATCTCTGAAAGCAAGCAATCCAGAAAGACTTAAAG 1140
DB 1081 AAAAGAAAAAGATGCTAAATAATCTCTGAAAGCAAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAGAGTTCAAAAGCAAGTGAATAATATCCAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAGAGTTCAAAAGCAAGTGAATAATATCCAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATTAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATTAAG 1260
QY 1261 AAGCATAAAGTAAATTAATGAGGATTTACTAGAAAACTGACTAATGTTGTCACGTGCGC 1320
DB 1261 AAGCATAAAGTAAATTAATGAGGATTTACTAGAAAACTGACTAATGTTGTCACGTGCGC 1320
```


Qy	1321	AAATGATATATGATTTAATTTCTTCAAGAGAGACAGAACACCTGAAATACACAAATTT	1380
Dp	1321	AAATGATATATGATTTAATTTCTTCAAGAGAGACAGAACACCTGAAATACACAAATTT	1380
Qy	1381	CTTGACACGAAGTATAGACAGTATCACAGAAATTTCCGAATTAGTTTCTGACTACAAAGAA	1440
Dp	1381	CTTGACACGAAGTATAGACAGTATCACAGAAATTTCCGAATTAGTTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
Dp	1441	AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGAAAGATGCACAAAGGCTTGAGGCACTGAAAATTTGGCCAGCCGAGACTTGAAGAT	1560
Dp	1501	TCAGAGAAAGATGCACAAAGGCTTGAGGCACTGAAAATTTGGCCAGCCGAGACTTGAAGAT	1560
Qy	1561	TTTATGGCTATTCGAGAGAAATGAAAGACGCGAGATCTCATGTGCGATTTCCAGAAAC	1620
Dp	1561	TTTATGGCTATTCGAGAGAAATGAAAGACGCGAGATCTCATGTGCGATTTCCAGAAAC	1620
Qy	1621	CTGACTATATGTCGCCACTCTGGCAATGGTATGATATGATTAATTTCCCTCCAAAGAAAGC	1680
Dp	1621	CTGACTATATGTCGCCACTCTGGCAATGGTATGATTAATTTCCCTCCAAAGAAAGC	1680
Qy	1681	AGAACACCTGAAAGCCGAGCAATTTCCCTGCACACTGGAATGGAAGATCACAGTACAGAA	1740
Dp	1681	AGAACACCTGAAAGCCGAGCAATTTCCCTGCACACTGGAATGGAAGATCACAGTACAGAA	1740
Qy	1741	CAAAATGATATCTAGAGCAATTTTGTGAAGACAGAACACTCTGCAATTTACACGATAGC	1800
Dp	1741	CAAAATGATATCTAGAGCAATTTTGTGAAGACAGAACACTCTGCAATTTACACGATAGC	1800
Qy	1801	ATTCTGATTCATGAAGAAAGACAGATAGAGAGTGTGAAGAAATTAATTTCTGACCTTCT	1860
Dp	1801	ATTCTGATTCATGAAGAAAGACAGATAGAGAGTGTGAAGAAATTAATTTCTGACCTTCT	1860
Qy	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGCTAGCTGGGGAAGAAATTT	1920
Dp	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGCTAGCTGGGGAAGAAATTT	1920
Qy	1921	GCATGCTTAAGATGAGCTAGACACAAATGAACATTCAGAGCCAGACTTAAAAA	1980
Dp	1921	GCATGCTTAAGATGAGCTAGACACAAATGAACATTCAGAGCCAGACTTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Dp	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

```

RESULT 2
: Sequence 374, Application US/09288946
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C7
: CURRENT APPLICATION NUMBER: US/09/288,946
: CURRENT FILING DATE: 1999-04-09
: NUMBER OF SEQ ID NOS: 381
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-288-946-374

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Query Match	100.0%	Score 2000;	DB 16;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 2.6e-271;		
Matches 2000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	ATGTTGGTGAAGTTGATTCTCATGCCGGCGCTCTTCTGTGTAAGAAGCAATTGGTTC	60
Dd	1	ATGGTGTTGAGTTGATTTCCATGCCGGCGCTCTTCTGTGTAAGAAGCAATTGGTTC	60
OY	61	AGGAGCAAGATGGGCAGTGGTGTGCGCGTTCCTCCGTGTGAGGAGACGGCGCAG	120
Dd	61	AGGAGCAAGATGGGCAGTGGTGTGCGCGTTCCTCCGTGTGAGGAGACGGCGCAG	120
OY	121	AGCAACGTGGCACATTCTTGAGACAACAGACACTGTCTATTAAGACACTGAGAGCAG	180
Dd	121	AGCAACGTGGCACATTCTTGAGACAACAGAGACTGTCTATTAAGACACTGAGAGCAG	180
OY	181	ATGGGCAAGTGTGTCGCCCACTGTCTTCCCCTGCTGACGGGGAGTGGCAAGCACTG	240
Dd	181	ATGGGCAAGTGTGTCGCCCACTGTCTTCCCCTGCTGACGGGGAGTGGCAAGCACTG	240
OY	241	GGGCGTTCTGSAAGCCAGACGACTGCTGTATGAACACTGAGAACAAAGTGGGCAG	300
Dd	241	GGGCGTTCTGSAAGCCAGACGACTGCTGTATGAACACTGAGAACAAAGTGGGCAG	300
OY	301	TGGTGTCCACACTCTTCCCCCTGCTGACGGGGAGGGCAAGCAAGTGGGCGCTTGG	360
Dd	301	TGGTGTCCACACTCTTCCCCCTGCTGACGGGGAGGGCAAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTTCATGAGACCAGGTACACGTCCGTGGAGAAATCTG	420
Dd	361	GGAGACTACGATGACAGTGCCTTTCATGAGACCAGGTACACGTCCGTGGAGAAATCTG	420
OY	421	GACAAAGCTCCACAGAGCTGGCTGGTGGGGTAAAGTCCCAAAAAGATCTCATTCGTATG	480
Dd	421	GACAAAGCTCCACAGAGCTGGCTGGTGGGGTAAAGTCCCAAAAAGATCTCATTCGTATG	480
OY	481	CTCAGGGAACACTGACGTGAACAAGAGAACAAACAAGACACTGTACATCTGACC	540
Dd	481	CTCAGGGAACACTGACGTGAACAAGAGAACAAACAAGACACTGTACATCTGACC	540
OY	541	TC TGCCAATGGGAATTCAGAGTAGTAAAACTCTCTGTGACAGACGATGTCACTTAAT	600
Dd	541	TC TGCCAATGGGAATTCAGAGTAGTAAAACTCTCTGTGACAGACGATGTCACTTAAT	600
OY	601	GTCCTGACAACAAAAGAGACAGCGCTAATAAGCGGCTACAMTGCAGGAAGATGAA	660
Dd	601	GTCCTGACAACAAAAGAGACAGCGCTGATTAAGCGGCTAACAATGCCAGGAAGATGAA	660
OY	661	TGTGCGTTAATGTTGCTGCGAACAATGACACTGATCCAAATATTCACAGTAGATGGAAT	720
Dd	661	TGTGCGTTAATGTTGCTGCGAACAATGACACTGATCCAAATATTCAGATGAGATGGAAT	720
OY	721	ACCACTGTGACCTACGCTATCTAATGAAGATAAATTAAATGSCCAAGCACTGCTTGA	780
Dd	721	ACCACTGTGACCTACGCTATCTAATGAAGATAAATTAAATGSCCAAGCACTGCTTGA	780
OY	781	TATGTTGCTGATATTCGAATCAAAAAACAGATGGGCTCACACCACTGTACTTGGTGA	840
Dd	781	TATGTTGCTGATATTCGAATCAAAAAACAGCAAGGCTCACACCACTGTACTTGGTGA	840
OY	841	CATGAGCAAAAACAGCAAGCTGGAATTTTTATCAAGAAAAAGCGAATTTAAATGCA	900
Dd	841	CATGAGCAAAAACAGCAAGCTGGAATTTTTATCAAGAAAAAGCGAATTTAAATGCA	900
OY	901	CTGATAGATATGGAAGAGACTGCTCATACTGTGATGTTGTTGATCAGCAAGTATA	960
Dd	901	CTGATAGATATGGAAGAGACTGCTCATACTGTGATGTTGTTGATCAGCAAGTATA	960
OY	961	GTCAGCTTCTACTTAGCAAAAATATTGATGTTCTTCAAGATCTATCTGGACAGAGC	1020
Dd	961	GTCAGCTTCTACTTAGCAAAAATATTGATGTTCTTCAAGATCTATCTGGACAGAGC	1020
OY	1021	GCCAGAGAGTGTGCTGTTCTTAGCATCATCATGTAATTTGGCAGTTACTTCTGACATC	1080
Dd	1021	GCCAGAGAGTGTGCTGTTCTTAGCATCATCATGTAATTTGGCAGTTACTTCTGACATC	1080
OY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGTGAANAACAGCAATCCAGAACAACTTAAAG	1140

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|||||
Db 1081 AAAAAGAGATGCTAAAAATCTCTTCTAAAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGACTCAGAAAGGTTCAAGAGCAGTGAATATAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGACTCAGAAAGGTTCAAGAGCAGTGAATATAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGAGTGTATAGAGAGGTTGAAGAAATTAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGAGTGTATAGAGAGGTTGAAGAAATTAAG 1260
QY 1261 AAGCATGAATATATATGTGGATTAATAGAAAACCTGACTAATGGTGTACTGTGGC 1320
Db 1261 AAGCATGAATATATATGTGGATTAATAGAAAACCTGACTAATGGTGTACTGTGGC 1320
QY 1321 AATGGTATATATGATTAATCTCAAGAGAGAGCAGAACACCTGAAATCAGCAATTT 1380
Db 1321 AATGGTATATATGATTAATCTCAAGAGAGAGCAGAACACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTAAGTTTCTGACTACAAAGA 1440
Db 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTAAGTTTCTGACTACAAAGA 1440
QY 1441 AAACAGATGCCAAATTAATCTTTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACAAAGGCTTGAGAGAGTGAATTTGCGAGCCAGAGCTGAGAAAT 1560
Db 1501 TCAGAGAGAGAGTACAAAGGCTTGAGAGAGTGAATTTGCGAGCCAGAGCTGAGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAACAGCAGGAAGTACTCATGTGCGATTTCCAGAAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAACAGCAGGAAGTACTCATGTGCGATTTCCAGAAAAC 1620
QY 1621 CTGACTATATGTCGCTGCTGCGCAATGTGTATGATGATTAATTTCTCCAGAGAGAGC 1680
Db 1621 CTGACTATATGTCGCTGCTGCGCAATGTGTATGATGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGACACCTGAAAGCAGACATTTCTGACACTGAGATGAAGATCACAGTGACGAA 1740
Db 1681 AGACACCTGAAAGCAGACATTTCTGACACTGAGATGAAGATCACAGTGACGAA 1740
QY 1741 CAAATATGATCTCAGAAAGCAATTTGTGAAGAACAGAACTGGAATTTACAGATGAG 1800
Db 1741 CAAATATGATCTCAGAAAGCAATTTGTGAAGAACAGAACTGGAATTTACAGATGAG 1800
QY 1801 ATTTGATTTCTGAAGAAACAGATAGAGTGGTTGAAAAATGAATTTGAGAGCTTTCT 1860
Db 1801 ATTTGATTTCTGAAGAAACAGATAGAGTGGTTGAAAAATGAATTTGAGAGCTTTCT 1860
QY 1861 CTTAGTTGTAGAAGAAAGAGACATCTTGATGAAATATAGCTTCGGGAGAAATTT 1920
Db 1861 CTTAGTTGTAGAAGAAAGAGACATCTTGATGAAATATAGCTTCGGGAGAAATTT 1920
QY 1921 GCCATGCTAAGAGCTGAGAGCTAGACAAATGAAGACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGAGCTGAGAGCTAGACAAATGAAGACATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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RESULT 3

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US-09-289-198-302
; Sequence 302, Application US/09289198
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
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```
;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;; FILE REFERENCE: 210121.419C5
;; CURRENT APPLICATION NUMBER: US/09/289, 198
;; CURRENT FILING DATE: 1999-04-09
;; EARLIER APPLICATION NUMBER: US 09/062,451
;; EARLIER FILING DATE: 1998-04-17
;; EARLIER APPLICATION NUMBER: US 08/991,789
;; EARLIER FILING DATE: 1997-12-11
;; EARLIER APPLICATION NUMBER: US 08/838,762
;; EARLIER FILING DATE: 1997-04-09
;; EARLIER APPLICATION NUMBER: PCT/US97/00485
;; EARLIER FILING DATE: 1997-01-10
;; EARLIER APPLICATION NUMBER: US 08/700,014
;; EARLIER FILING DATE: 1996-08-20
;; EARLIER APPLICATION NUMBER: US 08/585,392
;; EARLIER FILING DATE: 1996-01-01
;; NUMBER OF SEQ ID NOS: 312
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO: 302
;; LENGTH: 2000
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-289-198-302
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Query Match 100.0%; Score 2000; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGTGCTTGAAGTGTGATTCATGCGCGCTGCTTCTTGTGAAACCAATTTGCTGTC 60
Db 1 ATGTGCTTGAAGTGTGATTCATGCGCGCTGCTTCTTGTGAAACCAATTTGCTGTC 60
QY 61 AGAGCAAGATGAGGCAATGCTGCTGCGGTTGCTTCCCTGCTGAGAGAGCGCAAG 120
Db 61 AGAGCAAGATGAGGCAATGCTGCTGCGGTTGCTTCCCTGCTGAGAGAGCGCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACAGACTCTGCTATGAAGACACTAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACAGACTCTGCTATGAAGACACTAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAACTG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAACTG 240
QY 241 GCGCTTCTGAGACACAGACAGACTCTGCTATGAAGACACTAGAGCAAGTGGCGCAAG 300
Db 241 GCGCTTCTGAGACACAGACAGACTCTGCTATGAAGACACTAGAGCAAGTGGCGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCTGACAGGGGAGCGCAAGCAAGTGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGCTGACAGGGGAGCGCAAGCAAGTGGCGCTTGG 360
QY 361 GGAGACTGATGACAGTGCCTTCATGAGGCCAGGTCCAGCTCCGCGGAGAAATG 420
Db 361 GGAGACTGATGACAGTGCCTTCATGAGGCCAGGTCCAGCTCCGCGGAGAAATG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGAGGTAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGCTGAGGTAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACGTGACAGAGAGAGCAAGCAAAAGAGAGCTCTCATCTGCGC 540
Db 481 CTCAGGACACTGACGTGACAGAGAGAGCAAGCAAAAGAGAGCTCTCATCTGCGC 540
QY 541 TCTGCAATGGGAATTCAGAGTAGTAATACTCTGCGGAGAGAGCTGCACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAGTAGTAATACTCTGCGGAGAGAGCTGCACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGAGCTGATTAAGGCGCTACAAATGACAGGAAGATGAA 660
Db 601 GTCCCTGACAAACAAAAGAGAGAGAGCTGATTAAGGCGCTACAAATGACAGGAAGATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGGCAGTCAATCAATATTTCCAGATGAGTAAT 720
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|||||
Db 661 TGTGGTAAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAAGCCCAACACTGCTTCT 780
Db 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAAGCCCAACACTGCTTCT 780
Oy 781 TATGCTGTATGTAATCAAAAAACAAGCATGGCTCACACTGTTACTGGTGA 840
Db 781 TATGCTGTATGTAATCAAAAAACAAGCATGGCTCACACTGTTACTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGA 900
Oy 901 CTGGATATGATGAAGAGCTGCTCATCTGCTGATGTTGGATGATCAGCAAGTATA 960
Db 901 CTGGATATGATGAAGAGCTGCTCATCTGCTGATGTTGGATGATCAGCAAGTATA 960
Oy 961 GTGACCCCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCGACAGAG 1020
Db 961 GTGACCCCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTGGCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTGGCAGTTACTTTCTGACTAC 1080
Oy 1081 AAGAAAAACATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACACTTAAAG 1140
Db 1081 AAGAAAAACATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
Oy 1201 ATGCTCAAGAACCAAAATTAATAGATGCTGATAGAGAGTTGAAGAGAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATAGATGCTGATAGAGAGTTGAAGAGAATGAAG 1260
Oy 1261 AAGCATGAAGATTAATAGTGGATTAATCAAGAAACCTGATTAAGTGTCTACTGTCG 1320
Db 1261 AAGCATGAAGATTAATAGTGGATTAATCAAGAAACCTGATTAAGTGTCTACTGTCG 1320
Oy 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGACAGCAACCTGAAATAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGACAGCAACCTGAAATAGCAATTT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
Oy 1441 AAGCATGACCAAAATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAGCATGACCAAAATCTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAGTCAACAAAGCTTGAAGGAGTGAATAATGGCCAGCAGAGCTAGAAAAAT 1560
Db 1501 TCAGAGAGAGTCAACAAAGCTTGAAGGAGTGAATAATGGCCAGCAGAGCTAGAAAAAT 1560
Oy 1561 TTTATGCTATGCAAGAAATGAAGAACAGCAAGTACTCATGTGCGATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATGCAAGAAATGAAGAACAGCAAGTACTCATGTGCGATTTCCAGAAAAAC 1620
Oy 1621 CTGACATTAATGCTGCAAGTGTGATGATGATTAATCTCTCAAGAGAAAGAC 1680
Db 1621 CTGACATTAATGCTGCAAGTGTGATGATGATTAATCTCTCAAGAGAAAGAC 1680
Oy 1681 AGAAGACCTGAAGAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTGCAGAA 1740
Db 1681 AGAAGACCTGAAGAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTGCAGAA 1740
Oy 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
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Db 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGCATGAG 1800
Oy 1801 ATTCTGATTCATGAAGAAAGCAGATAGAGGTTTGAAGAAATGATTTCTGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAGGTTTGAAGAAATGATTTCTGAGCTTCT 1860
Oy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCATGGAATAATGATGTTGGGGAGAAATTT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCATGGAATAATGATGTTGGGGAGAAATTT 1920
Oy 1921 GCCATGCTAAGAGCTGAGCTAGACACATGAATGAACATCAGAGCCAGCTAAAAAAGAAA 1980
Db 1921 GCCATGCTAAGAGCTGAGCTAGACACATGAATGAACATCAGAGCCAGCTAAAAAAGAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-429-755-302
; Sequence 302, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGCTGCTTGAAGTTCATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGCTGCTTGAAGTTCATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Oy 61 AGAGCAAGATGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Oy 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCCCGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGTGG 240
Db 181 ATGGGCAAGTGTGCCCGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGTGG 240
Oy 241 GGGGCTTGTGAGACCAAGCAAGTGTGATGAAGACCTGAGAAACAAGATGGGCAAG 300
Db 241 GGGGCTTGTGAGACCAAGCAAGTGTGATGAAGACCTGAGAAACAAGATGGGCAAG 300
Oy 301 TGGTCTGCACTGCTTCCCTGCTGCGAGGAGAGCGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCGAGGAGAGCGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTACAGTACAGTCCCTTCATGAGAGCCAGGATCACAGTCCGTGGAGAAATGTCG 420
Db 361 GGAGACTACAGTACAGTCCCTTCATGAGAGCCAGGATCACAGTCCGTGGAGAAATGTCG 420
```


[illegible]

Db	1141	CTGACATCAGAGGAGGTACCAAGGTTCAAAGGCGTGAATAATGCGCCAGAGAA	1200
Qy	1201	ATGTCCTAAGAACCCAGAAATAAATAAGGATGGTGATAGAGAGTGTGAAGAAATGAG	1260
Db	1201	ATGTCTCAAGACACAGAAATAAATAAAGATGGTGATAGAGAGTGTGAAGAAATGAG	1260
Qy	1261	AAGCATGAAGATAAATAATGTGGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGATAAATAATGTGGGATTACTAGAAAACCTGACTAATGTGTCACTGTGGC	1320
Qy	1321	AATGGTGTAAATGGATTTAATTCCTCAAAGGAGACGACGACCTGAAAATCAGCAATT	1380
Db	1321	AATGGTGTAAATGGATTTAATTCCTCAAAGGAGAGCAGAACCTGAAAATCAGCAATT	1380
Qy	1381	CCTGACCAACGAAAGTGAAGAGTATCAACAGATTTGGCATTTAGTTCTTGACTACAAAGA	1440
Db	1381	CCTGACCAACGAAAGTGAAGAGTATCAACAGATTTGGCATTTAGTTCTTGACTACAAAGA	1440
Qy	1441	AAACAGATGCCAAATATCTCTTGTGA AAAACAGCACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTGTGA AAAACAGCACCCAGAACAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAAGGTACAAAAGGCTTGAGGGCAGTGA AAAATGGCCACCGAGCTTGA AAT	1560
Db	1501	TCAGAGGAAAGGTACAAAAGGCTTGAGGGCAGTGA AAAATGGCCACCGAGCTTGA AAT	1560
Qy	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAGCAAGTACTCATGTGGATTTCCACAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAGCAAGTACTCATGTGGATTTCCACAGAAAC	1620
Qy	1621	CTGACTAATGTGGTCCACTGTGCGCAATGTGATGATGATTAAATTCCTCCAAAGAGAGC	1680
Db	1621	CTGACTAATGTGGTCCACTGTGCGCAATGTGATGATGATTAAATTCCTCCAAAGAGAGC	1680
Qy	1681	AGAACACCTGAAACCCAGCAATTTCTCGACACCTGGAATGAAGAGTATCACAGTACGAA	1740
Db	1681	AGAACACCTGAAACCCAGCAATTTCTCGACACCTGGAATGAAGAGTATCACAGTACGAA	1740
Qy	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGACACAACTGCAATATTACACATGAG	1800
Db	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGACACAACTGCAATATTACACATGAG	1800
Qy	1801	ATTCTGATTCATGAAGAAAGACAGATAGAAGTGGTGA AAAAATGAAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGACAGATAGAAGTGGTGA AAAAATGAAATTCGAGCTTCT	1860
Qy	1861	CTTAGCTGTAAAGAAAGAAAGACATCTTGCAATGA AAAATGATGCTGGGGAGCAAAAT	1920
Db	1861	CTTAGCTGTAAAGAAAGAAAGACATCTTGCAATGA AAAATGATGCTGGGGAGCAAAAT	1920
Qy	1921	GCCATGCTAACAACGAGGAGTACAGACACAATGA AACATCAGAGCAGCTTAAAAA AAAAA	1980
Db	1921	GCCATGCTAACAACGAGGAGTACAGACACAATGA AACATCAGAGCAGCTTAAAAA AAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 6			
US-09-483-672A-374			
Sequence 374, Application US/09483672A			
GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan Louise			
; APPLICANT: Jiang Yungui			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			

Db 1561 TTTATGGCTATCGAAGAAATGAAGACAGGAAAGTACTCATGTTCGGATTCCCAAGAAAC 1620
Qy 1521 CTGACTAATGGTGGCTACTGCTGGCAATGGTGATGATGGATTAAATTCCTCCAGAGAGAGC 1680
Db 1621 CTGACTAATGGTGGCTACTGCTGGCAATGGTGATGATGGATTAAATTCCTCCAGAGAGAGC 1680
Qy 1681 AGAACCCTGGAACCCAGCAATTTCTTGACACTGAGAAATGAAGATACACAGTACGAA 1740
Db 1681 AGAACCCTGGAACCCAGCAATTTCTTGACACTGAGAAATGAAGATACACAGTACGAA 1740
Qy 1741 CAAATATATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATTTACAGATAG 1800
Db 1741 CAAATATATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATTTACAGATAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAAAATGAATTTCTGACCTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAAAATGAATTTCTGACCTTCT 1860
Qy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATGACAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATGACAGCCAGCTAAAAAAGAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 8

US-09-536-857-374
Sequence 3/4, Application US/09536857

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Scolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536,857
NUMBER OF SEQ ID NOS: 592
SOFTWARE: FastSeq for Windows Version 3.0
SEQUENCE ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-374

Query Match 100.0%; Score 2000; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGTTGATTCATCCGCGCTGCTCTTCTGTGAAGAGCAATTTGTCTC 60
Db 1 ATGGTGGTTGAGTTGATTCATCCGCGCGCTGCTCTTCTGTGAAGAGCAATTTGTCTC 60
Qy 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGACAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGACAGGAGCGGCAAG 120
Qy 121 AGCAAGTGGCACTTCTGAGACCCAGAGACTCTCTATGAAGACACTGAGGCAAG 180
Db 121 AGCAAGTGGCACTTCTGAGACCCAGAGACTCTCTATGAAGACACTGAGGCAAG 180

Db 121 AGCAAGTGGCACTTCTGAGACCCAGAGACTCTCTATGAAGACACTGAGGCAAG 180
Qy 181 ATGGCAAGTGGTGGCTGGCTGCTTCCCTGCTGACAGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGGTGGCTGGCTGCTTCCCTGCTGACAGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCTTCTGAGACACAGGACTCTGCTATGAAGACACTGAGAACAGATGGCAAG 300
Db 241 GGGCTTCTGAGACACAGGACTCTGCTATGAAGACACTGAGAACAGATGGCAAG 300
Qy 301 TGGTGGCCCACTGCTTCCCTGCTGACAGGGAGGGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGGTGGCCCACTGCTTCCCTGCTGACAGGGAGGGGAGGAGGAGGAGGAGGAGG 360
Qy 361 GGAGACTACATGACAGTGGCTTCTGATGAGCCAGGTACACAGTCCGCTGAGAAATCTG 420
Db 361 GGAGACTACATGACAGTGGCTTCTGATGAGCCAGGTACACAGTCCGCTGAGAAATCTG 420
Qy 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCCAGAAAGATCTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCCAGAAAGATCTCATG 480
Qy 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGAGAGTGGCTCATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGAGTGGCTCATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTCTGCTGACAGACATGCTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTCTGCTGACAGACATGCTCACTTAAT 600
Qy 601 GTCTTTCACAAACAAAGAGAGGACAGCTCTGATTAAGCCCGTACATGCGAGAAATGAA 660
Db 601 GTCTTTCACAAACAAAGAGAGGACAGCTCTGATTAAGCCCGTACATGCGAGAAATGAA 660
Qy 661 TGTGCTTAAATGTTGCTGGAACATGGACATGATCAAAATATTCAGATGAGATGAAAT 720
Db 661 TGTGCTTAAATGTTGCTGGAACATGGACATGATCAAAATATTCAGATGAGATGAAAT 720
Qy 721 ACCACTGCACTACGCTATCTATTAATGAAGATTAATGAGCAAGCAAGCTGCTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGAAGATTAATGAGCAAGCAAGCTGCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAGACAGATGGCTCACACCACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAGACAGATGGCTCACACCACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAGACAGAGTGTGAATTTTAATCAAGAAAGAAATTTAAATGCA 900
Db 841 CATGAGCAAAAGACAGAGTGTGAATTTTAATCAAGAAAGAAATTTAAATGCA 900
Qy 901 CTGGATGATATGGAAGGACTGCTCTCATACTTCTGTATGTTGGATGACGAATGATA 960
Db 901 CTGGATGATATGGAAGGACTGCTCTCATACTTCTGTATGTTGGATGACGAATGATA 960
Qy 961 GTACAGCTTCTACTTGAACAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTACAGCTTCTACTTGAACAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGGCCGATCTTCTGATAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGGCCGATCTTCTGATAC 1080
Qy 1081 AAAGAAAAAGATGCTTAATAATCTCTTGTGAAGACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAAGAAAAAGATGCTTAATAATCTCTTGTGAAGACAGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAAGAGAAAGTCAAAAGGTTCAAGGCAAGTAAATATGACAGCAGAGAAA 1200
Db 1141 CTGACATCAAGAGAAAGTCAAAAGGTTCAAGGCAAGTAAATATGACAGCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGATGGTATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGATGGTATGAGAGGTTGAAGAAATGAAG 1260

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OY 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACCTGACATATGTCACCTGCTGGC 1320
      |||||||
Db 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACCTGACATATGTCACCTGCTGGC 1320
OY 1321 AATGGTAAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
      |||||||
Db 1321 AATGGTAAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
OY 1381 CCTGACACGAAAGTGAAGATATCAGACAAATTTGCGAATTAATTTCTGACATCAAGAA 1440
      |||||||
Db 1381 CCTGACACGAAAGTGAAGATATCAGACAAATTTGCGAATTAATTTCTGACATCAAGAA 1440
OY 1441 AAACGATGCCAAATATCTTCTGAAAACAGAACCCAGAACCAACTTAAGCTGACGACA 1500
      |||||||
Db 1441 AAACGATGCCAAATATCTTCTGAAAACAGAACCCAGAACCAACTTAAGCTGACGACA 1500
OY 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCAGAGCTAGAAAAT 1560
      |||||||
Db 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCAGAGCTAGAAAAT 1560
OY 1561 TTATATGCTATGAGAGAAATGAAGAGCAGAGAGTACTCATGTGCGAATTTCCAGAAAAC 1620
      |||||||
Db 1561 TTATATGCTATGAGAGAAATGAAGAGCAGAGAGTACTCATGTGCGAATTTCCAGAAAAC 1620
OY 1621 CTGACTAATGTGCGCCTGCTGCAATGGATGATGATTAATTTCTCCAGAGAGAGAG 1680
      |||||||
Db 1621 CTGACTAATGTGCGCCTGCTGCAATGGATGATGATTAATTTCTCCAGAGAGAGAG 1680
OY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGTATCAGATGACGAA 1740
      |||||||
Db 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGTATCAGATGACGAA 1740
OY 1741 CAAATATGATCTCAGAGCAATTTTGTGAAGACAGACACTGGAATTTTACACGATGAG 1800
      |||||||
Db 1741 CAAATATGATCTCAGAGCAATTTTGTGAAGACAGACACTGGAATTTTACACGATGAG 1800
OY 1801 ATTCTGATTCATGAAAGAAAGCAGATAGAAGTGTGAAAATTAATTTCTGACCTTCT 1860
      |||||||
Db 1801 ATTCTGATTCATGAAAGAAAGCAGATAGAAGTGTGAAAATTAATTTCTGACCTTCT 1860
OY 1861 CTATAGTTGTAGAAAGAAAGACATCTTGCAATGAATAATGATGCTTGGCGGAGAAAT 1920
      |||||||
Db 1861 CTATAGTTGTAGAAAGAAAGACATCTTGCAATGAATAATGATGCTTGGCGGAGAAAT 1920
OY 1921 GCCATGCTTAAGACTGAGCTAGACACAAATGAAGACATCAGAGCCAGCTTAAAAA 1980
      |||||||
Db 1921 GCCATGCTTAAGACTGAGCTAGACACAAATGAAGACATCAGAGCCAGCTTAAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAA 2000
      |||||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000

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RESULT 9
US-09-100A-374
; Sequence 374, Application US/09568100A
; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun

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; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42713C13
; CURRENT APPLICATION NUMBER: US/09/568,100A
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-568-100A-374

Query Match      100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATGGTGTGAGGTGATTCATGCGGGCTGCTTCTGTGAAGAGCAATTTGGTCTC 60
      |||||||
Db 1 AATGGTGTGAGGTGATTCATGCGGGCTGCTTCTGTGTGAAGAGCAATTTGGTCTC 60
OY 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
      |||||||
Db 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
OY 121 AGCAAGCTGGGCACTTCTGAGACACAGACGATCTGCTATGAAGACACTCAGAGCAAG 180
      |||||||
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACGATCTGCTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGTGCGGCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
      |||||||
Db 181 ATGGGCAAGTGTGCGGCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
OY 241 GGGCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
      |||||||
Db 241 GGGCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
OY 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
      |||||||
Db 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
OY 361 GGAGCTACGATGACAGTGGCTTCATGAGACCCAGTACCACTGCTGAGAGATCTG 420
      |||||||
Db 361 GGAGCTACGATGACAGTGGCTTCATGAGACCCAGTACCACTGCTGAGAGATCTG 420
OY 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
      |||||||
Db 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
OY 481 CTCAGGACACTGACGTGAACAAAGAGACAGCAAAAGAGACTGCTATCTGAGCC 540
      |||||||
Db 481 CTCAGGACACTGACGTGAACAAAGAGACAGCAAAAGAGACTGCTATCTGAGCC 540
OY 541 TCTGCCAATGGAATTCAGAAAGTAAATCTGCTGCTGAGAGAGAGATCTCAACTTAAT 600
      |||||||
Db 541 TCTGCCAATGGAATTCAGAAAGTAAATCTGCTGCTGAGAGAGATCTCAACTTAAT 600
OY 601 GTCCCTTGACAAACAAAAGAGACAGCTGTGATTAAGGCGGTACATGCCAGAAATGAA 660
      |||||||
Db 601 GTCCCTTGACAAACAAAAGAGACAGCTGTGATTAAGGCGGTACATGCCAGAAATGAA 660
OY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATTTCAATGATGTGAAAT 720
      |||||||
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATTTCAATGATGTGAAAT 720
OY 721 ACCACTCTGACATACGCTATCTAATTAATGAAGATTAATTAATGCGCAAGAGACTGCTTA 780
      |||||||
Db 721 ACCACTCTGACATACGCTATCTAATTAATGAAGATTAATTAATGCGCAAGAGACTGCTTA 780
OY 781 TATGATGCTGATATGAAATCAAAAGCAAGCATGGCTCAGACCACTGTTACTTGTGTA 840
      |||||||
Db 781 TATGATGCTGATATGAAATCAAAAGCAAGCATGGCTCAGACCACTGTTACTTGTGTA 840

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QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
QY 901 CTGATAGATATGGAAGACGCTCTCATCTTGTGTATGTGTGGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGACGCTCTCATCTTGTGTATGTGTGGATCAGCAAGTATA 960
QY 961 GTCAGCCCTTCTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATCGACAGAG 1020
Db 961 GTCAGCCCTTCTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATCGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAAGAAACAGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAAAGAAACAGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAGGCAAGTGAATATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAGGCAAGTGAATATAGCCAGCAGAGAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATTAATATGTGGGATTAATAGAAAACCTGACTAATGGTGTACTGTGCG 1320
Db 1261 AAGCATGAAATTAATATGTGGGATTAATAGAAAACCTGACTAATGGTGTACTGTGCG 1320
QY 1321 AATGCTGTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAGCAATTT 1380
Db 1321 AATGCTGTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAACGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAAGTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCAAAATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGTGCACA 1500
Db 1441 AAAAGATGCAAAATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGTGCACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATGSCCAAGCCAGACTGAAAT 1560
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATGSCCAAGCCAGACTGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAGCAGAGTACTCATGTGCGAATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAGCAGAGTACTCATGTGCGAATTTCCAGAAAAAC 1620
QY 1621 CTGACTAATGCTGCTGCTGCGCAATGCTATGATGATTAATTTCTCCAAAGAGAGC 1680
Db 1621 CTGACTAATGCTGCTGCTGCGCAATGCTATGATGATTAATTTCTCCAAAGAGAGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATACAGAGTACGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATACAGAGTACGAA 1740
QY 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATAG 1800
Db 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATAG 1800
QY 1801 ATTCTGATCTCATGAAGAAACAGATAGAGTGTGAAAAATGAATTTCTGACCTTTCT 1860
Db 1801 ATTCTGATCTCATGAAGAAACAGATAGAGTGTGAAAAATGAATTTCTGACCTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTGATGAAAAATAGTAGTTGGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTGATGAAAAATAGTAGTTGGGGAAGAAAT 1920

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QY 1921 GCCATGCTAAGACCTGAGACTGAGACAAATGAATACTAGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAAGACCTGAGACTGAGACAAATGAATACTAGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-09-577-505B-302
Sequence 302, Application US/09577505B
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C8
CURRENT APPLICATION NUMBER: US/09/577.505B
CURRENT FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-577-505B-302

Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGGTGATTCATGCGCGCTGCTCTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGGTGTTGAGGTGATTCATGCGCGCTGCTCTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTCTGCGAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTCTGCGAGGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGAGCAGACGACCTCTGTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGAGCAGACGACCTCTGTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTCCCTGCTGTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGGCACTGCTCCCTGCTGTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGACACACAGACGACTCTGTATGAAGACACTGAGAACCAATGGGCAAG 300
Db 241 GGGCTTCTGAGACACACAGACGACTCTGTATGAAGACACTGAGAACCAATGGGCAAG 300
QY 301 TGTGTCTGCCACTGCTTCCCTGCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
Db 301 TGTGTCTGCCACTGCTTCCCTGCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
QY 361 GGAAGCTGATGAGAGAGTCTTCTATGAGAGCCAGAGTACAGTCCGCTGGAGAGATCTG 420
Db 361 GGAAGCTGATGAGAGAGTCTTCTATGAGAGCCAGAGTACAGTCCGCTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAGTCCCAAGAAAGATCTCATCTGCTATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAGTCCCAAGAAAGATCTCATCTGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAAAGAGACTGCTCTATCATCTGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAAAGAGACTGCTCTATCATCTGCC 540

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QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATACTCTGCTGGACAGACGATGCAACTTAT 600
 DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATACTCTGCTGGACAGACGATGCAACTTAT 600
 QY 601 GTCTTTGACAAACAAAAGAGAGACGCTGATPAAGCCGCTCAATGCCAGGAAGATGA 660
 DB 601 GTCTTTGACAAACAAAAGAGAGACGCTGATPAAGCCGCTCAATGCCAGGAAGATGA 660
 QY 661 TGTGGTAAATGTTGCTGGAACATGGCAATGCCAAATATCCAGATGATGTAAT 720
 DB 661 TGTGGTAAATGTTGCTGGAACATGGCAATGCCAAATATCCAGATGATGTAAT 720
 QY 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCAGCTGCTTA 780
 DB 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCAGCTGCTTA 780
 QY 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTTACTTGGTGA 840
 DB 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAAAAAGCGAATTTAAATGCA 900
 DB 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGATATGATATGGAAGAGCTGCTCATACTTGTGATGTTGATGATCAGCAAGTATA 960
 DB 901 CTGATATGATATGGAAGAGCTGCTCATACTTGTGATGTTGATGATCAGCAAGTATA 960
 QY 961 GTGACCCCTTCTACTTGTGACAAATAATGATGATCTTCTCAAGATCTATCTGGACAGACG 1020
 DB 961 GTGACCCCTTCTACTTGTGACAAATAATGATGATCTTCTCAAGATCTATCTGGACAGACG 1020
 QY 1021 GCCAAGAGTATGCGTTTCTAGTATCATCATATTAATTTGGCAGTTACTTTCTGACTAC 1080
 DB 1021 GCCAAGAGTATGCGTTTCTAGTATCATCATATTAATTTGGCAGTTACTTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
 DB 1081 AAAGAAAAACAGATCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGGAAGAGTCAACAAAGTTCAAGGCAAGTGAATAATAGCCAGCAGAAA 1200
 DB 1141 CTGACATCAGAGGAAGAGTCAACAAAGTTCAAGGCAAGTGAATAATAGCCAGCAGAAA 1200
 QY 1201 ATGCTCAAGAACGAAATTAATAAGATGATGATAGAGAGGTTGMAAGAAATGAAG 1260
 DB 1201 ATGCTCAAGAACGAAATTAATAAGATGATGATAGAGAGGTTGMAAGAAATGAAG 1260
 QY 1261 AAGCATGAAGATTAATGTTGGATTACTAGAAAACCTGACTAATGGTCTCACTGCTGGC 1320
 DB 1261 AAGCATGAAGATTAATGTTGGATTACTAGAAAACCTGACTAATGGTCTCACTGCTGGC 1320
 QY 1321 AATGTTGATATGATTAATCTCTCAAAAGGAGAGCAACCTGAAAAATCAGCAATTT 1380
 DB 1321 AATGTTGATATGATTAATCTCTCAAAAGGAGAGCAACCTGAAAAATCAGCAATTT 1380
 QY 1381 CCTGCAACGAAGTGAAGATGATCACAAGATTTTGGGATTAAGTTTCTACTACACAAAGAA 1440
 DB 1381 CCTGCAACGAAGTGAAGATGATCACAAGATTTTGGGATTAAGTTTCTACTACACAAAGAA 1440
 QY 1441 AAACAGATGCCAAATACTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 DB 1441 AAACAGATGCCAAATACTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAATGGCCAGGCAAGCTAGAAAAT 1560
 DB 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAATGGCCAGGCAAGCTAGAAAAT 1560
 QY 1561 TTTAAGGCTATGCAAGAAATGAAGAACGCAAGTACTCATGTGGATTTCCAGAAAAC 1620
 DB 1561 TTTAAGGCTATGCAAGAAATGAAGAACGCAAGTACTCATGTGGATTTCCAGAAAAC 1620

QY 1621 CTGACTAATGATGTCGCCACTGCTGCAATGGTATGATGATTAATTCCTCCAAAGAAAGC 1680
 DB 1621 CTGACTAATGATGTCGCCACTGCTGCAATGGTATGATGATTAATTCCTCCAAAGAAAGC 1680
 QY 1681 AGAACACTGGAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCACAGTACGAA 1740
 DB 1681 AGAACACTGGAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCACAGTACGAA 1740
 QY 1741 CAAATGATACACAGAAAGCAATTTTGTGAAGAACACACACATGATATTAACAGATGAG 1800
 DB 1741 CAAATGATACACAGAAAGCAATTTTGTGAAGAACACACACATGATATTAACAGATGAG 1800
 QY 1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGGTTGAAAAATGATTTGAGCTTTCT 1860
 DB 1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGGTTGAAAAATGATTTGAGCTTTCT 1860
 QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATCGTTGGCGGAAGAAAT 1920
 DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATCGTTGGCGGAAGAAAT 1920
 QY 1921 GCCATGCTAAGACTGAGCTAGACACATGAACATCAGACCCAGCTAAAAA 1980
 DB 1921 GCCATGCTAAGACTGAGCTAGACACATGAACATCAGACCCAGCTAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 11
 US-09-583-302
 ; Sequence 302, Application us/09590583
 ; GENERAL INFORMATION:
 ; APPLICANT: Frudakis, Tony N.
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Smith, John M.
 ; APPLICANT: Misher, Linda E.
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; FILE REFERENCE: 210121.419C9
 ; CURRENT APPLICATION NUMBER: US/09/590,583
 ; CURRENT FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 324
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 302
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-590-583-302

Query Match 100.0%; Score 2000; DB 22; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 2.6e-271;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTTGAGGTGATTCATGCCGCTGCTCTTCTGTGAAGAACCAATTTGGTCTC 60
 DB 1 ATGTTGTTGAGGTGATTCATGCCGCTGCTCTTCTGTGAAGAACCAATTTGGTCTC 60
 QY 61 AGAGCAAAATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
 DB 61 AGAGCAAAATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
 QY 121 AGCAAGCTGGGCACTTCTGAGACCAAGAGACTGCTATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAAGCTGGGCACTTCTGAGACCAAGAGACTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGT 240
 DB 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGT 240

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QY 241 GGGCTTCTGGAGACACGAGACTCTGTAATGAACACTCAGGAACAAGATGGCAAG 300
    |||||
Db 241 GGGCTTCTGGAGACACGAGACTCTGTAATGAACACTCAGGAACAAGATGGCAAG 300
QY 301 TGGTGCTGCCACTGCTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
    |||||
Db 301 TGGTGCTGCCACTGCTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTCTGATGAGGCCAGTACCAAGTCCGAGGAGAGATCTG 420
    |||||
Db 361 GGAGACTACGATGACAGTGGCTTCTGATGAGGCCAGTACCAAGTCCGAGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGGCTGGTGGGCTAAAGTCCCAAGAAAGATCTCATGTCATG 480
    |||||
Db 421 GACAAGCTCCACAGAGCTGGCTGGTGGGCTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAGAGACAGCAAGAAAGAGACTGCTTACATCTGGCC 540
    |||||
Db 481 CTCAGGGACACTGACGTGAACAGAGACAGCAAGAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTCTGCTGGAGACAGATGTCACCTTAAT 600
    |||||
Db 541 TCTGCCAATGGGAATTCAGAACTCTGCTGGAGACAGATGTCACCTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGAGAGCTCTGATAAAGCCGTAACATGCGAGAGATGAA 660
    |||||
Db 601 GTCCCTGACAAACAAAAGAGAGAGAGCTCTGATAAAGCCGTAACATGCGAGAGATGAA 660
QY 661 TGTGCGCTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATAGATGAAT 720
    |||||
Db 661 TGTGCGCTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATAGATGAAT 720
QY 721 ACCACTGTGACACTGCTATCTATATGAAGATTAATGAAGCCCAAGACCTGCTCTTA 780
    |||||
Db 721 ACCACTGTGACACTGCTATCTATATGAAGATTAATGAAGCCCAAGACCTGCTCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCCTCACACACCTGTTACTTGCTTA 840
    |||||
Db 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCCTCACACACCTGTTACTTGCTTA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
    |||||
Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATGATATGGAAGAGACTGCTCTCATCTGCTGATGTTGATGATGCAAGTATA 960
    |||||
Db 901 CTGGATGATATGGAAGAGACTGCTCTCATCTGCTGATGTTGATGATGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
    |||||
Db 961 GTGAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGAGATGCTGTTTCTAGTCATCATCTATTAATTTGCCAGTTACTTTCGACTAC 1080
    |||||
Db 1021 GCCAGAGAGATGCTGTTTCTAGTCATCATCTATTAATTTGCCAGTTACTTTCGACTAC 1080
QY 1081 AAAGAAAAAGAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAACAAAGATTAAAG 1140
    |||||
Db 1081 AAAGAAAAAGAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAACAAAGATTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGCAGTGAATAATACGCCAGAGAAA 1200
    |||||
Db 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGCAGTGAATAATACGCCAGAGAAA 1200
QY 1201 ATGTCTTAACAGCAAGAAATTAATAGAGATGATAGAGAGTTGAAGAAATGAAG 1260
    |||||
Db 1201 ATGTCTTAACAGCAAGAAATTAATAGAGATGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGTTGGATTACTAGAAAACCTGACTATATGTTGACAGTGGCC 1320
    |||||
Db 1261 AAGCATGAAGTAAATATGTTGGATTACTAGAAAACCTGACTATATGTTGACAGTGGCC 1320

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QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGACAGACACTGAATAATCAGCAATTT 1380
    |||||
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGACAGACACTGAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAATGAAAGATATCAGAGATTTGGCAATTAATGTTTCTGATACAGAA 1440
    |||||
Db 1381 CCTGACAAACGAATGAAAGATATCAGAGATTTGGCAATTAATGTTTCTGATACAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTGAATAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
    |||||
Db 1441 AAACAGATGCCAAATATCTCTTGAATAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAAGGCTTGAAGGAGTGAAGAAATGGCCAGCAGAGACTGAAAT 1560
    |||||
Db 1501 TCAGAGAGAGAGTCAAAAAGGCTTGAAGGAGTGAAGAAATGGCCAGCAGAGACTGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATTAAGAGACAGGAAAGTACTCTATGTCGATTTCCAGAAAC 1620
    |||||
Db 1561 TTTATGCTATCGAAGAAATTAAGAGACAGGAAAGTACTCTATGTCGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGCTGACGCTGCGCAATGATGATGATGATTAATTTCTCCAAAGAGAGC 1680
    |||||
Db 1621 CTGACTAATGCTGACGCTGCGCAATGATGATGATGATTAATTTCTCCAAAGAGAGC 1680
QY 1681 AGAACACCTGAAACCCAGCAATTTCTGACACTGAGATGAAGATATCAACAGTACGAA 1740
    |||||
Db 1681 AGAACACCTGAAACCCAGCAATTTCTGACACTGAGATGAAGATATCAACAGTACGAA 1740
QY 1741 CAAATATGATCTCGAAGCAATTTTGTGAGAAACAGAACTGGAATTTACAGATGAG 1800
    |||||
Db 1741 CAAATATGATCTCGAAGCAATTTTGTGAGAAACAGAACTGGAATTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAACAGATGAAGTGGTTGAAAAATGAATTTGACACTTCT 1860
    |||||
Db 1801 ATTCTGATTCATGAAGAAACAGATGAAGTGGTTGAAAAATGAATTTGACACTTCT 1860
QY 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATAGTACGTTGGGGAAGAAAT 1920
    |||||
Db 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATAGTACGTTGGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACCTGAGCTGAGACAAATGAACATCAGAGCCAGTAAAAAAGAAAA 1980
    |||||
Db 1921 GCCATGCTAAGACCTGAGCTGAGACAAATGAACATCAGAGCCAGTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

```

RESULT 12
 US-09-593-793A-374
 : Sequence 374, Application US/09593793A
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jlangchun
 : APPLICANT: Dillon, Davin C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yugu
 : APPLICANT: Reed, Steven G.
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: Fanger, Gary R.
 : APPLICANT: Retter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Carter, Darrick
 : APPLICANT: Li, Samuel
 : APPLICANT: Wang, Aijun
 : APPLICANT: Skeiky, Yasir A.W.
 : APPLICANT: Helpert, William
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 : TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 : FILE REFERENCE: 210121.42715C15

```

1 CURRENT APPLICATION NUMBER: US/09/593,793A
2 CURRENT FILING DATE: 2000-06-13
3 NUMBER OF SEQ. ID NOS.: 814
4 SOFTWARE: FastSeq for Windows Version 3.0
5 SEQ. ID NO. 374
6 LENGTH: 2000
7 TYPE: DNA
8 ORGANISM: Homo sapien
9 US-09-593-793A-374

```

Query Match	100.0%	Score 2000;	DB 22;	Length 2000;
Best Local Similarity	100.0%	Pred. No. 2,66-271;		
Matches 2000; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	ATGATGGTTAGAGTTAATTTCCATGACCGGCTGCTTTCTGTGAAGAAAGCAATTTGGTCTC	60
Db	1	ATGATGGTTAGAGTTGAAATTCATGACCGGCGCCCTCTTCTGTGAAGAAAGCAATTTGGTCTC	60
QY	61	AGCAGCAAGATGGGCAAGTGGTGGCTGGCGCTGGCTGCTCCCTGCTGCAAGGAGACGGGCAAG	120
Db	61	AGAGAGCAAGATGGGCAAGTGGTGGCGCTGGCTGGCTGCTCCCTGCTGCAAGGAGACGGGCAAG	120
QY	121	AGCAAGCTGGGCACTTTCTGGAGACCAAGACAGACTCTGCTATGAAGACACTCAGAGGCAAG	180
Db	121	AGCAAGCTGGGCACTTTCTGGAGACCAAGACAGACTCTGCTATGAAGACACTCAGAGGCAAG	180
QY	181	ATGAGGCAAGAGGTGCGCCGCACTGGCTTCCCGTGGCGAGGGGGAGTGGCAGAGCAACGTG	240
Db	181	ATGAGGCAAGAGTGTGCGCCGCACTGGCTTCCCGTGGCGAGGGGGAGTGGCAGAGCAACGTG	240
QY	241	GGCGCTTCTGGAGACCAAGACAGACTTGTCTATGAAGACACTCAGGAACAAGATGGGCAAG	300
Db	241	GGCGCTTCTGGAGACCAAGACAGACTTGTCTATGAAGACACTCAGGAACAAGATGGGCAAG	300
QY	301	TGGTGTGCGCAACTGCTTCCCTGCTGAGGGGGAGCGGCAAGCAAGTGGGCGCTTG	360
Db	301	TGGTGTGCGCAACTGCTTCCCTGCTGAGGGGGAGCGGCAAGCAAGTGGGCGCTTG	360
QY	361	GGAGACTACGATGACAGTGGCTTTCATGGAGCCACAGTACCAGTCCCTGGAGAAATCTG	420
Db	361	GGAGACTACGATGACAGTGGCTTTCATGGAGCCACAGTACCAGTCCCTGGAGAAATCTG	420
QY	421	GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTATG	480
Db	421	GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTATG	480
QY	481	CTCAGGCGACACTGACGTGTAACAAAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	540
Db	481	CTCAGGCGACACTGACGTGTAACAAAGAGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	540
QY	541	TCTGCCAATGGGAATTCAGAAATGTAAACTCTGCTGAGCAGACAGTGTCAACTTAAT	600
Db	541	TCTGCCAATGGGAATTCAGAAATGTAAACTCTGCTGAGCAGACAGTGTCAACTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGAGACAGCTGTGATAAAGCCGTACATCCAGAGAAATGAA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACAGCTGTGATAAAGCCGTACATCCAGAGAAATGAA	660
QY	661	TGTGCGTTAATGTGCTGGGAACATAGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
Db	661	TGTGCGTTAATGTGCTGGGAACATAGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
QY	721	ACCACTGTGCACTACGCTATCTATAATGAGAGATTAATTAATGGCCAAAGCACTGCTTTA	780
Db	721	ACCACTGTGCACTACGCTATCTATAATGAGAGATTAATTAATTAATGGCCAAAGCACTGCTTTA	780
QY	781	TATGATGCTGATATTCGAATCAAAAACAGAGTGGCTTCACACACTGTTACTGGTGA	840
Db	781	TATGATGCTGATATTCGAATCAAAAACAGAGTGGCTTCACACACTGTTACTGGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900

QY	901	CTGATAGATATGGAAGGACTGCTCTCATTTCTGCTGATGTGTTGGATCAGCAAGTATA	960
Db	901	CTGGATATGATATGGAAGGACTGCTCTCATTTCTGCTGATGTGTTGGATCAGCAAGTATA	960
QY	961	GTCACCCCTTCACTTGAGCAAAATATTCATGATCTTCAAGATCTATTCGACAGACG	1020
Db	961	GTCACCCCTTCACTTGAGCAAAATATTCATGATCTTCAAGATCTATTCGACAGACG	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTACTTTTGACTTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTACTTTTGACTTAC	1080
QY	1081	AAAGAAAAACGATGCTAAAAATCTCTCTGAAAAACCAATCCAGAACCAAGACTTAAAG	1140
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTCTGAAAAACCAATCCAGAACCAAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAGAGTCAACAAAGTCTTCAAGCAGTGAATAATAGCCACGAGAGAA	1200
Db	1141	CTGACATCAGAGGAGAGTCAACAAAGTCTTCAAGCAGTGAATAATAGCCACGAGAGAA	1200
QY	1201	ATGTCTCAAGAACGAAAAATAATATAGGATGCTGATAGAGGCTTGAAAGAAATGTAAG	1260
Db	1201	ATGTCTCAAGAACCCGAAATATATATAGATGCTGATAGAGGCTTGAAAGAAATGTAAG	1260
QY	1261	AGCATGGAAGTAATAATGTTGGATTACTAGAAAACTGCATTAATGCTGCTACGCTGGC	1320
Db	1261	AGCATGGAAGTAATAATGTTGGATTACTAGAAAACTGCATTAATGCTGCTACGCTGGC	1320
QY	1321	AATGTTGATTAATGATTAATTTCTTCAAGGAAGCAGACACCTGAAATATCAGCAATTT	1380
Db	1321	AATGTTGATTAATGATTAATTTCTTCAAGGAAGCAGACACCTGAAATATCAGCAATTT	1380
QY	1381	CCTGCAACGGAAGGAAGAGATACAGAAATTTCCGATTATGTTTGACTACAAAGAA	1440
Db	1381	CCTGCAACGGAAGGAAGAGATACAGAAATTTCCGATTATGTTTGACTACAAAGAA	1440
QY	1441	AAACGATGCCAAAATACTCTTCTGAAAAACAGCAACCAGAAACAGACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCAAAATACTCTTCTGAAAAACAGCAACCAGAAACAGACTTAAAGCTGACA	1500
QY	1501	TGAGAGGAAGATCCACAAAGGCTTGAAGGCACTGAAAAATGGCCACGACGACTAGAAAT	1560
Db	1501	TGAGAGGAAGATCCACAAAGGCTTGAAGGCACTGAAAAATGGCCACGACGACTAGAAAT	1560
QY	1561	TTTATGGCTATGGAAGAAATGAAGAAGCAGCACTCATGTCTGGATTTCCAGAAAAC	1620
Db	1561	TTTATGGCTATGGAAGAAATGAAGAAGCAGCACTCATGTCTGGATTTCCAGAAAAC	1620
QY	1621	CTGACTAATGTTGTCACCTGCTGGCAATGCTGATGATTAATTTCTTCCAGGAAGAGC	1680
Db	1621	CTGACTAATGTTGTCACCTGCTGGCAATGCTGATGATTAATTTCTTCCAGGAAGAGC	1680
QY	1681	AAACACCTGGAAGCAGCAATTTCTCTCAACCTGGAATGAAGATATCACAGTACGAA	1740
Db	1681	AAACACCTGGAAGCAGCAATTTCTCTCAACCTGGAATGAAGATATCACAGTACGAA	1740
QY	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACGAACACTGGAATATTACAGATGAG	1800
Db	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACGAACACTGGAATATTACAGATGAG	1800
QY	1801	ATTCTGATTCAATGAAGAAAGCAGATAGCAATGCTGTTGAAAAATGAATTTCTGAGCTTCT	1860
Db	1801	ATTCTGATTCAATGAAGAAAGCAGATAGCAATGCTGTTGAAAAATGAATTTCTGAGCTTCT	1860
QY	1861	CTTAGTGTGAATAAAGAAAAACACATCTTGATGAATAATAGTACGTTGGGGAACAAATTT	1920
Db	1861	CTTAGTGTGAATAAAGAAAAACACATCTTGATGAATAATAGTACGTTGGGGAACAAATTT	1920
QY	1921	GCCATGCTAAGACTGGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAATAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAATAAAAA	1980

QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 13
US-09-605-783A-374
Sequence 374, Application US/09605783A
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,783A
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQUENCE ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-783A-374

Query Match 100.0%; Score 2000; DB 23; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e+271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGATCTC 60
Db 1 ATGGTGGTTAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGATCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAG 120

QY 121 AGCAACTGGGCACTTCTGAGACACAGACAGACTCTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTCTGAGACACAGACAGACTCTCTATGAAGACACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240

QY 241 GGGGCTTCTGAGACACAGACAGACTCTGCTATGAAGACACTCAGAGAACAGATGGCAAG 300
Db 241 GGGGCTTCTGAGACACAGACAGACTCTGCTATGAAGACACTCAGAGAACAGATGGCAAG 300

QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTGG 360
Db 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGCAAGTGGGCGCTGG 360

QY 361 GGAAGACTAGATGACAGTGCCTTCATGAGAGCCAGAGTACCAGTCCGTGGAGAGATCTG 420
Db 361 GGAAGACTAGATGACAGTGCCTTCATGAGAGCCAGAGTACCAGTCCGTGGAGAGATCTG 420

QY 421 GACAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480

Db 421 GACAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGAGCACTGACGTGACCAAGAGACAGCAAGAAAGAGACTGCTACATCTGGCC 540
Db 481 CTCAGGAGCACTGACGTGACCAAGAGACAGCAAGAAAGAGACTGCTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTGAGAGTAGTAAACTCTGCTGGAGACAGAGATCTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTGAGAGTAGTAAACTCTGCTGGAGACAGAGATCTCAACTTAAT 600

QY 601 GTCTTCACACAAACAAAGAGACAGCTCTGATTAAGGCCCTACAAATCCGAGAAAGTAA 660
Db 601 GTCTTCACACAAACAAAGAGACAGCTCTGATTAAGGCCCTACAAATCCGAGAAAGTAA 660

QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGAGTAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGAGTAAT 720

QY 721 ACCACTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA 780

QY 781 TATGTCCTGATATCCGAATCAAAAAACAAGCATGGCCTCACACACTGTTACTGGTGA 840
Db 781 TATGTCCTGATATCCGAATCAAAAAACAAGCATGGCCTCACACACTGTTACTGGTGA 840

QY 841 CATGAGCAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900

QY 901 CTGGATAGATATGGAAGAGACTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGGAAGAGACTGCTCATCTGCTGATGTTGTGGATCAGCAAGTATA 960

QY 961 GTGACCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATGTCAGACAGAG 1020
Db 961 GTGACCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATGTCAGACAGAG 1020

QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080

QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAACAGCTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAACAGCTTAAAG 1140

QY 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGCGCTGAATAATGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGCGCTGAATAATGCCAGCCAGAGAA 1200

QY 1201 ATGCTCTCAAGAACAGAAATTAATTAAGATGATGATAGAGGTTGAAAGAAATGAAG 1260
Db 1201 ATGCTCTCAAGAACAGAAATTAATTAAGATGATGATAGAGGTTGAAAGAAATGAAG 1260

QY 1261 AAGCATGAAGATTAATTAATGTTGGAATTAATGAAAACTGACTAATGTTGCTGCTGGC 1320
Db 1261 AAGCATGAAGATTAATTAATGTTGGAATTAATGAAAACTGACTAATGTTGCTGCTGGC 1320

QY 1321 AATGGTATTAATGATTAATTTCTCAAGAGAGAGCAAGACACTGAAATTCAGCAATTT 1380
Db 1321 AATGGTATTAATGATTAATTTCTCAAGAGAGAGCAAGACACTGAAATTCAGCAATTT 1380

QY 1381 CTTGACAAACGAAGTGAAGATATCACAGAAATTTGCAATTTAGTTTCTGACTCAAAAGAA 1440
Db 1381 CTTGACAAACGAAGTGAAGATATCACAGAAATTTGCAATTTAGTTTCTGACTCAAAAGAA 1440

QY 1441 AAACAGATGCCAAATTAATCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500

QY 1501 TCAAGAGAGAGATCACAAGAGCTTGAAGGCGATGAGAAATTTGCCAGAGAGCTAGAAAT 1560
Db 1501 TCAAGAGAGAGATCACAAGAGCTTGAAGGCGATGAGAAATTTGCCAGAGAGCTAGAAAT 1560

QY	1561	TTTATGGCTATCCAAATAATGAAGAAGCAGCGAAGTACTCATGTGGATTTCCAGAAAC	1620
Db	1561	TTTATGGCTATCCAAATAATGAAGAAGCAGCGAAGTACTCATGTGGATTTCCAGAAAC	1620
QY	1621	CTGACTAATGTGGCCACTGCTGGCAGTGGTGTGATGTGATTAATTCCTCCAAAGAAAGC	1680
Db	1621	CTGACTAATGTGGCCACTGCTGGCAGTGGTGTGATGTGATTAATTCCTCCAAAGAAAGC	1680
QY	1681	AGAACACCTGAAGCCAGCAATTTCTGTGACTGTGAATGAAGATATCACAGTACGAA	1740
Db	1681	AGAACACCTGAAGCCAGCAATTTCTGTGACTGTGAATGAAGATATCACAGTACGAA	1740
QY	1741	CAAAATGATACTCAGAAGCAATTTGTGAAGAACAGAACACTGTGAATTTACAGATGAG	1800
Db	1741	CAAAATGATACTCAGAAGCAATTTGTGAAGAACAGAACACTGTGAATTTACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAGAAAAGCAGATGAAGTGGTTGAAAAATTAATTTCTGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAAGCAGATGAAGTGGTTGAAAAATTAATTTCTGAGCTTCT	1860
QY	1861	CTTAGTGTGTAAGAAAGAAAAGACATCTTGATGAAAATAGTAGCTTGGGGAGAAATT	1920
Db	1861	CTTAGTGTGTAAGAAAGAAAAGACATCTTGATGAAAATAGTAGCTTGGGGAGAAATT	1920
QY	1921	GCCATGCTAAGACTGAGTAGACACAAATGAACAATCAGAGCCAGCTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGTAGACACAAATGAACAATCAGAGCCAGCTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

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RESULT 14
US-09-636-215-374
: Sequence 374, Application US/09636215
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636, 215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-374

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Query Match	100.0%	Score 2000;	DB 24;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 2,6e+211;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0;
Gaps 0;				
1 ATGCTGCTTGAGCTTGATTCATGCCGCGTCGCTTCTGTGTAAGAAGCATTTTGTCTC 60				

D	1	ATGTGGTTGAGTTGATTCATGCGGGCTGCTTCTGTGAAAGAACATTTGGTCTC	60
Q	61	AGAGCAAGATGGGCAAGTGTGTGTCGCCGTTGCTTCCCTGTCTGCAAGGAGACGGCCAAAG	120
D	61	AGAGCAAGATGGGCAAGTGTGTGTCGCCGTTGCTTCCCTGTCTGCAAGGAGACGGCCAAAG	120
Q	121	AGCAAGGTGGGCACTTCTGTGGAACACAGACACTCTGCTATGAAGACACTCAGAAACAGATGGGCAAG	180
D	121	AGCAAGGTGGGCACTTCTGTGGAACACAGACACTCTGCTATGAAGACACTCAGAAACAGATGGGCAAG	180
Q	181	ATGGGCAAGTGTGTCGCCGCTGCTTCCCTGTCTGCAAGGAGGAGTGGCAAGACACTG	240
D	181	ATGGGCAAGTGTGTCGCCGCTGCTTCCCTGTCTGCAAGGAGGAGTGGCAAGACACTG	240
Q	241	GCGGCTTCTGTGAGACACAGACACTCTGCTATGAAGACACTCAGAAACAGATGGGCAAG	300
D	241	GCGGCTTCTGTGAGACACAGACACTCTGCTATGAAGACACTCAGAAACAGATGGGCAAG	300
Q	301	TGCTGCTGCCACTGCTTCCCTGTCTGCAAGGAGGAGCGGCAAGAGATGGGCGCTTGG	360
D	301	TGCTGCTGCCACTGCTTCCCTGTCTGCAAGGAGGAGCGGCAAGAGATGGGCGCTTGG	360
Q	361	GAGAGCTACGATGACAGTGCCTTCATGGAAGCCAGGTATCCAGCTCCGTGGAGAAAGATCTG	420
D	361	GAGAGCTACGATGACAGTGCCTTCATGGAAGCCAGGTATCCAGCTCCGTGGAGAAAGATCTG	420
Q	421	GACAGCTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCCAGAAAGATTCATGCTCATG	480
D	421	GACAGCTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCCAGAAAGATTCATGCTCATG	480
Q	481	CTCAGGAGACACTGACGTGAACAAGAGACACGCAAAAAGAGAGCTCTTACATCTGGCC	540
D	481	CTCAGGAGACACTGACGTGAACAAGAGAGACACGCAAAAAGAGAGCTCTTACATCTGGCC	540
Q	541	TCGTGCCAATGGGAATTCAGAACTACTAAACTCCGTGGACAGAGATTCACACTTAAT	600
D	541	TCGTGCCAATGGGAATTCAGAACTACTAAACTCCGTGGACAGAGATTCACACTTAAT	600
Q	601	GTCCTTGACAAACAAAAGAGACACTCTGATTAAGGCGGTACATATGCCAGAAAGATGAA	660
D	601	GTCCTTGACAAACAAAAGAGAGACACTCTGATTAAGGCGGTACATATGCCAGAAAGATGAA	660
Q	661	TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
D	661	TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
Q	721	ACCACTCTGACCTACGCTATCTATTAATAAATTAATGGCCAAAGAGACTGCTCTTA	780
D	721	ACCACTCTGACCTACGCTATCTATTAATAAATTAATGGCCAAAGAGACTGCTCTTA	780
Q	781	TATGTGTGATGATGCAATCAAAAAACAAGATGGCCCTACACACTGTACTTGGTGTGA	840
D	781	TATGTGTGATGATGCAATCAAAAAACAAGATGGCCCTACACACTGTACTTGGTGTGA	840
Q	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
D	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
Q	901	CTGGATATGATATGGAAGGACTGCTCTACTTGTCTGATATGTTGTGGATCAGCAATATA	960
D	901	CTGGATATGATATGGAAGGACTGCTCTACTTGTCTGATATGTTGTGGATCAGCAATATA	960
Q	961	GTCAGCCTTCTACTTGAGCAAAAATTTATATCTCTCAAGATCTATCTGACAGACAG	1020
D	961	GTCAGCCTTCTACTTGAGCAAAAATTTATATCTCTCAAGATCTATCTGACAGACAG	1020
Q	1021	GCCAGAGAGTATGCTTTCTAGTATCATCATGTAATTTGCCAGATTACTTCTGACTAC	1080
D	1021	GCCAGAGAGTATGCTTTCTAGTATCATCATGTAATTTGCCAGATTACTTCTGACTAC	1080
Q	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAACAGACTTAAAG	1140
D	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAACAGACTTAAAG	1140

Db 1081 AAGAGAGAGATGCTAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
 Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
 QY 1261 AAGATTAAGTAAATTAATTAATTAAGAGTGTATAGAGAGTTGAAGAGTTGAGG 1320
 Db 1261 AAGATTAAGTAAATTAATTAATTAAGAGTGTATAGAGAGTTGAAGAGTTGAGG 1320
 QY 1321 AATGTGATTAATTAATTAATTAATTAAGAGTGTATAGAGAGTTGAAGAGTTGAGG 1380
 Db 1321 AATGTGATTAATTAATTAATTAATTAAGAGTGTATAGAGAGTTGAAGAGTTGAGG 1380
 QY 1381 CTTGACACAGAGAGTGAAGAGTATCAGAGAAATTTGCGAATTAATTAATTAAGAG 1440
 Db 1381 CTTGACACAGAGAGTGAAGAGTATCAGAGAAATTTGCGAATTAATTAATTAAGAG 1440
 QY 1441 AAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1500
 Db 1441 AAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1500
 QY 1501 TCAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1560
 Db 1501 TCAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1560
 QY 1561 TTTTGTGCTATCGAAGAAATGAAGAGCAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1620
 Db 1561 TTTTGTGCTATCGAAGAAATGAAGAGCAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1620
 QY 1621 CTGACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680
 Db 1621 CTGACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680
 QY 1681 AGAAGACCTGAAGAGCAGCAATTTCTGACACTGAGATGAAGTGAAGTGAAGTGAAG 1740
 Db 1681 AGAAGACCTGAAGAGCAGCAATTTCTGACACTGAGATGAAGTGAAGTGAAGTGAAG 1740
 QY 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATTAATTAAG 1800
 Db 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATTAATTAAG 1800
 QY 1801 ATGTGATTAAGTGAAGAGCAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
 Db 1801 ATGTGATTAAGTGAAGAGCAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
 QY 1861 CTTAGTGAAGAGAGAGAGAGATCTTGCATGAATTAATTAAGTGAAGTGAAGTGAAG 1920
 Db 1861 CTTAGTGAAGAGAGAGAGAGATCTTGCATGAATTAATTAAGTGAAGTGAAGTGAAG 1920
 QY 1921 GCCATGCTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1980
 Db 1921 GCCATGCTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 15

US-09-651-236-374
 ; Sequence 374, Application US/09651236
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jlangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jlang, Yugu
 ; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.42718C18
 ; CURRENT APPLICATION NUMBER: US/09/651,236
 ; NUMBER OF SEQ. ID NOS: 865
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 374
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-651-236-374

Query Match 100.0%; Score 2000; DB 25; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 2,6e-271;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 60
 Db 1 ATGTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 60
 QY 61 AGGAGCAAGAGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 61 AGGAGCAAGAGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 121 AGCAAGTGGGCACTTCTGAGACACAGACAGTCTGCTATGAAGACACTCAGAGCAAG 180
 Db 121 AGCAAGTGGGCACTTCTGAGACACAGACAGTCTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 ATGGGCAAGTGGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 GGGCTTCTGAGAGCCAGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 241 GGGCTTCTGAGAGCCAGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Db 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 361 GGAAGCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
 Db 361 GGAAGCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
 QY 421 GACAAGCTCCACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Db 421 GACAAGCTCCACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 481 CTCAGGACACTGACGTGAACAG 540
 Db 481 CTCAGGACACTGACGTGAACAG 540
 QY 541 TCTGCTCAATGGGAATTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600
 Db 541 TCTGCTCAATGGGAATTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600
 QY 601 GTCCCTTGACAAAG 660
 Db 601 GTCCCTTGACAAAG 660
 QY 661 TGTGCTTAATGTTGCTGGAACATGGCATGATCAATTAATTCAGATGAATGAAGTGAAGTGA 720

|||||
Db 661 TGTGGTTAATGTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGAAT 720
Qy 721 ACCACTCTGCTAGCTATCTATATATGAAGTAAATTAATGGCCAAAGCACTGCTTAA 780
|||||
Db 721 ACCACTCTGCTAGCTATCTATATATGAAGTAAATTAATGGCCAAAGCACTGCTTAA 780
Qy 781 TATGGTGTGATATGGAATCAAAAAACAAGCATGGCTCACACCACTGTACTGGTGA 840
|||||
Db 781 TATGGTGTGATATGGAATCAAAAAACAAGCATGGCTCACACCACTGTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCACTGCTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGA 900
841 CATGAGCAAAAAACAGCACTGCTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCACTGCTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGA 900
Qy 901 CTGGATAGTATGGAAGGACTGCTCATATCTGTATGTTGTGATCAGCAAGTATA 960
|||||
Db 901 CTGGATAGTATGGAAGGACTGCTCATATCTGTATGTTGTGATCAGCAAGTATA 960
Qy 961 GTACAGCTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGAG 1020
|||||
Db 961 GTACAGCTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATCTGTTTCTAGTCATCATGTATTTGGCCAGTTACTTTCTGACTAC 1080
|||||
Db 1021 GCCAGAGATATCTGTTTCTAGTCATCATGTATTTGGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAGAAAAACATGCTAAAAATCTCTTGAAACAGCAATCCAGACACAGACTTAAAG 1140
|||||
Db 1081 AAGAGAAAAACATGCTAAAAATCTCTTGAAACAGCAATCCAGACACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCGAGTGAATATGCCAGCAGAGAA 1200
|||||
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCGAGTGAATATGCCAGCAGAGAA 1200
Qy 1201 ATGTCTCAAGAAACGAGAAATTAATAGATGGTATGAGAGGTTGGAAGAAATGAAG 1260
|||||
Db 1201 ATGTCTCAAGAAACGAGAAATTAATAGATGGTATGAGAGGTTGGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTATATATGTGGATTACTAGAAACCTGACTATATGGTCTGCTGCGC 1320
|||||
Db 1261 AAGCATGAAAGTATATATGTGGATTACTAGAAACCTGACTATATGGTCTGCTGCGC 1320
Qy 1321 AATGGTATATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATACGCAATTT 1380
|||||
Db 1321 AATGGTATATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATACGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTTAGTTCTGACTACAAAGA 1440
|||||
Db 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTTAGTTCTGACTACAAAGA 1440
Qy 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
|||||
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGATTCACAAAGGCTTGAGGCGAGTGAATGGCCAGCAGAGCTAGAAAT 1560
|||||
Db 1501 TCAGAGGAAGATTCACAAAGGCTTGAGGCGAGTGAATGGCCAGCAGAGCTAGAAAT 1560
Qy 1561 TTTATGGCTATGCAAGAAATGAAGACAGCAAGTACTCATGTGCGATTTCCAGAAAAAC 1620
|||||
Db 1561 TTTATGGCTATGCAAGAAATGAAGACAGCAAGTACTCATGTGCGATTTCCAGAAAAAC 1620
Qy 1621 CTGACTAATGTGGCCACTGCTGCAATGGTATGATGATTAATTCCTCAAGGAAGAGC 1680
|||||
Db 1621 CTGACTAATGTGGCCACTGCTGCAATGGTATGATGATTAATTCCTCAAGGAAGAGC 1680
Qy 1681 AGAACAACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGAGTATCAGAGTGAGAA 1740
|||||
Db 1681 AGAACAACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGAGTATCAGAGTGAGAA 1740
Qy 1741 CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
|||||

Db 1741 CAAAATGATACTCAGAAAGCAATTTTGTGAAGAAACAGAACACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAAAGCATAGAAAGTGTGAAAAAATGAATCTGAGCTTTCT 1860
|||||
Db 1801 ATTCTGATTCATGAGAAAAAGCATAGAAAGTGTGAAAAAATGAATCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAGAAAAAGCAATCTTGATGAAATATGATGCTTGGGGAAAGAAAT 1920
|||||
Db 1861 CTTAGTTGTAGAAAAAGCAATCTTGATGAAATATGATGCTTGGGGAAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACATGAACATCAGAGCCAGCTAAAAA 1980
|||||
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAACATGAACATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
|||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

Search completed: November 8, 2002, 08:45:42
Job time : 3948.08 secs

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? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Laureen
? APPLICANT: Deforge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Geriltsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Tumanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3330R1C139
? CURRENT APPLICATION NUMBER: US/10/131, 813A
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 21
? LENGTH: 1041
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-131-813A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

? 378 TGCTTCATGAGACCCAGGACGTCGCTGGAGAAGATCTGGACAAGCTCCACAGAGC 437
? 300 TGCTTCGACATTTCCCAATACCCCAATTAAACCGTATCATCTGAAGAGATCCACAGAGC 359
? 438 TGCTGGTGGGTAAGTCCCAAGAAAGTATCATGCTGATGCTGAGGACGTCGCT 437
? 360 TGCTTCATGATGTAATCTAGAGAAAGTAA--GTACCTTCTGCTCCAGTATTAAGAGC 416
? 498 GAACAAGAGAGACAGAAAAGAGAGACTGCTCTACATCTGCGCTTGCATGGGAATTC 557
? 417 CATTAAGAGAGACAGAAAGAGAGACCGCCCTACATTTGGCTGCGCCACCTGCGCAC 476
? 558 AGAAGTAGTAAACTCTGCTGAGACAGAGATCTCAACTTAATGCTCTTGACAAACAAA 617
? 477 GGAAGTAGTACATCTCTGCTGTCAGAAAGATGTGAGCTTAACCTCTGCGACCGTGA 536
? 618 GAGAGAGCTCTGATTAAGCGCTTACATCCCAAGAAAGATGATGCGCTTATGTTGCT 677
? 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGGACGAGGCTTGTCACACTCTTCTGCT 596
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? 678 GGAACATGGACATGATCCAAATATTCCAGATGATGAAATACCACTGTGACACTAGC 737
? 597 GCAAAATGGCCCCAATCCAAATATTAGGATTTCTTGGAAAGACCTGCTGCACTAGC 656
? 738 TATCTATTAAGATGAATTAATTAATGCGCAAGACACTGCTTTATATGCTGATATGA 797
? 657 TGCTATTAATGAAGATACATCATGATAGAAAACCTTCTTACATGATGTAATATATGA 716
? 798 ATCAAAAACAG 810
? 717 AGAATGACAGAG 729

RESULT 3
US-10-131-819A-21
? Sequence 21, Application US/10131819A
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Laureen
? APPLICANT: Deforge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Geriltsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Tumanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3330R1C134
? CURRENT APPLICATION NUMBER: US/10/131, 819A
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 21
? LENGTH: 1041
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-131-819A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

? 378 TGCTTCATGAGACCCAGGACGTCGCTGGAGAAGATCTGGACAAGCTCCACAGAGC 437
```

```
Db 300 TGGCTTCGCAATTTCCCAATACCCCATTAACCGTATCATCTGAGAGAGATCCACAGAGC 359
Qy 438 TGCCCTGGGGGTAAAGTCCCAAGAGATCTCATGCTCATGCTCAGGAGACAGAGT 497
Db 360 TGTCTTACATGTAATCTAGAGAAACTGAA--GTACCTTCTGCTCAGCTATATGAGAGC 416
Qy 498 GAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
Db 417 CAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
Qy 558 AGAGTAGTAAATCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
Db 477 GGAATGAGTACATCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
Qy 618 GAGGACAGCTCTGATTAAGGCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
Db 537 GAGGACAGCTCTGATTAAGGCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
Qy 678 GGAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 737
Db 597 GGAATGAGTACATCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
Qy 738 TATCTATATGAAGATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797
Db 657 TGTGTATATGAAGATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716
Qy 798 ATCAAAAAACAAG 810
Db 717 AGAATGAGAGAGAG 729
```

RESULT 4

US-10-131-823A-21

Sequence 21, Application US/10131823A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zhen

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C143

CURRENT APPLICATION NUMBER: US/10/131,823A

PRIOR APPLICATION NUMBER: 2002-04-24

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/045911

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-823A-21
Query Match
Best Local Similarity 8.5%; Score 170.6; DB 6; Length 1041;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
Qy 378 TGCCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
Db 300 TGGCTTCGCAATTTCCCAATACCCCATTAACCGTATCATCTGAGAGAGATCCACAGAGC 359
Qy 438 TGCCCTGGGGGTAAAGTCCCAAGAGATCTCATGCTCATGCTCAGGAGACAGAGT 497
Db 360 TGTCTTACATGTAATCTAGAGAACTGAA--GTACCTTCTGCTCAGCTATATGAGAGC 416
Qy 498 GAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
Db 417 CAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
Qy 558 AGAGTAGTAAATCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
Db 477 GGAATGAGTACATCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
Qy 618 GAGGACAGCTCTGATTAAGGCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
Db 537 GAGGACAGCTCTGATTAAGGCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
Qy 678 GGAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 737
Db 597 GGAATGAGTACATCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656
Qy 738 TATCTATATGAAGATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797
Db 657 TGTGTATATGAAGATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716
Qy 798 ATCAAAAAACAAG 810
Db 717 AGAATGAGAGAGAG 729
```

RESULT 5

US-10-131-824A-21

Sequence 21, Application US/10131824A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zhen

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C143

CURRENT APPLICATION NUMBER: US/10/131,824A

PRIOR APPLICATION NUMBER: 2002-04-24

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/045911

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C126
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-21

Query Match 8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 378 TGCCTTCATGAGCCAGGACGACGTCCTGCGAAGATCTGGACAGAGCTCCACAGAGC 437
DB 300 TGGCTTCGATGATTCCTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCACAGAGC 359
QY 438 TGCCTGCTGGGTAAGTCCCGCAGAAAGATTCATGCTGTCAGGAGACACTGAGCT 497
DB 360 TGTCTTACATGCTATATAGAGAACTGAA---GTACCTTCTGCTCAGTATTTATGACGC 416
QY 498 GAACAAGAGACAGCAAGCAAAAGAGACTGCTCTACATCTGCGCTTCCCAATGGGAATTC 557
DB 417 CAATTAAGAGAGAGAGAAAGAGACCGCCCTACATTTGGCGTGGCCACTGGCCAGC 476
QY 558 AGAAGTAGTAAACTCTGCTGAGACAGATGTCACACTTAATGTCTCTTGACACAAAAAA 617
DB 477 GGAATGTGTACATCTCTGCTGTCTCCAGAAAGATGTGAGCTTAACCTTGCAGACCGTGAAG 536
QY 618 GAGACAGCTCTGATTAAGCCCGCTACCAATGCGAGAGATGAATGTGCTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGGAGAGAGGCTTGTCAACTCTTCTGCT 596
QY 678 GGAACATGAGCATGATCAAAATATTCAGATGATGAAATACCACTCTGCACTAGCG 737
DB 597 GCAAAATGGCGCAATCAAAATATTAAGGATTTCTTTGGAAGAGACGCTCTGCACTAGCG 656
QY 738 TATCTATAATGAAGATTAATTAATGCGCAAGACACTGCTTATATGTGCTGATATGCA 797
DB 657 TGTGTATAATGAAGATATCATTCATGATGAAAAACTTCTTCACTAGTGTCAATATATGA 716
QY 798 ATCAAAAAACAAG 810
DB 717 AGAATGCAAGCAAG 729

RESULT 6
US-10-131-826A-21
Sequence 21, Application US/10131826A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-21

Query Match 8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 378 TGCCTTCATGAGCCAGGACGACGTCCTGCGAAGATCTGGACAGAGCTCCACAGAGC 437
DB 300 TGGCTTCGATGATTCCTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCACAGAGC 359
QY 438 TGCCTGCTGGGTAAGTCCCGCAGAAAGATTCATGCTGTCAGGAGACACTGAGCT 497
DB 417 CAATTAAGAGAGAGAGAAAGAGACCGCCCTACATTTGGCGTGGCCACTGGCCAGC 476
QY 498 GAACAAGAGACAGCAAGCAAAAGAGACTGCTCTACATCTGCGCTTCCCAATGGGAATTC 557
DB 417 CAATTAAGAGAGAGAGAAAGAGACCGCCCTACATTTGGCGTGGCCACTGGCCAGC 476
QY 558 AGAAGTAGTAAACTCTGCTGAGACAGATGTCACACTTAATGTCTCTTGACACAAAAAA 617
DB 477 GGAATGTGTACATCTCTGCTGTCTCCAGAAAGATGTGAGCTTAACCTTGCAGACCGTGAAG 536
QY 618 GAGACAGCTCTGATTAAGCCCGCTACCAATGCGAGAGATGAATGTGCTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGGAGAGAGGCTTGTCAACTCTTCTGCT 596

QY	678	GGAACATGAGCAGCTCATCAATATTCAGATGAGTAAGAAATACCACTGTGCATCGC	727
Db	597	GCAAAAAGGGCCATCCAAATATTACGATTTCTTTTGGAAGGCTGTGCATCAAGC	656
QY	738	TATCTATATGATGAATATAATTATGGCCAAGCACCTCTTATATGGTGCTGATATGA	797
Db	657	TGTTATTAATGAMGATCATTCATCATGATGAAAACTTCTTTCACATGGTACAAATATTGA	716
QY	798	ATCAAAAAACAAG	810
Db	717	AGAATGCAGCAG	729

RESULT 7
US-10-131-829A-21
; Sequence 21, Application US/10131829A
; GENERAL INFORMATION.

1 GENERAL INFORMATION:
 2 APPLICANT: Baker, Kevin P.
 3 APPLICANT: Beresini, Maureen
 4 APPLICANT: DeForge, Laura
 5 APPLICANT: Desnoyers, Luc
 6 APPLICANT: Filvaroff, Ellen
 7 APPLICANT: Gao, Wei-Qiang
 8 APPLICANT: Gerlitsen, Mary E.
 9 APPLICANT: Goddard, Audrey
 10 APPLICANT: Godowski, Paul J.
 11 APPLICANT: Gurney, Austin L.
 12 APPLICANT: Sherwood, Steven
 13 APPLICANT: Smith, Victoria
 14 APPLICANT: Stewart, Timothy A.
 15 APPLICANT: Tumas, Daniel
 16 APPLICANT: Watanabe, Colin K
 17 APPLICANT: Wood, William
 18 APPLICANT: Zhang, Zemin
 19 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 20 ACIDS ENCODING THE SAME
 21 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 22 FILE REFERENCE: P9330R1C138
 23 CURRENT APPLICATION NUMBER: US/10/131,829A

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CURRENT FILING DATE: 2002-04-27
PRIORITY APPLICATION NUMBER: 60/049911
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059194
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remainder prior application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-829A-21

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Query Match 8.5%; Score 170.6; DB 6; Length 1041;
 Best Local Similarity 63.7%; Pred. No. 9e-32;
 Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

378 TGCCCTCATGAGCCACGACGTCGCGTGGAGAAAGATCTGCGACAGCTCCAGAGC 437
 || |||| ||| ||||| | | ||||| | | ||||| |||||

Db 300 TGCGTTGGCATTTCGCCCAATTAACCCATTAAACGCTATCATCTGAAGAGATCCACAGAG 359

QY 438 TGCCTGGTGGGTAAAGTCTCCCGACAAAGATCTCATCTGTCATGCTCAGGAGACGTACGT 497

Db 360 TGTCTTACATGTTAAATCTAGAGAACTGAA---GTACCTCTGCTCGTACGTAATTATGACG 416

QY 498 GAAACAAGAGACACAGCAAGCAAAAAGAGACTGCTCTACATCTGGCCCTTGCCATGTGGAAATTC 557

Db 417 CAATAAGAGAGACAGGAAGGAAGGACCGCCCTACATTTGGCCTGTGGCCACTGGCAACC 476

QY 558 AGAAGTAGTAAACTCCTGCTGGACAGACATGTCAACTTAATGTCTTACACAACAAAA 617

Db 477 GGAATATGTAATCTCCCTGGGTGTCCAAAGAAATGTGACCTTGACCTGGCAGCGTGAAG 536

QY 618 GAGACACGCTCTGTATAAAGGCCGTACAAATGCCAGGAATGTAATGTGCCTTAATGTTCG 677

Db 537 CAGAGACACGCTCTGTATCAAGGCTGTACAACTGAGGACAGAGGCTTGTCACACTTCTGCT 596

QY 678 GGAACATAGGCACGTAGTCAAAATATTCCAGATAGTATGAGAAATACCACTGTGCATACG 727

Db 597 GCAAAATGGGCCCAATCCAAATATTACGAGATTCTTTGGAAGGCTGTCTTGCACTPACG 656

QY 738 TATCTATATGAAGATTAATTAATTAAGGCCAAGACACTGCTCTTAATATGGTCTGATACGA 797

Db 657 TGTGTATATATGAAGATTCATTCATGATAGAAAAAATCTTTTCACATGGTACAAATATTGA 716

QY 798 ATCAAAAAACAG 810

Db 717 AGAATGCAGCAG 729

RESULT 8
US-10-125-926A-21
: Sequence 21, Application US/10125926A

```

1 GENERAL INFORMATION:
2 APPLICANT: Baker, Kevin P.
3 APPLICANT: Beresini, Maureen
4 APPLICANT: DeForge, Laura
5 APPLICANT: Desnoyers, Luc
6 APPLICANT: Filvaroff, Ellen
7 APPLICANT: Gao, Wei-Qiang
8 APPLICANT: Gerritsen, Mary E.
9 APPLICANT: Goddard, Audrey
10 APPLICANT: Godowski, Paul J.
11 APPLICANT: Gurney, Austin L.
12 APPLICANT: Sherwood, Steven
13 APPLICANT: Smith, Victoria
14 APPLICANT: Stewart, Timothy A.
15 APPLICANT: Tumas, Daniel
16 APPLICANT: Watanabe, Colin K
17 APPLICANT: Wood, William
18 APPLICANT: Zhang, Zemin
19 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
20 ACIDS ENCODING THE SAME
21 FILE REFERENCE: P3330R1C80
22 CURRENT APPLICATION NUMBER: US/10/125,926A
23 CURRENT FILING DATE: 2002-10-15
24 PRIOR APPLICATION NUMBER: 60/049911
25 PRIOR FILING DATE: 1997-06-18
26 PRIOR APPLICATION NUMBER: 60/056974
27 PRIOR FILING DATE: 1997-08-26
28 PRIOR APPLICATION NUMBER: 60/059113
29 PRIOR FILING DATE: 1997-09-17
30 PRIOR APPLICATION NUMBER: 60/059115
31 PRIOR FILING DATE: 1997-09-17
32 PRIOR APPLICATION NUMBER: 60/059117
33 PRIOR FILING DATE: 1997-09-17
34 PRIOR APPLICATION NUMBER: 60/059122
35 PRIOR FILING DATE: 1997-09-17
36 PRIOR APPLICATION NUMBER: 60/059184
37 PRIOR FILING DATE: 1997-09-17
38 PRIOR APPLICATION NUMBER: 60/059263
39 PRIOR FILING DATE: 1997-09-18

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; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-926a-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTATGAGCCCGGACGATCCGCTGAGAGATCTGGACAAAGCTCCACAGC 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 TGGCTTCGCATTTCCCAATACCCGATTAACCGTATCATCTGAAGAGATCCACAGC 359
QY 438 TGCCTGGTGGGTAAGTCCCGCAGAAAGATCTCATGCTGCTCAGGACACTGACGT 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTCTTACATGTAATCTAGAGAACTGAA--GTACTTCTGCTCAGATTTATGACGC 416
QY 498 GAACAGAGAGACAAGCAAAAGAGACTGCTTACATCTGCGCTTCCCAATGGAAATTC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 CAATTAAGAGAGACAGAAAGAGACCGCCCTACATTTGGCGTGCCTGCGCAAC 476
QY 558 AGAAGTAACTCTGCTGACACAGATGCAACTTAATCTCTTGACACAACAAA 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GGAATGTACATCTCTGCTGTCACAGAAAGATGAGCTTAACCTTGAACCGCTGAGA 536
QY 618 GAGGACAGCTCTGTATAAGCCGCTACATGCAAGATGATGATGCTTAATGTTGCT 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGGACAGAGGCTTGTCACTCTTCTGCT 596
QY 678 GGAACATGCACTGATCCAAATATTCAGATGATGAAATACCACTGTGACACTGACG 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 GCAAAATGGCGCCCAATCAATATTTACGATTTCTTGAAGAGACTCTCTGCACTACGC 656
QY 738 TATCTATAATGAAGATTAATTAATGCCCCAAGCCTGCTTATATGCTGTATATGCA 797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 TGTGTATAATGAAGATCATCATCATGATAGAAAACTTCTTCACTGATCAATATATGA 716
QY 798 ATCAAAAACAG 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 AGAATGCAGCAG 729

RESULT 9
US-10-127-829a-21
; Sequence 21, Application US/10127829a
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Mei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowskl, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
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; CURRENT APPLICATION NUMBER: US/10/127,829a
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829a-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTATGAGCCCGGACGATCCGCTGAGAGATCTGGACAAAGCTCCACAGC 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 TGGCTTCGCATTTCCCAATACCCGATTAACCGTATCATCTGAAGAGATCCACAGC 359
QY 438 TGCCTGGTGGGTAAGTCCCGCAGAAAGATCTCATGCTGCTCAGGACACTGACGT 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTCTTACATGTAATCTAGAGAACTGAA--GTACTTCTGCTCAGATTTATGACGC 416
QY 498 GAACAGAGAGACAAGCAAAAGAGACTGCTTACATCTGCGCTTCCCAATGGAAATTC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 CAATTAAGAGAGACAGAAAGAGACCGCCCTACATTTGGCGTGCCTGCGCAAC 476
QY 558 AGAAGTAACTCTGCTGACACAGATGCAACTTAATCTCTTGACACAACAAA 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GGAATGTACATCTCTGCTGTCACAGAAAGATGAGCTTAACCTTGAACCGCTGAGA 536
QY 618 GAGGACAGCTCTGTATAAGCCGCTACATGCAAGATGATGATGCTTAATGTTGCT 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGGACAGAGGCTTGTCACTCTTCTGCT 596
QY 678 GGAACATGCACTGATCCAAATATTCAGATGATGAAATACCACTGTGACACTGACG 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 GCAAAATGGCGCCCAATCAATATTTACGATTTCTTGAAGAGACTCTCTGCACTACGC 656
QY 738 TATCTATAATGAAGATTAATTAATGCCCCAAGCCTGCTTATATGCTGTATATGCA 797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 TGTGTATAATGAAGATCATCATCATGATAGAAAACTTCTTCACTGATCAATATATGA 716
QY 798 ATCAAAAACAG 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 AGAATGCAGCAG 729

RESULT 10
US-10-127-831a-21
; Sequence 21, Application US/10127831a
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C107
CURRENT APPLICATION NUMBER: US/10/127,831A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-831A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
Db 597 GCAAAATGGCGCCAAATCCAAATATATACGATTTCTTGGAGAGACTGCTGCACATACG 656
Qy 738 TATCTATATGAAGATTAATATGCGCAAGACAGCTGCTTATATGCGTGATTCGA 797
Db 657 TGTGTATATGAAGATACATCATGATAGAAAACCTTCTTCACATGATCAAAATTTGA 716
Qy 798 ATCAAAAACAG 810
Db 717 AGATGCAGCAAG 729

RESULT 11
US-10-127-835A-21
; Sequence 21, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C102
CURRENT APPLICATION NUMBER: US/10/127,835A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-835A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
QY 438 TGCCTGGTGGGTAAGTCCCGAGAAAGATCTCATGCTCAGGGACACTGACGT 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTCTTACATGTATCTCTAGAGAAACTGAA---GTACCTTCTGCTACGATATATGACGC 416
QY 498 GAACAAGAGACAGCAAGAAAGAGACTGCTCTACATCTGGCCCTTCCCATGGGAATTC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 CAATTAAGAGACAGCAAGAAAGAGACCGCTACATTTGGCCCTGCTGACCTGGCCAAAC 476
QY 558 AGAAGTAGTAAACTCTGCTGGACAGACATGTCACATTAATGCTTGCACAACAAAA 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GGAATGTGATCATCTCTGCTGCTGACAGAAATGTGACCTTACCTTGCACCGCTGAAGA 536
QY 618 GAGACAGCTCTGTATTAAGGCGCCGTACATGCCAGGAAGATGATGCTTAAATGTTGCT 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 CAGGACACCTCTGTATCAAGGCTGTACAACTGAGGACAGAGGCTGTGCAACTCTTCTGCT 596
QY 678 GGAACATGACGACATGCCAATATTCAGATGAGTATGGAATACCACTGCTGCACTACGC 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 GCAAAATGGCGCCCAATCCAAATATTTACGATTTCTTTGGAAGGACCTCTGCACTACGC 656
QY 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTCTTATATGCTGATATCGA 797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 TGTGTATATGAAGATATCATCATCATGATAGAAAACTCTTTCACATGTGTACAAATATTTGA 716
QY 798 ATCAAAAAACAG 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 AGAATGCAGCAAG 729
```

```
RESULT 12
US-10-127-837A-21
; Sequence 21, Application US/10127837A
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C96
; CURRENT APPLICATION NUMBER: US/10/127, 837A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
```

```
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-127-837A-21
```

```
Query Match 8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
QY 378 TGCCTCATGAGAGCCAGTACACAGCTCCGTCGAGAAATCTGCAAGCTCCACAGAGC 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 TGCCTTGCATTTCCCAATACCCCATTTAAACGCTATCATCTGAAAGAGATCCACAGAGC 359
QY 438 TGCCTGGTGGGTAAGTCCCGAGAAAGATCTCATGCTCATGCTCAGGGACACTGACGT 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTCTTACATGTATCTAGAGAAACTGAA---GTACCTTCTGCTACGATATATGACGC 416
QY 498 GAACAAGAGACAGCAAGAAAGAGACTGCTCTACATCTGGCCCTTCCCATGGGAATTC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 CAATTAAGAGACAGCAAGAAAGAGACCGCTACATTTGGCCCTGCTGCACTGGCCAAAC 476
QY 558 AGAAGTAGTAAACTCTGCTGGACAGACATGTCACATTAATGCTTGCACAACAAAA 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GGAATGTGATCATCTCTGCTGCTGACAGAAATGTGACCTTACCTTGCACCGCTGAAGA 536
QY 618 GAGACAGCTCTGTATTAAGGCGCCGTACATGCCAGGAAGATGATGCTTAAATGTTGCT 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 CAGGACACCTCTGTATCAAGGCTGTACAACTGAGGACAGAGGCTGTGCAACTCTTCTGCT 596
QY 678 GGAACATGACGACATGCCAATATTCAGATGAGTATGGAATACCACTGCTGCACTACGC 737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 GCAAAATGGCGCCCAATCCAAATATTTACGATTTCTTTGGAAGGACCTCTGCACTACGC 656
QY 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTCTTATATGCTGATATCGA 797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 TGTGTATATGAAGATATCATCATCATGATAGAAAACTCTTTCACATGTGTACAAATATTTGA 716
QY 798 ATCAAAAAACAG 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 AGAATGCAGCAAG 729
```

```
RESULT 13
US-10-127-842A-21
; Sequence 21, Application US/10127842A
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C100
; CURRENT APPLICATION NUMBER: US/10/127, 842A
```

```

: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-842A-21

```

```

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```

```

QY 378 TCCCTTCATGAGCCAGGTACCGTCCGTGAGAGATCTGAGACAGCTCCACAGAGC 437
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTCGATTTCCCAATACCCATTAACCGTATCTGAAGAGATCCACAGAGC 359
QY 438 TCCCTGCTGGTAAAGTCCCAAGAGATCTCATCGTCACTGAGGAGACATGAGCT 497
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGCTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGTATTAATGACGC 416
QY 498 GAACAAGAGAGCAAGCAAAAGAGAGAGCTGCTACATCTGCGCTCCCAATGGAAATTC 557
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
+DB 417 CAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 476
QY 558 AGAAGTAGTAATCTCTGCTGAGACAGATGCTCACTTAATGTCCTTGACACAAAAA 617
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATGTGACATCTCTGCTGCTCCAGAGAGATGAGCTTAACCTCTGCGACCGTGAAGA 536
QY 618 GAGGACAGCTGTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 677
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACAGCTGTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 596
QY 678 GGAACATGAGCACTGATCAATATTTCCAGATAGTATGGAATACACACTGACATGAC 737
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 597 GCAATATGGCGGCAATCCAAATATTATAGGATTTCTTGAAGAGAGAGAGAGAGAGAGC 656
QY 738 TATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTATATGTCGATATGCA 797
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 657 TGTGATATATGAGATACATCATGATAGAAAAAATCTTCTTCAATGATGCAATATTTGA 716
QY 798 ATCAAAAAAACAAG 810
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 717 AGAATGACGCAAG 729

```

```

RESULT 14
US-10-127-850A-21
: Sequence 21, Application US/10127850A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura

```

```

: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C110
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-850A-21

```

```

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```

```

QY 378 TCCCTTCATGAGCCAGGTACCGTCCGTGAGAGATCTGAGACAGCTCCACAGAGC 437
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTCGATTTCCCAATACCCATTAACCGTATCTGAAGAGATCCACAGAGC 359
QY 438 TCCCTGCTGGTAAAGTCCCAAGAGATCTCATCGTCACTGAGGAGACATGAGCT 497
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGCTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGTATTAATGACGC 416
QY 498 GAACAAGAGAGCAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 557
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 CAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 476
QY 558 AGAAGTAGTAATCTCTGCTGAGACAGATGCTCACTTAATGTCCTTGACACAAAAA 617
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATGTGACATCTCTGCTGCTCCAGAGAGATGAGCTTAACCTCTGCGACCGTGAAGA 536
QY 618 GAGGACAGCTGTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 677
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACAGCTGTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 596
QY 678 GGAACATGAGCACTGATCAATATTTCCAGATAGTATGGAATACACACTGACATGAC 737
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

